

GenCore version 4.5  
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OM nucleic - nucleic search, using sw\_model

Run on: May 29, 2002, 20:42:01 ; Search time 6499.83 Seconds  
(without alignments)  
2520.909 Million cell updates/sec

Title: US-08-982-272-3  
Perfect score: 783  
Sequence: 1 ATGATCGAATACATCAACCA.....TTGGCTTACTCAAACTCTCA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 3595312  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	751	95.9	818	6	AR044778	Sequence
2	751	95.9	818	6	AR171646	Sequence
3	751	95.9	1250	6	AX208160	Sequence
4	749.4	95.7	783	6	AR076918	Sequence
5	749.4	95.7	783	6	AR078308	Sequence
6	749.4	95.7	783	6	AR085411	Sequence
7	749.4	95.7	783	6	AR103367	Sequence
8	749.4	95.7	783	6	AR169224	Sequence
9	749.4	95.7	783	6	187865	Sequence 5
10	749.4	95.7	1250	10	MMCD40	X65453 M.musculus
11	688.6	87.9	783	10	AF013985	Rattus no
12	685.4	87.5	783	10	AF116582	Rattus no
13	631.4	80.6	878	6	AR076933	Sequence
14	631.4	80.6	878	6	AR078323	Sequence
15	631.4	80.6	878	6	AR085426	Sequence
16	631.4	80.6	878	6	AR103382	Sequence
17	631.4	80.6	878	6	AR169239	Sequence
18	592.4	75.7	786	6	187864	Sequence 3
19	592.4	75.7	840	6	AR044779	Sequence
20	592.4	75.7	840	6	AR076926	Sequence
21	592.4	75.7	840	6	AR078316	Sequence
22	592.4	75.7	840	6	AR085419	Sequence
23	592.4	75.7	840	6	AR103375	Sequence
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25	592.4	75.7	840	6	AR169232	Sequence
26	592.4	75.7	840	6	AR171647	Sequence
27	592.4	75.7	840	6	123893	Sequence 1
28	592.4	75.7	840	6	127345	Sequence 7
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39	573.2	73.2	975	9	AF344844	AF344844 Callithri
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41	536.6	68.5	788	4	AF079105	AF079105 Felis cat
42	528.6	67.5	788	4	AF086711	AF086711 Canis fam
43	467.6	59.7	904	9	AF344853	AF344853 Macaca ne
44	446.2	57.0	1425	6	AR076929	Sequence
45	446.2	57.0	1425	6	AR078319	Sequence

ALIGNMENTS

RESULT	1	AR044778	Sequence 1 from patent US 5817516.	818 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR044778	Sequence 1 from patent US 5817516.					
DEFINITION	AR044778	Sequence 1 from patent US 5817516.					
ACCESSION	AR044778.1	GI:5966243					
VERSION	Unknown.						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 818)						
AUTHORS	Kehry, M. and Castle, B.						
TITLE	Methods for proliferating and differentiating B cells with high density membrane CD40 ligand						
JOURNAL	Patent: US 5817516-A 1 06-OCT-1998;						
FEATURES	Location/Qualifiers						
source	1. .818						
BASE COUNT	249 a	170 c	186 g	213 t			
ORIGIN							
Query Match							95.9%; Score 751; DB 6; Length 818;

[illegible]

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 818)  
Kehry M. and Castle B.  
B cell culture system comprising high density membrane bound CD40

[illegible]



DEFINITION Sequence 1 from Patent WO0156602.  
ACCESSION AX208160  
VERSION AX208160.1 GI:15422583  
KEYWORDS Mus sp.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Tripp, R.A., Anderson, L.J., and Brown, M.P.  
TITLE Cd40 ligand adjuvant for respiratory syncytial virus  
JOURNAL Patent: WO 0156602-A 1 09-AUG-2001;  
The Secretary, Department of Health and Human Services (US)  
FEATURES Location/Qualifiers  
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          /db\_xref="taxon:10095"  
BASE COUNT 379 a 273 c 285 g 313 t  
ORIGIN

Query Match 95.9%; Score 751; DB 6; Length 1250;  
Best Local Similarity 97.4%; Pred. No. 8.9e-185;  
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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DB 133 CTTTTCCTGCTGATCTTCTAGAGATTTGATAAGTTCGAAGAGGAGTAACCTTCAT 192  
QY 181 GAAGATTTTCTATCATAAAAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCC 240  
DB 193 GAAGATTTTCTATCATAAAAGCTTAAGAGATGCAACAAAGAGAGATCTTTATCC 252  
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DB 253 TTGCTGAACCTGAGGAGTGAAGGCAATTTGAAGACCTTGTCAAGGATATAACCTTA 312  
QY 301 AACAAAGAGAGAAAAGAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAA 360  
DB 313 AACAAAGAGAGAAAAGAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAA 372  
QY 361 ATTGCAGCACAGTGTGAAGCGAAGCAACAGTAATGCAGCATCCGTTCTACAGTGGGCC 420  
DB 373 ATTGCAGCACAGTGTGAAGCGAAGCAACAGTAATGCAGCATCCGTTCTACAGTGGGCC 432  
QY 421 AAGAAAGGATTTATACCATGAAAGCAACTTGGTATGCTTGAATGCGAAGACAGCTG 480  
DB 433 AAGAAAGGATTTATACCATGAAAGCAACTTGGTATGCTTGAATGCGAAGACAGCTG 492  
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DB 493 ACGGTTAAAAGAGAGAGGACTTATTATGCTACACTCAAGTCAAGTCAAGTCAAGTCA 552  
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DB 613 GAGAGATCTTACTCAGGCGGCAATACCCAGATTCCTCCAGCTTTCGGAGCAGCAG 672  
QY 661 TCTGTTTCACTTGGCGGAGTGTGTAATACAAAGCTGGTCTCTGTTGTTGCAACGCTG 720  
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QY 721 ACTCAAGCAAGCCAAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAAC 780  
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QY 781 TGA 783  
DB 793 TGA 795  
RESULT 4  
LOCUS AR076918  
DEFINITION Sequence 1 from patent US 5961974.  
ACCESSION AR076918  
VERSION AR076918.1 GI:10003664  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.  
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same  
JOURNAL Patent: US 5961974-A 1 05-OCT-1999;  
FEATURES Location/Qualifiers  
          1..783  
          /organism="unknown"  
BASE COUNT 243 a 159 c 178 g 203 t  
ORIGIN

Query Match 95.7%; Score 749.4; DB 6; Length 783;  
Best Local Similarity 97.3%; Pred. No. 2.3e-184;  
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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DB 121 CTTTTCCTGCTGATCTTCTAGAGATTTGATAAGTTCGAAGAGGAGTAACCTTCAT 180  
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DB 301 AACAAAGAGAGAAAAGAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAA 360  
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QY 481 ACGGTTAAAAGAGAGAGGACTTATTATGCTACACTCAAGTCAAGTCTCTGCTTAATCGG 540  
DB 481 ACGGTTAAAAGAGAGAGGACTTATTATGCTACACTCAAGTCAAGTCTCTGCTTAATCGG 540  
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Thu May 30 05:46:00 2002

us-08-982-272-3.rge

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Db 601 GAGAAATCTTTACTCAAGGGGGAATACCCAGAGTTCTCCAGCTTTCCGAGCAGCAG 660  
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Db 661 TCTGTTCACTTTGGGGGAGTGTGTTGAATACCAAGCTGGTCTCTGTTGTCAACGTG 720  
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Qy 781 TGA 783  
Db 781 TGA 783  
RESULT 5  
AR078308 AR078308 783 bp DNA linear PAT 31-AUG-2000  
LOCUS Sequence 1 from patent US 5962406.  
DEFINITION AR078308  
ACCESSION AR078308  
VERSION AR078308.1 GI:10005054  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical  
composition containing the same  
JOURNAL Patent: US 5962406-A 1 05-OCR-1999;  
FEATURES Location/Qualifiers  
source 1..783  
BASE COUNT 243 a 159 c 178 g 203 t  
ORIGIN  
Query Match 95.7%; Score 749.4; DB 6; Length 783;  
Best Local Similarity 97.3%; Pred. No. 2.3e-184;  
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
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Db 61 ATGAAATTTTATGATTTTACTTCTTTTCTTATCACCAGATGATTGGTTCAGCA 120  
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Db 121 CTTTGTGCTGTATCTTCATAGAGATTTGGATAGGTTCGAGAGAGTAAACCTTCAT 180  
Qy 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTATCC 240  
Db 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTATCC 240  
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Db 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
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Db 481 ACGGTTAAAGAGAGAGAGTCTTATATCTTACACTCAAGTCACTTCTGCTCTTAATCGG 540  
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Db 781 TGA 783  
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LOCUS Sequence 1 from patent US 5981724.  
DEFINITION AR085411  
ACCESSION AR085411  
VERSION AR085411.1 GI:10012180  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40  
JOURNAL Patent: US 5981724-A 1 09-NOV-1999;  
FEATURES Location/Qualifiers  
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BASE COUNT 243 a 159 c 178 g 203 t  
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Query Match 95.7%; Score 749.4; DB 6; Length 783;  
Best Local Similarity 97.3%; Pred. No. 2.3e-184;  
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Qy	421	AAGAAAGGATATTATACCATGAAGAAGCAACTTGGTATGTTGAAATGGGAACACAGCTG	480
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AUTHORS	Arimaige,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.
TITLE	Method of augmenting a vaccine response by administering CD40 ligand
JOURNAL	US 6290972-A 1 18-SEP-2001;
FEATURES	Patent: Location/Qualifiers
source	1. .783 /organism="unknown"
BASE COUNT	243 a 159 c 178 g 203 t
ORIGIN	

95.78; Score 749.4; DB 6; Length 783;



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X65453.
VERSION X65453.2 GI:13872516
KEYWORDS CD4 antigen.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1250)
Armitage, R., Fanslow, W., Sato, T.A., Clifford, K.N., Strockbine, L.,
Macduff, B.M., Anderson, D.M., Gimpel, S.D., Davis-Smith, T.,
Maliszewski, C.R., Clark, E.A., Smith, C.A., Grabstein, K.H., Cosman, D.
and Spriggs, M.K.
Molecular and biological characterization of a murine ligand for
CD40
Nature 357 (6373), 80-82 (1992)
92244364
2 (bases 1 to 1250)
Spriggs, M.K.
Direct Submission
Submitted (07-APR-1992) M.K. Spriggs, Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
revised by [3]
3 (bases 1 to 1250)
Spriggs, M.K.
Direct Submission
Submitted (24-APR-2001) Strockbine, L. Immunex Research &
Development, Molecular Biology, 51 University Street, Seattle,
Washington, 98101, USA
On Apr 27, 2001 this sequence version replaced gi:50351.
FEATURES
source Location/Qualifiers
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/gene="CD40L"
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/product="CD40 surface protein"
/protein_id="CAA46448.2"
/db_xref="GI:13872517"
/db_xref="SWISS-PROT:P27548"
/translation="MIETISQSPRSVATGLPASMKIFWILTVLITOMISGLVAV
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QQSVHLGGVYFELQAGASVFVNVTESQVTHRVGFSSFGLLKL"
BASE COUNT 379 a 273 c 286 g 312 t
ORIGIN
Query Match 95.7%; Score 749.4; DB 10; Length 1250;
Best Local Similarity 97.3%; Pred. No. 2.3e-184;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGATCGAAACATACAAACCAACTCTCCCGGATCTCGCGCCACTGGCATGCCCATCAGC 60
Db 13 ATGATGAAACATACAGCAACCTTCCCGGATCTCGCGCACTCGGCACTGGCATGCCAGC 72
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATATCCAGATGATGGTCCAGCA 120
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QY 121 CTTTTCGTCTGTATCTTATAGAGATTGGATAAGTTCGAAGAGGAGTAACCTTCAT 180
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Db 193 GAAGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 252
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Db 253 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTGCAAGGATATAACGTTA 312
QY 301 AACAAAGACAGAAAAGAAAACAGCTTTCAATATGCAAGAGGTGATGAGGATCCCTCAA 360
Db 313 AACAAAGACAGAAAAGAAAACAGCTTTGAATATGCAAGAGGTGATGAGGATCCCTCAA 372
QY 361 ATTGCAGCACACCTTTGTAAGCGAAGCAACAGTAATCAGCATCCGTTCTACAGTGGGCC 420
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QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAACAGCTGCTGCTCTGTTGTTGTTCAAGCTG 720
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QY 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
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QY 781 TGA 783
Db 793 TGA 795

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RESULT 11
AF013985
LOCUS AF013985 783 bp mRNA linear ROD 26-JAN-1999
DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.
ACCESSION AF013985
VERSION AF013985.1 GI:4102613
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 783)
AUTHORS Daniel, K.C., Foss, Y., Moussavi, A., Macary, P., Kemeny, D.M.,
Farzaneh, F. and Gaken, J.A.
TITLE Cloning and sequencing of rat CD40 ligand
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 783)
AUTHORS Daniel, K.C., Foss, Y., Moussavi, A., Macary, P., Kemeny, D.M.,
Farzaneh, F. and Gaken, J.A.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-1997) Immunology, King's College School of
Medicine and Dentistry, 123 Coldharbourlane, London SE5 9NU, United
Kingdom
FEATURES
source Location/Qualifiers
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Query Match	87.9%	Score 688.6	DB 10	Length 783
Best Local Similarity	92.5%	Pred. No. 1.5e-168		
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DB	1	ATGATAGAAACATACAGCAACCTTC	CCCGAGATCTGGCTACTCGGCTTCCACGAGC	60
QY	61	ATGAAATTTTATGATTTTACTTTACT	TGTTTCTTTATCACCCAGATGATGGGTCGGTG	120
DB	61	ATGAGATTTTATGATTTTACTTTACT	TGTTTCTTTATCACCCAGATGATGGGTCGGTG	120
QY	121	CTTTTGTGCTGATCTTCATAGAGAT	TGGATAGAGTCGAAGAGGTCGAAGAGGAAGTAAACCTTCAT	180
DB	121	CTTTTGTGCTGATCTTCATAGAGAT	TGGATAGAGTCGAAGAGGTCGAAGAGGAAGTAAACCTTCAC	180
QY	181	GAAGATTTTGTATTTCATATAAAGCT	TAAAGAGATGCAACAAAGAGAGGATCTTTATCC	240
DB	181	GAGGATTTTGTATTCGTAAAAAGCT	TAAAGAGTGCACAAAGAGAGAGGTCCTTTATCC	240
QY	241	TTGCTGAACCTGTGAGGAGATGAGAG	GCAATTTGAGAGCCTTGTCGAAGGATATAACGGTTA	300
DB	241	TTGCTCAACTGTGAGGAGATGAGAG	GCAATTTGAGAGCCTTGTCGAAGGATATAACGGTTA	300
QY	301	ACCAAGAGAGAGAGAGAGAGAGAGCT	TGAAATGCAAGAGAGGTGATGAGGATCCCTCA	360
DB	301	ACCAAGAGAGAGAGAGAGAGAGAGCT	TGAAATGCAAGAGAGGTGATGAGGATCCCTCA	360
QY	361	ATTGACGACACCTGTTAGCGAGAGCA	AGCCACAGTATGAGCATCGTTCTACAGTGGGCC	420
DB	361	ATTGACGACACCTGTTAGCGAGAGCA	AGCCACAGTATGAGCATCTGTTCTACAGTGGGCC	420
QY	421	AAGAAAGGATATTATACCATGAAAGCA	AACTTGGTAATGCTTGAATGGGAACACAGCTG	480
DB	421	AAGAAAGGATATTATACCATGAAAGCA	AACTTGGTAGTCTGGAATGGGAACACAGCTG	480
QY	481	ACGGTTAAAGAGAGAGACTCTATTATG	CTCTACACTCAAGTCACCTCTGCTCTTAATCGG	540
DB	481	ACGGTTAAAGAGAGAGACTCTATTATG	CTCTACACCAGTCACCTCTGCTCTTAATCGG	540
QY	541	GAGCCTTCGAGTCAACGCCCAATTCAT	CGTGGGCTCTGGCTGAAGCCAGCATTTGGATCT	600
DB	541	GAACCTTTGAGTCAACGTCCTCAATTC	ATTCATCGTCAGCCTCTGGCTGAAGCCAGCATTTGGGTC	600
QY	601	GAGAGATCTTACTCAAGGCGGCAATACC	ACACAGTTCTCCAGCTTTGGCAGCAGAG	660
DB	601	GAGAGATCTTACTCAAGGCGGCAATACC	ACACAGTTCTCCAGCTTTGTGAGCAACAG	660
QY	661	TCGTGTTACTTTGGGCGGAGTGTTTGA	ATTACAAGCTGGTCTGTTGTTGTCACCGTG	720
DB	661	TCCATTCACTTGGGCGGAGTATTTGA	ATTACAAGCAGGTCCTGTTGTTGTCACCGTG	720
QY	721	ACTGAAGCAGCCAGGTGATCCACAGAG	TGGGCTTCATCTTTTGGCTTACTCAAACTC	780
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QY	781	TGA 783		
DB	781	TGA 783		

RESULT 12

RESULT 12

AF116582 783 bp mRNA linear ROD 12-JUL-2000

AF116582 Rattus norvegicus CD40 ligand mRNA, complete cds.

AF116582 Rattus norvegicus

AF116582.1 GI:4545249

Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 783)

Hallett, K.M. and Oaks, M.K.

Nucleotide sequence of the rat CD40 ligand

DNA Seq. 10 (6), 405-406 (2000)

20284949

MEDLINE

PUBMED

10826698

2 (bases 1 to 783)

Hallett, K.M. and Oaks, M.K.

Direct Submission

Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical  
Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA

Location/Qualifiers

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FEATURES

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61	ATGAAATTTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATTGGGTCAGCA	120			
61	ATGATAGAAATTTATCTATTTACTGTTTTCTTATCACCAGATGATTGGGTCGGTG	120			
121	CTTTTTGCTGTATCTTCATAGAAGATTGGATAAGTTCGAAGGAAGTAATAAOCCTTCAT	180			
121	CCTTTTGCTGTGTATCTTCATAGAAGATTGGATAAGTAGAGGAAGCAAGCCCTTCAC	180			
181	GAAGATTTTGTATTCATAAAAAGCTAAAGAGATCCACARAAGGAGAGGATCTTTATCC	240			
181	GAGGATTTTGTATTCGTAAAAAGCTAAAGAGGTGCCAAAGGAGAGAGGGTCTTATCC	240			
241	TTGCTGAACTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA	300			
241	TTGCTCAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGTCAAGGATATATCGTTA	300			
301	AACAAAGAAGAGAAAAAAGAAACAGCTTTGAAATGCCAAGAGGTGATGAGCATCCTCAA	360			
301	AACAAGAGAGAAAAAAGAAAGAGCTTTGAAATGCCAAGAGGTGATGAGGATCCTCAA	360			
361	ATTGCAGCACACCTTGTAAAGCGAAGCCACAGTAATGCAGCATCCCTTTCTACAGTGGGCC	420			
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QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAAATGGAAACAGCTG 480
DB 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAAATGGAAACAGCTG 480
QY 481 ACGTTTAAAGAGAGAGACTCTATATGTCTACACTCAAGTCACTTCTGCTCTTAATCGG 540
DB 481 ACGTTTAAAGAGAGAGACTCTATATGTCTACACTCAAGTCACTTCTGCTCTTAATCGG 540
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DB 661 TCCATTTCACCTTTGGCGGAGTATTGTAATTAACAAGCAGGTGCTTCTGTTGTTGTCACAGCTG 720
QY 721 ACTGAACAGCCAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
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QY 781 TGA 783
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RESULT 13
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LOCUS AR076933 878 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 22 from patent US 5961974.
ACCESSION AR076933
VERSION AR076933.1 GI:10003679
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 22 05-OCT-1999;
FEATURES
    Location/Qualifiers
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BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTCGAAGAGAGAGTAAACCTTCATCAAGATTTTGTATTCTATAAAGCTAAAG 210
DB 225 GATAAGGTCGAAGAGAGTAAACCTTCATCAAGATTTTGTATTCTATAAAGCTAAAG 284
QY 211 AGATGCAACAAAGAGAGAGTCTTTATCTTGTGTAACCTGTGAGGAGATGAGAAGCAA 270
DB 285 AGATGCAACAAAGAGAGAGTCTTTATCTTGTGTAACCTGTGAGGAGATGAGAAGCAA 344
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DB 345 TTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGAGAGAGAGAGAGAGTTT 404
QY 331 GAAATGCAAGAGAGTGTAGGATCTTCAAAATTCAGCACACGTTGTAAAGCAAGCCAAAC 390
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QY 691 CAAGCTGTGCTTCTGCTTGTCAACCTGACTGAAGCAAGCCAGTCAACAGAGCTT 750
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RESULT 14
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LOCUS AR078323 878 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 22 from patent US 5962406.
ACCESSION AR078323
VERSION AR078323.1 GI:10005069
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 878)
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S., Gibson,M.G., Morris,A.E. and McGrew,J.T.
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same
JOURNAL Patent: US 5962406-A 22 05-OCT-1999;
FEATURES
    Location/Qualifiers
    source 1..878
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BASE COUNT 277 a 178 c 203 g 220 t
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTCGAAGAGAGTAAACCTTCATCAAGATTTTGTATTCTATAAAGCTAAAG 210
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DEFINITION Sequence 22 from patent US 5981724.  
ACCESSION AR085426  
VERSION AR085426.1 GI:10012195  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 878)  
AUTHORS Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40  
JOURNAL Patent: US 5981724-A 22 09-NOV-1999;  
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source location/Qualifiers  
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BASE COUNT 277 a 178 c 203 g 220 t  
ORIGIN

Query Match 80.68; Score 631.4; DB 6; Length 878;  
Best Local Similarity 99.88; Pred. No. 1.2e-153;  
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 151 GATAAGTCGAAGAGAGTAACCTTCATGAAGATTTCATTATCAATAAAGCTAAAG 210  
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Job time: 22004 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 18:49:50 ; Search time 5112.58 Seconds  
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Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: em\_htc:\*  
9: gb\_est1:\*  
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11: gb\_htc:\*  
12: gb\_gss:\*  
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15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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c 20	44	5.6	802	12	CNS0383B
c 21	43.8	5.6	329	9	AL513719
c 22	43.8	5.6	799	12	CNS011SA
c 23	43.8	5.6	1101	12	CNS0182P
c 24	43.6	5.6	458	9	AL514085
c 25	43.6	5.6	588	12	AQ451757
c 26	43.6	5.6	828	12	CNS018FA
c 27	43.6	5.6	1039	12	CNS02ADN
c 28	43.6	5.6	1101	12	CNS000D1
c 29	43.4	5.5	1201	12	CNS0168L
c 30	43.2	5.5	889	12	CNS006MT
c 31	43	5.5	642	10	BJ096268
c 32	42.8	5.5	534	12	CNS03DHB
c 33	42.8	5.5	597	9	AL514721
c 34	42.8	5.5	1101	12	CNS00LLD
c 35	42.6	5.4	307	12	CNS00A3W
c 36	42.6	5.4	415	10	R41111
c 37	42.6	5.4	595	12	AQ521025
c 38	42.6	5.4	633	9	AL513979
c 39	42.6	5.4	744	12	AG044338
c 40	42.6	5.4	805	9	AI557564
c 41	42.6	5.4	959	12	CNS00655
c 42	42.6	5.4	1007	12	CNS06X9S
c 43	42.6	5.4	1101	12	CNS0039L
c 44	42.6	5.4	1101	12	CNS0100X
c 45	42.2	5.4	330	9	AL513817

#### ALIGNMENTS

RESULT 1  
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001  
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF599437  
VERSION BF599437.1 GI:11695919  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
1 (bases 1 to 492)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pertes,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

TITLE  
JOURNAL Contact: Smith TPL  
MEDLINE 21180013  
COMMENT USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCATGACCAT  
BACKWARD: GTTTCCTCAGTCACGAG  
Plate: 33 row: N column: 5  
Seq primer: ATTTAGGTGACATATAG.  
Location/Qualifiers  
1. 492  
/organism="Bos taurus"  
/db\_xref="taxon:9913"

Thu May 30 05:46:04 2002

Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smithemail.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 20  
 and -minmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACACAGCTATGACCAT  
 BACKWARD: GTTTCCTCCAGTCACGAGC  
 Plate: 34 row: F column: 23  
 Seq primer: ATTAGGTGACACTATAG.  
 Location/Qualifiers  
 1. 398  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="MARC 1BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from lymph node, ovary,  
 fat, hypothalamus, and pituitary."  
 BASE COUNT 134 a 77 c 82 g 105 t  
 ORIGIN

/clone\_lib="MARC 3BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled tissue from marrow, alveolar  
 macrophage, ovary, fetal semitendinosus muscle, and fetal  
 longissimus muscle."  
 BASE COUNT 163 a 103 c 104 g 122 t  
 ORIGIN

Query Match 32.5%; Score 254.8; DB 9; Length 398;  
 Best Local Similarity 85.5%; Pred. No. 1.1e-43;  
 Matches 296; Conservative 0; Mismatches 47; Indels 3; Gaps 1;  
 Oy 1 ATGATCGAAACATACACCAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60  
 Db 53 ATGATCGAAACATACACCAACTTCTCCCGCTCCGCGCCACTGGCCACTGTTCAGT 112  
 Oy 61 ATGAAATTTTATGATTTTACTTTTCTTATCACCAGATGATGGGTGAGCA 120  
 Db 113 ATGAAATTTTATGATTTTACTTACAGTTTCTTATCACCAGATGATGGGTGAGCG 172  
 Oy 121 CTTTGTGCTGTATCTTCATAGAGATGATGATGATGATGATGATGATGATGATGAT 180  
 Db 173 CTTTGTGCTGTATCTTCATAGAGATGATGATGATGATGATGATGATGATGATGAT 232  
 Oy 181 GAAGATTTGTATCTTATCAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240  
 Db 233 GAAGATTTGTGTTTATCAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 292  
 Oy 241 TTGCTGAACCTGTGAGAGATGAGAGGATTTGAAGACCTTGTCAAGCATATAACGTTA 300  
 Db 293 TTACTGAACCTGTGAGAGATTTAGAACCGGTTTGAAGACTTGGTCAAGATATAATGCA 352  
 Oy 301 AACAAAGNAG---AGAAAAAGAAACAGCTTTGAATGCAAAAGAG 343  
 Db 353 AACAAAGNAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398

Query Match 39.9%; Score 312.2; DB 10; Length 492;  
 Best Local Similarity 82.9%; Pred. No. 9.1e-56;  
 Matches 369; Conservative 0; Mismatches 73; Indels 3; Gaps 1;  
 Oy 1 ATGATCGAAACATACACCAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60  
 Db 46 ATGATCGAAACATACACCAACTTCTCCCGCTCCGCGCCACTGGCCACTGTTCAGT 105  
 Oy 61 ATGAAATTTTATGATTTTACTTCTTATCACCAGATGATGGGTGAGCA 120  
 Db 106 ATGAAATTTTATGATTTTACTTACAGTTTCTTATCACCAGATGATGGGTGAGCG 165  
 Oy 121 CTTTGTGCTGTATCTTCATAGAGATGATAAGTTCGAGAGAGAGTAAACCTTCAT 180  
 Db 166 CTTTGTGCTGTATCTTCACAGAGATTTGCAAGATAGACAGCAAGAGGATCTTCAT 225  
 Oy 181 GAAGATTTGTATTCATCAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240  
 Db 226 GAAGATTTGTTCATCAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 285  
 Oy 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGGTTA 300  
 Db 286 TTACTGAACCTGTGAGAGATTTAGAGCGGTTTGAAGCTTGTCAAGGATATAAGTCAA 345  
 Oy 301 ACAAGAGAG---AGAAAAAGAAACACAGCTTTGAATGCAAAAGGAGGTGATGAGGATCC 357  
 Db 346 ACAAGAGAGTAAAG 405  
 Oy 358 CAAATTCAGCAGCAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417  
 Db 406 CAGATAGCGCAGATCTCATCAGTGGGCGCAGTAGTAAACAACTCTGTTCTCAGGAG 465  
 Oy 418 GCCAAGAGGATATTATACCATGA 442  
 Db 466 GCCCCCAAGAGACTACACCCCTAA 490

RESULT 3  
 LOCUS AI982044 638 bp mRNA linear EST 07-MAY-2001  
 DEFINITION pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus CDNA  
 clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.  
 ACCESSION AI982044  
 VERSION AI982044.1 GI:5885072  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 638)  
 Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J.  
 An expressed sequence tag database of T-cell-enriched activated  
 chicken splenocytes: sequence analysis of 5251 clones  
 Genomics 66 (2), 144-151 (2000)  
 JOURNAL 20318616  
 MEDLINE

RESULT 2  
 LOCUS AW486605 398 bp mRNA linear EST 25-APR-2001  
 DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION AW486605  
 VERSION AW486605.1 GI:7056711  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 398)  
 Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.P.,  
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrnkruug, S.C., Bennett,  
 G.L., Heaton, W.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G.,  
 Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and  
 Keefe, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)  
 JOURNAL 21180013  
 MEDLINE  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA

Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain *y<sup>+</sup>; cn bw sp*, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

FEATURES	source	Location/Qualifiers	BASE COUNT	ORIGIN
		1..997	89 a	99 c 13 g
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		/db_xref="taxon:7227"		
		/clone_lib="RPCI-98"		
		/clone="BAC12K22"		
		/note="END1 TET3"		
			258 t	538 others

Query Match 7.18; Score 55.8; DB 12; Length 997;

Query Match 7.1%; Score 55.8; DB 12; Length 997;  
Best Local Similarity 19.5%; Pred. No. 0.07;  
Matches 69; Conservative 131; Mismatches 153; Indels 0; Gaps 0;

Qy	140	ATAGAAGATTGGATAAGAGTGAAGAGGAAGTAAACCTTCATGAAGATTGTGATTCAATAA	199
		: : : :   :   : : :   :   : : :   :   : : :   :   : : :   :   : : :   :   : : :	
Db	881	ARARARRARAKAARAGARRRRRRRRRRRRRRRRRARGAGGRRGRRGRRRRARRR	822
Qy	200	AAAAGCTAAAGAGATCAACAAGAGGAGAAGGATCTTTATCCTTGCTGAACTCTGAGGAGA	259
		:   :	
Db	821	RAGAARARPRPARAARARPRRRRACRRRRRARGARRRRRGRRRGRRRRRA	762
Qy	260	TGAGAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTTAAACAAGAGAGAAAAAG	319
		: :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	761	ARRARARAGARAAARRRRRAGAAAAARRRRRRRRRGAGARPARRRRRARRARA	702
Qy	320	AAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCCTCAAAATGCGACACACGTGTAA	379
		: : : : :   : : : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	701	GACARRRRRRCRGAGARRRGRRGRRRGAGARRRRRRRRMRTFARRRRRRARGAA	642
Qy	380	GCGAAGCCACAGTAATGCAGCATCCGTTCTACAGTGGCCCAAGAAGATATTATACCA	439
		: :   :   : : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	641	RRRARGARRRA	582
Qy	440	TGAAAAGCAACTTGGTAATGCTTTGAAAATGGGAAACAGCTGCAGGTATAAAGA	492
		: : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :	
Db	581	GAGARRRRRRRRARRAAGARRRRRRARRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	529

RESULT	5				
AL534423		AL534423	797 bp	mRNA	linear EST 13-FEB-2001
LOCUS		AL534423	LTI_FL013_FBRn1	Homo sapiens	CDNA clone CSQDF004YD24 5
DEFINITION				prime, mRNA sequence.	

ACCESSION AL534423  
VERSION AL534423.1  
KEYWORDS EST.  
SOURCE human

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 797)

REFERENCE 1 (Pages 1 to 197)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)

CONTACT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES	Location/Qualifiers 1..797 /organism="Homo sapiens" /db_xref="taxon:9606"

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
Web : www.genoscope.cns.fr)  
COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBeloBAC11  
FEATURES Location/Qualifiers  
source 1..878  
/organism="Drosophila melanogaster"  
/plasmid="pBeloBAC11"  
/db\_xref="taxon:7227"  
/clone\_lib="DrosBAC"  
/clone="BACN04E04"  
/note="end : SP6"  
BASE COUNT 279 a 132 c 120 g 182 t 165 others  
ORIGIN  
Query Match 6.4% Score 49.8; DB 12; Length 878;  
Best Local Similarity 25.18; Pred. No. 1.3;  
Matches 60; Conservative 81; Mismatches 98; Indels 0; Gaps 0;  
QY 257 AGATGAGAGCAATTTTGAAGACCTTGTCAAGGATATTAACCTTAACAAAGAGAGAAA 316  
DB 88 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 147  
QY 317 AGAAAAACAGCTTTCAGATGCAAGAGGTGATGAGGATCTCAATTCGACGACACGTTG 376  
DB 148 AAAAAAATTTTTCGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 207  
QY 377 TAAGCAAGCAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436  
DB 208 WAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAG 267  
QY 437 CCATGAAAGCAACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 495  
DB 268 WMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 326  
RESULT 7  
CNS0145P/c 1043 bp DNA linear GSS-26-JUL-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
DEFINITION BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL103735  
VERSION AL103735.1 GI:5615346  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1043)  
Genoscope.  
AUTHORS Direct Submission.  
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
JOURNAL Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
COMMENT Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBeloBAC11  
FEATURES Location/Qualifiers

/clone="CSODF004VD24"  
/dev\_stage="pooled" tissue from post conception fetuses (20  
week - 24 week and 26 week)  
/lab\_host="DH10B"  
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand  
cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-stranded cDNA was digested with Not I  
and cloned into the Not I and Eco RV sites of the  
pCMVSPORT 6 vector. Library was constructed by Life  
Technologies. Contact : Feng Liang Life Technologies, a  
division of Invitrogen 9800 Medical Center Drive Rockville  
Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
filiang@life.techn.com URL :  
http://fulllength.invitrogen.com"  
BASE COUNT 407 a 43 c 120 g 152 t 75 others  
ORIGIN  
Query Match 6.7% Score 52.8; DB 9; Length 797;  
Best Local Similarity 38.9% Pred. No. 0.31;  
Matches 171; Conservative 36; Mismatches 233; Indels 0; Gaps 0;  
QY 140 ATAGAGATGGTGAAGCTGAGAGAGTAAACCTTCATGAAGATTTTGTATTCTATAA 199  
DB 240 AGAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 299  
QY 200 AAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTTCTGCTGAACTGTGAGAGA 259  
DB 300 AGGAAATRTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 359  
QY 260 TGAGAGCAATTTGAAGACCTTCTCAAGGATATAACGTTTAAACAAAGAGAGAAAAAAG 319  
DB 360 TCRWAAGAAGAAAGAAAGAAATAAATGAAATAAATAAATAAATAAATAAATAAATAA 419  
QY 320 AAAACAGCTTTCAATGCAAGAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 379  
DB 420 AAAAAAGTAWAGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 479  
QY 380 GCGAAGCAACAGTAAATGCAAGCTTCGTTCTACAGTGGCGCAAGAAAGGATATTATACCA 439  
DB 480 AAGGARATGGAATAATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 539  
QY 440 TGAAGCAACCTTGTGATGCTTGAATGGAACAGCTGACGCTTAAAGAGAGAGAC 499  
DB 540 TAAAAATWAAAAATGAAAGWAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 599  
QY 500 TCTATTATGCTTACACTCAAGTCACTTCTGCTCTAATCGGAGCTTCGAGTCAACGCC 559  
DB 600 MTATTGTGTTTMMTMTAAAGMMMTTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMT 659  
QY 560 CATTCACTCGCGCTCTGG 579  
DB 660 TMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMM 679  
RESULT 6  
CNS0187R 878 bp DNA linear GSS 26-JUL-1999  
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
DEFINITION BACN04E04 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL108993  
VERSION AL108993.1 GI:5629297  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 878)  
Genoscope.  
AUTHORS Direct Submission  
TITLE

## source

1. .1043  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="BACI-98"  
 /note="end : T7"

BASE COUNT 277 a 96 c 121 g 382 t 167 others  
 ORIGIN

Query Match 6.3%; Score 49.6; DB 12; Length 1043;  
 Best Local Similarity 35.8%; Pred. No. 1.4;  
 Matches 101; Conservative 48; Mismatches 133; Indels 0; Gaps 0;

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACAGATGTTGGTCCAGCA 120  
 Db 916 WTATTTGKTTTGTATRTDRTKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 857  
 QY 121 CTTTTCGTGTCATCTTCATAGAGATGAGTTCGAGAGAGAGAAAGTAAACCTTCAT 180  
 Db 856 TTWTWTATTTWATATATWTARRGGRAADDAAAAAAATTTTWTWWWWTTTWW 797  
 QY 181 GAAGATTTGTCATCAAAAAAGCTTAAGAGATGCAACAAGAGAGAGGATCTTTATCC 240  
 Db 796 WWWWWTTTWTTTTTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 737  
 QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
 Db 736 TATATAATTTAAWATATATATAATATAAATAAATAAATAAATAAATAAATAA 677  
 QY 301 AACAAAG 342  
 Db 676 TAWAAAAAANAWAAAAAATATATTTWWATAAANA 635

## RESULT 8

CNS0039G/C  
 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 BAC08K10 of RPI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL063921  
 GSS.  
 SOURCE fruit fly.

ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 JOURNAL Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 COMMENT - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammmer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

1. .1101

/organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="RPI-98"  
 /clone="BAC08K10"  
 /note="end : TET3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others  
 ORIGIN

Query Match 6.2%; Score 48.8; DB 12; Length 1101;  
 Best Local Similarity 13.7%; Pred. No. 2;  
 Matches 60; Conservative 221; Mismatches 155; Indels 2; Gaps 1;

QY 62 TGAATTTTATGATTTACTTACTTCTTCTTATCACCACAGATGTTGGTCCAGCAC 121  
 Db 1084 DDWDTKWTWKKRDRRRWAGDADRWDDGAGTWTATWWWATWDTWDDKWW 1025  
 QY 122 TTTTTCGTGTCATCTTCATAGAAGATTGTAAGGTGCAAGAGAGAAACCTTCATG 181  
 Db 1024 WWTAAKTTDTATWTWRTAWRADWAGRDRGAGKRDAAATDAGARRDGRKKDKDK 965  
 QY 182 AAGATTTTGTATTCATAAAAAGCTAAAGAGATCAACAAAGGAGAGATCTTTATCCT 241  
 Db 964 DDDDDKGGKKKRAAKAAKATKWWDDWKDKWOGAKORRADDGAGDKDDGKGR 905  
 QY 242 TCCTGAACCTGTGAGGAGATGAGAAGCA--ATTTGAAGACCTTGTCAAGGATATAACGTT 299  
 Db 904 DADDDTGTCTKDDDKDKWDDWAKAGTGWGATWAAATDWWGWADADWTTWDAADW 845  
 QY 300 AACAAAG 359  
 Db 844 WADRDWAWKWDADAWANGARTADRDWDRAGKRGARKRRDRKRRADRRD 785  
 QY 360 AATTCCACACACCTTGTAAAGCAAGCAACAGTATCCAGCATCCGTTCTACAGTGGC 419  
 Db 784 AATWTTTWTTRTDDWKKWTDTWRAADRTDRTDRTDRTDRTDRTDRTDRTDRT 725  
 QY 420 CAAGAAGGATATATACCATGAAAGCAACTTGTGTAATGCTTGAATGGAACACACT 479  
 Db 724 KRRTRWDDADDDTARDDRRRGGDDGADAGKKTGRRRRDRATWRTDRTDRTDRT 665  
 QY 480 GACGGTTAAAGAGAGAGG 497  
 Db 664 WTTTDTDTDDWKKRRR 647

## RESULT 9

CNS0108N  
 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
 BAC03L01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL098657  
 GSS.  
 SOURCE fruit fly.

ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
 JOURNAL Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 COMMENT - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector

Thu May 30 05:46:04 2002

```

FEATURES
  source      pBelobAC11.
              Location/Qualifiers
                1..1038
                /organism="Drosophila melanogaster"
                /plasmid="pBelobAC11"
                /db_xref="taxon:7227"
                /clone_lib="DrosBAC"
                /clone="BACN03101"
                /note="end : SP6"
BASE COUNT   372 a    6 c    119 g    219 t    322 others
ORIGIN
Query Match      6.1%; Score 47.8; DB 12; Length 1038;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 155; Conservative 20; Mismatches 273; Indels 0; Gaps 0;

QY 72 TATGTAATTACTTACTGTTTCTTATCCACCCAGATGATGGTCAAGCACTTTTGGCTGT 131
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 37 TTTTNNNTTTNNNNNTTTGGTTWANNACYWTTTATTTTATTTTATTTATTTTATTTA 96
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 132 GTATCTTCATAGAAGATTGGATAGGTCGAAGAGAGTAACCTTCATGACGATTTTGT 191
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 97 TTAATAAGYRCANCAACNCNTNNNNNNNNNNCYATAAAATNTNTNTAANAATAAAA 156
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 192 ATTCTATAAAAAGCTAAAGATGCAACAAGAGAGAGGATCTTTATCTCTGCTGAACGT 251
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 157 TTNNTTTTANNANNANNANNANNANNANNANNANNANNANNANNNTTNNNNATTNAAA 216
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 252 TCAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGA 311
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 217 NNNNTNANNNTAANAANAATTTATAAANAANAANAANAANAANAANAANAANAANA 276
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 312 GAAAAAGAAACACCTTTGAAATGCAAGAGGATGATGAGATCCTCAAAATTCGACGACA 371
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 277 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 336
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 372 CGTTGTAAGCGAGCAACAGTAATGTCAGATCCCTTCTACAGTGGGCCRAAGAGATA 431
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 337 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 396
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 432 TTATACCATGAAGCAACCTTTGGTATGCTTCAAAATGGGAAACAGCTGACGGTTAAAG 491
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 397 TAATAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 456
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
QY 492 AGAAGGACTCTATTATGCTCTACACTCAA 519
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1
Db 457 ADWDAAAANAATWDTGKGAASAAA 484
    ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1

RESULT 10
LOCUS      AZ691914
DEFINITION ENTM26FR Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000
            genomic, DNA sequence.
ACCESSION  AZ691914
VERSION     AZ691914.1 GI:11829180
KEYWORDS    GSS.
SOURCE      Entamoeba histolytica.
            Entamoeba histolytica.
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1 (bases 1 to 920)
AUTHORS     Loftus,B., Van Aken,S. and Fraser,C.
TITLE       Determination of clone end sequences from Entamoeba histolytica
            HMI:IMSS sheared DNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org

```

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library  
 Seq primer: M13-Reverse  
 Class: shotgun  
 High quality sequence start: 15  
 High quality sequence stop: 330.  
 Location/Qualifiers

## FEATURES

source Entamoeba histolytica  
 1..920  
 /organism="Entamoeba histolytica"  
 /strain="HMI:IMSS"  
 /db\_xref="taxon:5759"  
 /clone\_lib="Entamoeba histolytica Sheared DNA"  
 /note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.  
 Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds M. Vaudin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 354 a 54 c 131 g 381 t  
 ORIGIN

Query Match 5.9%; Score 46.4; DB 12; Length 920;  
 Best Local Similarity 54.8%; Pred. No. 6.7;  
 Matches 92; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 186 TTTTCTATTATAAAAGCTTAAAGAGATGCAACAAGAGGAGAGGATCTTTATCTCTGCT 245  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1  
 Db 687 TTTTCTTTTATTTTAAAGAGATATAAATAAATAAATAAATAAATAAATAAATAA 746  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1  
 QY 246 GAACGTGTGAGGATGCAAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAA 305  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1  
 Db 747 TTATGGGGGGGGGGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 806  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1  
 QY 306 AGAAGAGAAAAAAGAAACAGCTTTGAAATGCAAGAGGATGATGAGGA 353  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1  
 Db 807 AAAAAAGATGGAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGA 854  
 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1 ||||| 1:1

RESULT 11

CNS0181N

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence Sp6 end of BAC

BACN37P10 of DrosBAC library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL108773

GSS.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS0181N 1101 bp DNA linear GSS 26-JUL-1999  
 Drosophila melanogaster genome survey sequence Sp6 end of BAC  
 BACN37P10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL108773 GI:5629077  
 GSS.  
 fruit fly  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 Genoscope.  
 Direct Submission  
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila genome project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector

FEATURES source Location/Qualifiers  
 1. 1101  
 /organism="Drosophila melanogaster"  
 /plasmid="pBelobAC11"  
 /db\_xref="taxon:7227"  
 /clone\_lib="DrosBAC"  
 /clone="BACN37P10"  
 /note="end : SP6"  
 BASE COUNT 125 a 364 c 197 g 116 t 299 others  
 ORIGIN

Query Match 5.9%; Score 46.4; DB 12; Length 1101;  
 Best Local Similarity 20.8%; Pred. No. 6.5;  
 Matches 83; Conservative 133; Mismatches 184; Indels 0; Gaps 0;  
 QY 74 TGTATTACTTACTGTTTCTTATCACCAGATGATGGTCAGACATTTTGTGTGTG 133  
 DB 630 YBKTTTBKGTGTTTCTGGSYTTTGYGAGVGTCTKTKGKGTTTCTTTTMTV 689  
 QY 134 ATCTTCATAGAGATTGATAGGTCGAAGGAGTAAGTAACTTCATGAAGATTGTAT 193  
 DB 690 MAAAMADARGAVMGGSVAHDKGTWWDRTTKTSARAGRAAMGRSARMAAARTTH 749  
 QY 194 TCATAAAAGCTAAGAGATCAACAAAGGAGAGGATCTTTATCTTGTCTGAACTGTG 253  
 DB 750 WWAIAAARAARAAHARRAWTHHHVRARAGRRGRGGDRARRRHRRRRARAAR 809  
 QY 254 AGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTTAAACAAGAGAGA 313  
 DB 810 CRRRRARRGRMMNRNARNAARAGRRRAGRRARRARRARRARRRRGRGRGG 869  
 QY 314 AAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCTCAATTCGAGCACAG 373  
 DB 870 RGRRRRARRARARARARRRRRARRARARAGGRRGRRARRARRGRGRRRR 929  
 QY 374 TTGTAAGCGAACCCACAGTAATGCGATCCGTTTCTACAGTGGCCCAAGAGATATT 433  
 DB 930 RRRRRGRGRGRRGGAGAGRRAGARRRRGRGGGGGGGGGGGGRRRRRRARR 989  
 QY 434 ATACCATGAAGCAACTTGTGTAATGCTTGAATGGGAA 473  
 DB 990 GARRRAAGRARARRRRARRARARARAGAGARARRARRGGA 1029

RESULT 12  
 CNS011TX/c 828 bp DNA linear GSS 26-JUL-1999  
 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC  
 BACN06A02 of DrosBAC library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL100719.1 GI:5612330  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 828)  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome project (EDGP) -  
 http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC  
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
 d'Etude du Polymorphisme Humain) with funding provided by a MRC  
 project grant. The DNA was prepared from embryos by Alain Bucheton  
 and Genevieve Payan. It has been constructed in the vector

FEATURES source Location/Qualifiers  
 1. 828  
 /organism="Drosophila melanogaster"  
 /plasmid="pBelobAC11"  
 /db\_xref="taxon:7227"  
 /clone\_lib="DrosBAC"  
 /clone="BACN06A02"  
 /note="end : T7"  
 BASE COUNT 143 a 127 c 20 g 449 t 89 others  
 ORIGIN

Query Match 5.8%; Score 45.6; DB 12; Length 828;  
 Best Local Similarity 39.7%; Pred. No. 10;  
 Matches 120; Conservative 29; Mismatches 153; Indels 0; Gaps 0;  
 QY 194 TCATAAAAGCTAAGAGATGCAACAAAGGAGAGGATCTTTATCTTGTGTAAGTGTG 253  
 DB 600 TAAAAAAGAAATWAGAATAAGAAAGGTTTAAATWTATATGATATAAAWAAAAAGGAG 541  
 QY 254 AGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTTAAACAAGAGAGA 313  
 DB 540 AAAAAAGAGAGAAAGAGGATGAAGATGTWAAAAAATWGTTTAAWAAAAAGAAAAA 481  
 QY 314 AAAAAAGAAACAGCTTTTGAATGCAAGAGGTGATGAGATCTTCAAAATTCGAGCACAG 373  
 DB 480 AAWAAWATAAAGAAWAAATGAAWAAATGAWAAAGWAAAGAAATWTRAAAAAAGAAAA 421  
 QY 374 TTGTAAGCGAACCCACAGTAATGCGATCTTCTACAGTGGCCCAAGAGATATT 433  
 DB 420 AAAAAAGAAAGAAWAGAAWAAWAAAAAAGAAAAATGAAGAGGAAWAAWAAAAATTA 361  
 QY 434 ATACCATGAAGCAACTTGTGTAATGCTTGAATGGGAAACAGCTGACGGTTAAAAAGAG 493  
 DB 360 AWTWAAAAAATGTAAGAGAAWWTAAAAAAGAAAAAARAAWAAWAAAAA 301  
 QY 494 AA 495  
 DB 300 AA 299

RESULT 13  
 AL514085/c 458 bp mRNA linear EST 13-FEB-2001  
 LOCUS  
 DEFINITION AL514085 LTI\_NFL006\_PL2 Homo sapiens CDNA clone CL08A004ZE10 3  
 prime, mRNA sequence.  
 ACCESSION AL514085  
 VERSION AL514085.1 GI:12777579  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 458)  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 Location/Qualifiers  
 1. 458  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CL08A004ZE10"  
 /clone\_lib="LTI\_NFL006\_PL2"  
 /tissue\_type="placenta"  
 /note="Vector: pCWSport 6; Site: 1: NotI; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCWSport 6



vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com

BASE COUNT 186 a 13 c 3 g 207 t 49 others  
ORIGIN

Query Match 5.8%; Score 45.2; DB 9; Length 458;  
Best Local Similarity 42.2%; Pred. No. 13;  
Matches 116; Conservative 14; Mismatches 145; Indels 0; Gaps 0;

QY 68 TTTTATGATTTACTTACTGTTTTTTTATCACCAGATGATGGTCTGAGCACTTTTG 127  
DB 304 TTTTATGATTTACTTACTGTTTTTTTATCACCAGATGATGGTCTGAGCACTTTTG 245

QY 128 CTGTGATCTCATAGAGATTCGTAAGTTCGAAGGAGGAAGTAAACCTTCATGAAGATT 187  
DB 244 TTTTATGATTTTAAAGCAAGGCTGGGNAANNAANNNNNNAANNNNNNTAAAAA 185

QY 188 TTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCTCTCTGA 247  
DB 184 AATAAATAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 125

QY 248 ACTGTGAGGAGATGAGAGGCAATTTTCAAGACCTTTGCAAGGATATAACCTTAAACAAAG 307  
DB 124 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 65

QY 308 AAGAGAAAAAATAAACAGCTTTTGAATGCAAGA 342  
DB 64 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 30

RESULT 14  
AL514657 559 bp DNA linear GSS 20-MAY-1999  
LOCUS AL514657.LTI.NFL006.PL2 Homo sapiens genomic clone RPCI-11-14516,  
DEFINITION prime, mRNA sequence.  
ACCESSION AL514657.1 GI:4344262  
VERSION EST.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Zhao; S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter  
J.C. Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other GSSs: RPCI11-14516.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html  
Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers  
1. .559  
/organism="Homo sapiens"  
/db\_xref="GDB:7555493"

/db\_xref="taxon:9606"  
/clone="RPCI-11-14516"  
/clone\_lib="RPCI-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; Site\_1: ECORI; Site\_2: ECORI;  
RPCI11 Human Male BAC Library"

BASE COUNT 165 a 108 c 110 g 176 t  
ORIGIN

Query Match 5.8%; Score 45.2; DB 12; Length 559;  
Best Local Similarity 48.8%; Pred. No. 13;  
Matches 122; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 90 TTTTCTATCACCAGATGATGGTCTGAGCACTTTTGTGTGTATCTTCTCATGAAGATT 149  
DB 269 TTGACCTATCTCCCACTGATGGTCTACAGTATATTTATTTATCCACATAGTACAG 210

QY 150 GGATAAGTCTCAAGAGAGTAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAA 209  
DB 209 TTTTAGTCTGAGTGCATAGAAATGGACAGTCTTTAGGAGGCTATTTACCTTTT 150

QY 210 GAGATGCAACAAAGAGAGAGATCTTTATCTCTCTGAACTGTGAGGAGATGAGAGGCA 269  
DB 149 TTGCCCTTGAATTTCTGGAAGAAGATCTGCTCTGAAACACAGTATTTCTCAAGAGAAGGCC 90

QY 270 ATTTGAAGACCTTGTCAAGATATTAAGCTTAAACAAAGAGAGAGAGAGAGAGAGAGCCTT 329  
DB 89 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 30

QY 330 TGAATGCA 339  
DB 29 AGAAGTACAA 20

RESULT 15  
AL514657 529 bp mRNA linear EST 13-FEB-2001  
LOCUS AL514657.LTI.NFL006.PL2 Homo sapiens cDNA clone CL08B002ZE09 3  
DEFINITION prime, mRNA sequence.  
ACCESSION AL514657.1 GI:12778151  
VERSION EST.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
JOURNAL Full-length cDNA libraries and normalization  
COMMENT Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1. .529  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CL08B002ZE09"  
/clone\_lib="LTI.NFL006.PL2"  
/tissue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com



BASE COUNT 364 a 20 c 9 g 89 t 47 others  
ORIGIN

Query Match 5.7%; Score 44.6; DB 9; Length 529;  
Best Local Similarity 44.3%; Pred. No. 17;  
Matches 121; Conservative 13; Mismatches 139; Indels 0; Gaps 0;

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Qy 68 TTTTATGCTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCAGCTTTTGTG 127
Db 24 TTTTATGCTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCAGCTTTTGTG 83
Qy 128 CTGTCTATCTTCATAGAGATTCGATAGGTCGAGAGAGAGTAAACCTTCATGAAGATT 187
Db 84 TTTTAAATATATATATATAAAWATTTAAWAAAAAAWATATATAAAATTTTAAAAWYTY 143
Qy 188 TTGTATTCTATAAAAGCTAAAGAGATGCAACAAGGAGAGGATCTTTATCTTGCTGA 247
Db 144 CTTAAAAAAATTTAAAAAAATTTAAAAAAATTTAAAAAAATTTAAAAAAATTTAAAAAA 203
Qy 248 ACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAGGATATAACGTTAAACAAAG 307
Db 204 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 263
Qy 308 AAGAGAAAAAAGAACAGCTTTGAAATGCAAA 340
Db 264 AAAAAAAAAAAAAAAAAAAGGGGCAAAAAAAW 296
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Search completed: May 30, 2002, 01:00:01  
Job time: 22211 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 23:55:51 ; Search time 680.87 seconds

(without alignments)

1974.450 Million cell updates/sec

Title: US-08-982-272-3

Perfect score: 783

Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_032802.\*

- 1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.\*
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- 5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.\*
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- 8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.\*
- 9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.\*
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- 12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.\*
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- 15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.\*
- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.\*
- 17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.\*
- 18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.\*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19 AAV38999	Exemplary CD40 lig
2	773.4	98.8	783	19 AAV39001	Exemplary CD40 lig
3	751	95.9	783	19 AAV38998	CD40 ligand gene u
4	751	95.9	818	19 AAV61062	Murine CD40 ligand
5	749.4	95.7	783	15 AAQ63960	Mouse CD40-L type
6	749.4	95.7	783	19 AAV12853	CD40 ligand coding
7	749.4	95.7	783	20 AA227524	Mouse CD40-L codin
8	745.2	95.2	782	14 AAQ41507	Murine CD40-L DNA
9	648.6	82.8	783	19 AAV42184	Exemplary nucleoti

10	645.2	82.4	1477	22	AAH25527	Nucleotide sequenc
11	632.6	80.8	818	16	AAAT05762	Murine CD40 ligand
12	631.4	80.6	878	20	AAZ27538	Mouse trimeric CD4
13	592.4	75.7	786	15	AAQ63959	Human CD40-L type
14	592.4	75.7	786	19	AAV38997	Human CD40-L gene u
15	592.4	75.7	786	19	AAV12852	CD40 ligand gene u
16	592.4	75.7	840	14	AAQ41506	CD40-L DNA. Homo
17	592.4	75.7	840	15	AAQ67123	CD40 ligand gene.
18	592.4	75.7	840	16	AAAT05763	Human CD40 ligand
19	592.4	75.7	840	18	AAAT33782	CDNA of CD40L, a n
20	592.4	75.7	840	19	AAV61063	Human CD40 ligand
21	592.4	75.7	840	20	AAZ27525	Human CD40-L codin
22	592.4	75.7	879	22	AAAF5539	Nucleotide sequenc
23	592.4	75.7	1816	21	AAAS1745	Human CD40 ligand
24	592.4	75.7	1816	23	AAAS6571	DNA encoding novel
25	591	75.5	840	18	AAAT58122	Human CD40L mutain
26	589.2	75.2	840	15	AAQ57984	Genomic sequence o
27	587.6	75.0	840	16	AAQ94091	Human CD40-L CDNA.
28	582.8	74.4	786	19	AAV39002	Exemplary CD40 lig
29	570	72.8	786	19	AAV39000	Exemplary CD40 lig
30	560.4	71.6	786	19	AAV39003	Exemplary CD40 lig
31	541.2	69.1	864	19	AAV39004	CD40 ligand gene u
32	535	68.3	885	21	AAZ55540	Feline CD154 CDNA.
33	535	68.3	885	21	AAZ55541	Feline CD154 CDNA
34	532	67.9	780	21	AAZ55542	Feline CD154 CDNA
35	532	67.9	780	21	AAZ55543	Feline CD154 CDNA.
36	527	67.3	1878	21	AAZ55534	Canine CD154 CDNA.
37	527	67.3	1878	21	AAZ55535	Canine CD154 CDNA
38	524	66.9	780	21	AAZ55536	Canine CD154 CDNA
39	524	66.9	780	21	AAZ55537	Canine CD154 CDNA
40	454.6	58.1	1552	22	AAH25525	Nucleotide sequenc
41	449.2	57.4	865	22	AAAF82933	HIV-1 gp120 V3 loo
42	449.2	57.4	906	22	AAAF82932	HIV-1 gp120 V3 loo
43	449.2	57.4	2209	22	AAAF82929	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAAF82928	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/FC fu

## ALIGNMENTS

### RESULT 1

AAV38999 ID AAV38999 standard; DNA; 783 BP.

XX AC AAV38999;

XX DT 23-SEP-1998 (first entry)

XX DE Exemplary CD40 ligand gene used in the course of the invention:  
XX DE CD40 ligand; alteration; immunoreactivity; human cell;  
XX DE accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
XX DE autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX OS Chimeric - Mus sp.  
XX OS Chimeric - Homo sapiens.  
XX PN WO9826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

XX

PT Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX  
PS Disclosure: Page 105; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,  
CC comprising nucleotides encoding the extracellular domains (Domains III  
CC and IV) of the murine CD40 ligand gene (AAV38997) operatively linked to  
CC nucleotides encoding the extracellular domains (Domains III and IV) and  
CC transmembrane domain (Domain II) of human CD40 ligand gene (AAV38998).  
CC The sequence is used to exemplify the method of the invention. The  
CC specification describes a method for altering the immunoreactivity of  
CC human cells which comprises introducing a gene encoding an accessory  
CC molecule ligand (AML) into the cells so that the AML is expressed on the  
CC surface of the cells. Vectors containing the AML genes can be used in  
CC gene therapy for treating neoplasia or autoimmune disorders such as  
CC rheumatoid arthritis. They can also be used for vaccination to produce  
CC immunity against a virus cell, bacteria, protein, fungus or neoplasia.  
XX  
SQ Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 100.0%; Score 783; DB 19; Length 783;  
Best Local Similarity 100.0%; Pred. No. 3.8e-210;  
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGCATCTGCGGCCACTGAGTGGCCATCAGC 60  
DB 1 atgacgaaacatacaacaaactctcccgcatctgcgccactgactgcccatacagc 60  
QY 61 ATGAAATTTTATGTTACTTCTTCTTATACCCAGATGTTGGTGCAGCA 120  
DB 61 atgaaatTTTATGTTACTTCTTCTTATACCCAGATGTTGGTGCAGCA 120  
QY 121 CTTTGTGCTGTCTTCTATAGAGATTTGATAAGTTCGAAGAGGAAGTAAACCTTCAT 180  
DB 121 ctttGTGCTGTCTTCTATAGAGATTTGATAAGTTCGAAGAGGAAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATCATAAAAGCTAAAGATGCAACAGAGGAGAGATCTTTATCC 240  
DB 181 gaagATTTTGTATCATAAAAGCTAAAGATGCAACAGAGGAGAGATCTTTATCC 240  
QY 241 TTGCTGAACCTGTGAGGATGAGAGCAATTTGAAGACCTTTGTCAGGATATACCTTA 300  
DB 241 ttgctGAACCTGTGAGGATGAGAGCAATTTGAAGACCTTTGTCAGGATATACCTTA 300  
QY 301 AACAAAGAGAGAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCCTCAA 360  
DB 301 aacaaAGAGAGAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCCTCAA 360  
QY 361 ATTGCGACACACCTTGTAAAGCAAGCAACAGTAAATGTCAGATTCAGTGGGCC 420  
DB 361 attgCGACACACCTTGTAAAGCAAGCAACAGTAAATGTCAGATTCAGTGGGCC 420  
QY 421 AAGAAGGATATTTATCCATGAACCAACTTGTGTAATCTTGAATAAGGAAACAGCTG 480  
DB 421 aagaAGGATATTTATCCATGAACCAACTTGTGTAATCTTGAATAAGGAAACAGCTG 480  
QY 481 ACGGTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCACTTCTGCTCTAATCGG 540  
DB 481 acggTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCACTTCTGCTCTAATCGG 540  
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTGCTGGCTTGGCTGAAGCCAGCATTTGGATCT 600  
DB 541 gagcCTTCGAGTCAACGCCCATTCATCTGCTGGCTTGGCTGAAGCCAGCATTTGGATCT 600  
QY 601 GAGAGATCTTACTCAAGGGGCAAAATACCCAGATTTCTCCAGCTTTGCGAGCAGCAG 660  
DB 601 gagagaTCTTACTCAAGGGGCAAAATACCCAGATTTCTCCAGCTTTGCGAGCAGCAG 660  
QY 661 TCTGTCTACTTGGGCGGAGTGTGTTGAATTACAAAGCTGGTCTCTGTGTTGTCAACGTG 720  
DB 661 tctGTCTACTTGGGCGGAGTGTGTTGAATTACAAAGCTGGTCTCTGTGTTGTCAACGTG 720

DB 661 tctgttacttggcgaggtgtttgaattacaagctgtgtcttctgtgttgcacagctg 720  
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTCCTCTCATCTTTTGGCTTACTCAAACTC 780  
DB 721 actgaagcaagcaagTATCCACAGAGTTCCTCTCATCTTTTGGCTTACTCAAACTC 780  
QY 781 TGA 783  
DB 781 tga 783

RESULT 2

AAV39001

ID AAV39001 standard; DNA; 783 BP.

XX AC AAV39001;

XX 23-SEP-1998 (first entry)

XX Exemplary CD40 ligand gene used in the course of the invention.  
DE  
XX  
XX CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
XX WO9826061-A2.  
XX 18-JUN-1998.  
XX 08-DEC-1997; 97WO-US22740.  
XX 01-DEC-1997; 97US-0982272.  
XX 09-DEC-1996; 96US-0032145.  
XX (REGC) UNIV CALIFORNIA.  
XX Cantwell M, Kipps TJ, Sharma S;  
XX WPI; 1998-348521/30.  
XX Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells; particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX  
XX Disclosure: Page 106; 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,  
CC comprising nucleotides encoding the extracellular domains (Domains III  
CC and IV) and transmembrane domain (Domain II) the murine CD40 ligand gene  
CC (AAV38997) operatively linked to nucleotides encoding the cytoplasmic  
CC domain of the human CD40 ligand gene (AAV38998). The sequence is used to  
CC exemplify the method of the invention. The specification describes a  
CC method for altering the immunoreactivity of human cells which comprises  
CC introducing a gene encoding an accessory molecule ligand (AML) into the  
CC cells so that the AML is expressed on the surface of the cells. Vectors  
CC containing the AML genes can be used in gene therapy for treating  
CC neoplasia or autoimmune disorders such as rheumatoid arthritis. They can  
CC also be used for vaccination to produce immunity against a virus cell,  
CC bacteria, protein, fungus or neoplasia.  
XX  
SQ Sequence 783 BP; 243 A; 161 C; 175 G; 204 T; 0 other;

Query Match 98.8%; Score 773.4; DB 19; Length 783;  
Best Local Similarity 99.2%; Pred. No. 1.9e-207;  
Matches 777; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGCATCTGCGGCCACTGAGTGGCCATCAGC 60  
DB 1 atgacgaaacatacaacaaactctcccgcatctgcgccactgactgcccatacagc 60



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481	QY	ACG	TTAAAGAGAGAGGACTCTATTATGTCTACACTCAAGTCAACCTTCGTCTCTAATCGG	540
481	Db	acg	gttaaaagagaaggaactctattatgtctacactcaagtcaacctctgtcttaacg	540
541	QY	GAG	CTTTCGAGTCAACGCGCCATTTCATCTCGCGGCTCTGGCTGAAGCCGAGCATTCGATCT	600
541	Db	gag	ctcttcgagtcacgcgccattcatcgctcgccctggctgaagcccgagtgagatct	600
601	QY	GAG	AGAACTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTCCGAGCAGCAG	660
601	Db	gag	agaatcttactcaaggcggcaataaccacagttctcccaagcttctgagcagcag	660
661	QY	TC	TGTTCACTTTGGCGGAGTGTGTTGAATTACAGCTGTGCTCTCTGTCTTTGTCACG	720
661	Db	tct	gttctacttggcgaggtttgaattacaagctggtgtctctgtttgttccaacg	720
721	QY	ACT	GAAAGCAAGCAAGTGTCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACT	780
721	Db	act	gaagcaagcgaagtgtccacagagttggcttctcatcttttggcttactcaact	780
781	QY	TGA	783	
781	Db	tga	783	
RESULT 7				
AAZ27524				
ID	AAZ27524 standard; cDNA: 783 BP.			
XX	AAZ27524:			
AC				
XX	13-DEC-1999 (first entry)			
DT				
XX	Mouse CD40-L coding sequence.			
DE				
XX	CD40-L: CD40 receptor ligand; anti-human CD40-L monoclonal antibody;			
KW	binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;			
KW	peripheral blood B cell; proliferation inhibitor; ss.			
OS	Mus sp.			
XX	US5961974-A.			
PN	05-OCT-1999.			
XX	24-MAY-1994; 94US-0249189.			
XX	25-OCT-1991; 91US-0783707.			
PR	05-DEC-1991; 91US-0805723.			
PR	23-OCT-1992; 92US-0969703.			
XX	(TMW ) IMMUNEX CORP.			
XX	Spriggs MK, Fanslow WC, Armitage RJ;			
XX	WPI; 1999-579604/49.			
XX	P-PSDB; AAY39937.			
XX	Anti-human CD40-Ligand monoclonal antibodies -			
PI	Disclosure; Fig 1; 59pp; English.			
XX	This sequence encodes the mouse CD40 receptor ligand (CD40-L). The			
CC	invention relates to anti-human CD40-L monoclonal antibodies M90 se-			
CC	creted by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybrid			
CC	oma hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to C			
CC	cells and the ability of trimeric CD40-L and anti-Immunoglobulin M to in			
CC	duce proliferation of peripheral blood B cells.			
XX	Sequence 783 BP: 243 A; 159 C; 178 G; 203 T; 0 other;			
XX				

Query Match 95.7%; Score 749.4; DB 20; Length 783;

(IMVX) IMMUNEX CORP.

Spriggs MK, Srinivasan S;  
WPI: 1998-144799/13.  
P-PSDB; AA41179.

Soluble oligomeric fusion proteins - comprising leucine zipper fused to extracellular region of transmembrane protein

Example 1; column 23-24; 21pp; English.

This sequence is the coding sequence for the mouse CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the method of the invention. The method is for preparing soluble oligomeric protein by culturing a host cell transfected with a vector for the fusion protein. The soluble oligomeric proteins comprise a leucine zipper fused to the N terminus of the extracellular region of a heterologous mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane protein, where the leucine zipper is a peptide comprising at least part of AA41171 or AA41172, optionally that the peptide trimerises in solution. A substitutions, provided that the peptide trimerises in solution. A soluble fusion protein comprising the leucine zipper of AA41171 linked to the extracellular region of CD40-L (a type II transmembrane protein) that is found on activated T cells and acts as a ligand for the B-cell antigen CD40) stimulates B-cell proliferation and antibody production in a similar manner to membrane-bound CD40-L. A soluble fusion protein comprising the leucine zipper of AA41172 linked to the extracellular region of CD27-L (a type II transmembrane protein) that binds to the lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein) comprising the extracellular region of CD27 and a human IgG1 Fc region) to EBV-transformed B cells expressing CD27-L.

Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match. 95.7%; Score 749.4; DB 19; Length 783;  
Best Local Similarity 97.3%; Pred. No. 1.1e-200; Indels 0; Gaps  
Matches 762; Conservative 0; Mismatches 21;

QY 1 ATGATCGAACATACAAACCAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 60  
DB 1 atgataagaacatacagcaaaccttcccccagatcctgtggcaactggacttccagagc 60  
QY 61 ATGAAATTTTATGATTTTACTGTTTCTTATCACCAGATGATGGGTACGA 120  
DB 61 atgaagattttatgtattactactgttttccctatcccccagaagattggtatctg 120  
QY 121 CTGTTTCTGTGATCTTCATAGAAGATTGGATAAGGTGGAAGGAAGTAAACCTTCAT 180  
DB 121 ctttttctgtgtatcttcataagaagattggataaggttcgaagaggaagtaaaccttcat 180  
QY 181 GAAGATTTTGTATTCATAAAAGCTTAAGAGATGCAACAAAGGAGAAGGATCTTTATCC 240  
DB 181 gaagattttgtattcataaaagagctaaagagatgcaacaaggagaagatctttatcc 240  
QY 241 TTGCTGAACCTGAGGAGATGAGAAGCAATTTCAGACCTTGTCAAGATATAACGTTA 300  
DB 241 ttgctgaactgtgaggagatgagaagcaatttcagaccttgcgaagatatcaagtta 300  
QY 301 AACAAAGAGAAAGAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCA 360  
DB 301 aacaagaagagaaaaaagaaacagctttgaaatgcaagaccttgcgaagatatcaagtta 360  
QY 361 ATTGCAGCACAGTTGTGAAGCGAAGCCAAACAGTATCCAGATCCGTTCTACAGTGGCC 420  
DB 361 attgcagcacagtgtgaagcgaagcgaacagctttgaaatgcaagaccttgcgaagttatcaagttggcc 420  
QY 421 AGAAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATGCTTGAATGGAAATGGAAACAGCTG 480  
DB 421 aagaagagatattatccattgaaagcaacttggtaattgcttgaataatgggaacagctg 480





421 aagaagagatattataccatgaaagcaacttgtaattgcttgaaatgggaacagctg 480  
 481 ACGGTTAAAGAGAGAGGACTCTATATGCTTACACTCAAGTCACTTCTGCTCTAAATCGG 540  
 481 acggttaaagagagagactctattatgcttaccactcaagtcacactctctctataatcg 540  
 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGCCCTCTGGCTGAAGCCGAGCATTTGGATCT 600  
 541 gagccttcagtcacagccattcatcgctcgtcgctgaagccagcagtgatct 600  
 601 GAGAGANTCTTACTCAAGCGGCAATACCCACAGTTCCTCCAGCTTTCGAGCAGCAG 660  
 601 gagagantcttactcaagcggaataaccacagttctccacagcttctgagcagcag 660  
 661 TCTGTTCACTTGGCGGAGCTGTTGAATACAGCTGGTCTGCTGTTGTTGTTCAACTG 720  
 661 tctgttcaacttggcgagagctgttggaattacaagctggtgctctgtgtgtgcaactg 720  
 721 ACTGAAGCAGCAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
 721 actgaagcagcagcaagtatccacagagttggtctctcactcttcttggcttactcaactc 780  
 781 TG 782  
 781 tg 782

RESULT 9  
 AAV42184  
 ID AAV42184 standard; DNA: 783 BP.  
 XX AAV42184;  
 AC AAV42184;  
 XX AAV42184;  
 DT 23-SEP-1998 (first entry)  
 XX Exemplary nucleotide sequence of a chimeric accessory molecule.  
 DE Human; alteration: immunoreactivity; human cell;  
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.  
 XX Chimeric - Homo sapiens.  
 OS Chimeric - Mus sp.  
 XX W09826061-A2.  
 PN 18-JUN-1998.  
 XX 08-DEC-1997; 97WO-US22740.  
 XX 01-DEC-1997; 97US-0982272.  
 PR 09-DEC-1996; 96US-0032145.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Cantwell M, Kipps TJ, Sharma S;  
 PI WPI; 1998-348521/30.  
 XX Vectors containing accessory molecule ligand genes - used for  
 PT altering immunoreactivity of cells, particularly for treatment of  
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
 XX Disclosure; Page 116; 167pp; English.  
 PS The present sequence represents an exemplary nucleotide sequence,  
 CC where nucleotides encoding human domain III have been replaced with  
 CC nucleotide encoding mouse domain III. The sequence is used to exemplify  
 CC the method of the invention. The specification describes a method for  
 CC altering the immunoreactivity of human cells which comprises introducing  
 CC a gene encoding an accessory molecule ligand (AML) into the cells so that  
 CC the AML is expressed on the surface of the cells. Vectors containing the  
 CC AML genes can be used in gene therapy for treating neoplasia or

CC autoimmune disorders such as rheumatoid arthritis. They can also be  
 CC used for vaccination to produce immunity against a virus cell,  
 CC bacteria, protein, fungus or neoplasia.  
 XX Sequence 783 BP; 252 A; 167 C; 156 G; 198 T; 0 other;  
 SO

Query Match 82.8%; Score 648.6; DB 19; Length 783;  
 Best Local Similarity 89.3%; Pred. No. 2.4e-172;  
 Matches 699; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGATCGAATACATACCAAACTTCTCCCGATCTGGCCGACCTGGAGTCCCATCAGC 60  
 Db 1 atgatacgaaatcacaccacacttctcccgatctggccgacctggagtcgcatcagc 60  
 QY 61 ATGAAAATTTTATGTTATTTACTTACTGTTTCTTATCACCAGATGTTGGGTACGA 120  
 Db 61 atgaaaattttattgtatttacttactgtttttcttatcaccagatgattgggtacga 120  
 QY 121 CTTTGTGCTGTATCTTCATAGATTTGGATTAAGGTGGAAGAGAACTTAACCTTCAT 180  
 Db 121 ctttgtgctgtatcttcatagatttggataaaggtcgaagaggaagtaaaccttcat 180  
 QY 181 GAAGATTTTGTATTAATAAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
 Db 181 gaagattttgtattcataaaaaagcttaagagatgcaacaaagagagagattttatcc 240  
 QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAGACCTTGTCAAGGATATAAGCTTA 300  
 Db 241 ttgctgaacctgtgaggagatgagagcaatttgaagaccttgcgaaggatacaagctta 300  
 QY 301 AACAAAG 360  
 Db 301 aacaaag 360  
 QY 361 ATTGAGCAGACAGCTGTGAAGCGAAGCAACAGTAAATGAGAGATCCGTTCTACAGTGGCC 420  
 Db 361 attgagcacatgcatcagaagtgaggccagcagtaaaacacatctgtttacagtggtt 420  
 QY 421 AAGAAGAGATATTATACCATGAAAGCAACTTGTGTAATGCTTGAATAATGGGAAACAGCTG 480  
 Db 421 gaagaagagatattatcaccatgaaagcaacttgtgtaattgcttgaataatgggaaacagctg 480  
 QY 481 ACGGTTAAAG 540  
 Db 481 accgtttaaag 540  
 QY 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGCCCTCTGGCTGAAGCCGAGCATTTGGATCT 600  
 Db 541 gagccttcagtcacagccattcatcgctcgtcgctgaagccagcagtgatct 600  
 QY 601 GAGAGANTCTTACTCAAGCGGCAATACCCACAGTTCCTCCAGCTTTCGAGCAGCAG 660  
 Db 601 gagagantcttactcaagcggaataaccacagttctccacagcttctgagcagcag 660  
 QY 661 TCTGTTCACTTGGCGGAGCTGTTGAATACAGCTGGTCTGCTGTTGTTGTTCAACTG 720  
 Db 661 tctgttcaacttggcgagagctgttggaattacaagctggtgctctgtgtgtgcaactg 720  
 QY 721 ACTGAAGCAGCAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
 Db 721 actgaagcagcagcaagtatccacagagttggtctctcactcttcttggcttactcaactc 780  
 QY 781 TGA 783  
 Db 781 tga 783

RESULT 10  
 AAH25527  
 ID AAH25527 standard; DNA: 1477 BP.  
 XX AAH25527;  
 AC AAH25527;

XX 22-AUG-2001 (first entry)  
 XX Nucleotide sequence of surfactant protein D fused to CD40 ligand.  
 DE  
 XX Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;  
 KW pulmonary surfactant protein D; SPD; immunocompetent cell;  
 KW cell antigenicity; vaccine adjuvant; chimera; ss.  
 XX  
 OS Chimeric - Mus sp.  
 OS Chimeric - Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 32..1444  
 FT CDS /\*tag= a  
 FT sig\_peptide 32..88  
 FT /\*tag= b  
 FT /note= "signal peptide from murine surfactant protein D"  
 XX WO200142298-A1.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 20-MAR-2000; 2000WO-US07380.  
 XX  
 XX 09-DEC-1999; 99US-0454223.  
 XX (KORN/) KORNBLUTH R S.  
 XX Kornbluth RS;  
 XX WPI; 2001-381642/40.  
 XX P-PSDB; AAB84421.  
 XX  
 XX Producing tumor necrosis factor superfamily proteins as multimeric  
 PT ligands fused onto collectin molecules e.g. pulmonary surfactant  
 PT protein D, useful as vaccine adjuvants against infectious agents and  
 PT tumours  
 XX  
 XX Claim 1; Page 65-68; 74pp; English.  
 XX  
 CC The present sequence encodes a fusion protein comprising the mature  
 CC murine surfactant protein D (including hub region, collagenous portion,  
 CC and neck) fused to the murine CD40 ligand extracellular region (including  
 CC stalk). The specification describes a method for constructing stable  
 CC bioactive fusion proteins of the difficult to express tumor necrosis  
 CC factor superfamily (TNFSF) proteins (especially CD40 ligand) as  
 CC multimeric ligands fused onto branched protein backbones such as  
 CC collectin molecules e.g. pulmonary surfactant protein D (SPD). The fusion  
 CC proteins of the invention are useful for stimulating immune response in  
 CC potentially immunocompetent cells (e.g., resting B cells). They are also  
 CC useful for increasing antigenicity of cells such as tumor cells or human  
 CC immunodeficiency virus (HIV) positive cells. They are also useful as a  
 CC vaccine adjuvant since they stimulate B cells, macrophages and dendritic  
 CC cells. Since the large size of the soluble fusion protein makes them  
 CC less likely to diffuse into the circulation, they can be advantageously  
 CC used as a vaccine adjuvant or tumor immunotherapy agent, injected locally  
 CC to prevent them from diffusing away. Also, the TNFSF-collectin fusion  
 CC proteins present new possibilities for the expression of highly active,  
 CC multimeric, soluble TNFSF members. CD40L was a powerful stimulant for  
 CC macrophages and dendritic cells.  
 XX  
 XX Sequence 1477 BP; 418 A; 339 C; 421 G; 299 T; 0 other;  
 SQ  
 Query Match 82.4%; Score 645.2; DB 22; Length 1477;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-171;  
 Matches 647; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 134 ATCTTCATAGAGATTGGTAAGCTGAAGAGGAAGTAACCTTCATCAAGATTTCAT 193  
 || |||||  
 Db 795 atggccatagaagattggataaggtcgaaaggaaggaacccctcatgaagatttgat 854

QY 194 TCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTTGTGTAACGTG 253  
 |||||  
 Db 855 tcataaaaaagctaaagagatgcaaaaggaagagatctttatccttctgctgaacgtg 914  
 QY 254 AGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGAGTATATAACCTTTAAACAAGAGAGA 313  
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 Db 915 aggagatgagaaggaagcaatttgaagacctgtcaagagataataacgttaacaaagaagaga 974  
 QY 314 AAAAAGAAACAGCTTTGAAATGCAAAAGAGGTGATGAGGATCTCAATATGCACACACG 373  
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 Db 975 aaaaagaaaacagctttgaaatgcaagaggtgatgaggatcctcaattgacgacacg 1034  
 QY 374 TTGTAAGCGAAGCCAACAGTAATGACAGCATCCGTTCTACAGTGGCCCAAGAAAGATATT 433  
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 Db 1035 ttgtaagcgaagccaaacagtaattgacagcctgtttcacagtgggccaagaagatatt 1094  
 QY 434 ATACCATGAAGAACAACCTTGGTAATGCTTGAATGGAAGAAACAGCTGACGGTTAAAGAG 493  
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 Db 1095 ataccatgaaaagcaacttgtaattgcttgaaatgggaaacagctgacggttaaaagag 1154  
 QY 494 AAGGACTCTATTATGCTACACTCAAGTCACTTCTCTCTTAATCGGAGCCTTCGAGTC 553  
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 Db 1155 aaggactctattatgctcacactcaagtcacacttctctcttaacggtgagccttcgagtc 1214  
 QY 554 AACGCCCATTCATCGTCGGCTCTGCTGAGCCAGCAGCATTTGGATCTGAGAGAACTCTTAC 613  
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 Db 1215 aagccattcatcgctgcgctctgctgctgaagccagcattggtatcgagaaatcttac 1274  
 QY 614 TCAGGCGGCAATACCACAGTTCTCCAGCTTTCCAGCTTTGGAGCAGCAGCTGTCTTCACTTGG 673  
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 Db 1275 tcaaggcggcaaataccacagttctccacagcttgcgagcagcagctgttctacttgg 1334  
 QY 674 GCGGAGTGTGTAATTACAGCTGCTGCTCTGCTGTTGTGTTGTTCAACGCTGACTGAACCAAGCC 733  
 |||||  
 Db 1335 gcggagcgtttgtaattacaagcgtggtgctctctgctgttgcacagtgactgaagcaagcc 1394  
 QY 734 AAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTTACTCAAACTCTGA 783  
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 Db 1395 aagtgatccacagagttggcttctcatctctttgtggttactctcaactctga 1444  
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 ID AAT05762 standard; DNA; 818 BP.  
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 AC AAT05762;  
 XX  
 DT 18-MAR-1996 (first entry)  
 XX  
 DE Murine CD40 ligand DNA.  
 XX  
 KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;  
 KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;  
 KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 13..795  
 FT CDS /\*tag= a  
 FT  
 XX WO9529935-A1.  
 XX  
 XX 09-NOV-1995.  
 XX  
 XX 28-APR-1995; 95WO-US05448.  
 XX  
 XX 28-APR-1994; 94US-0234580.  
 XX  
 XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX Castle BE, Kehry M;  
 XX

QY	151	GATAAGCTCGAAGAGGAAGTAAACCTTCATGAGATTTTGTATTATATAAAGAGCTTAAG	215
Db	225	gataaggtcgaaagagaagtataaccttcataagattttgtattcataaaagctcaag	284
QY	211	AGATGCAACAAGGACAAGATCTTTATCCCTTGCTGAACCTGTGAGAGATGTAGAAGGCAA	270
Db	285	agatgcacacaagagaagagctcttataccttctgaacctgtgaggagatgagaagggcaa	344
QY	271	TTTCAACACCTTGCTCAAGGATATACGTTTAAACAAGAGAGAAAAGAAAACAGCTTT	330
Db	345	tttgaagacctgtcaaggatataaacgtttaacaaagagaagaaaaagaaacagcttt	404
QY	331	GAATGCAAGAGGCTGATGAGNATCTCTAAATTCAGCACACAGCTTGTAAAGCGAAGCAAC	390

Db 405 gaaatcgaagaggtgatgagatcctcaaatgagcacacgctgtgtaagcgaagccaac 464  
 Qy 391 AGTAATGAGCATCCGTTCTACAGTGGCCCAAGAAAGGATATTATACCATGAAAGCAAC 450  
 Db 465 agtaatgcagcatccgttctacagtgaggcaagaaagatattataccatgaaagccaac 524  
 Qy 451 TTGGTAATGCTTGAATGGAACAGCTGACGCTTAAAGAGAGAGAGACTCTATTAATGTC 510  
 Db 525 ttggtaatgcttgaatggaagacagctgacggtttaaagagagagagactctattatgc 584  
 Qy 511 TACACTCAAGTCACTCTGCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCCTC 570  
 Db 585 tacactcaagtcaccttctgcttaatacggagccttcgagtcacgcccattcatcgtc 644  
 Qy 571 GGCCTCTGGCTGAAGCCAGCATTTGGATCTGAGAGAAATCTTACTCAAGCGGCAAAATACC 630  
 Db 645 ggcctctggctgaagccagcagtgatctgagagaatcttactcaagcggaataacc 704  
 Qy 631 CACAGTTCCTCCAGCTTTGGAGAGCAGCTGTTTCACTTTGGGGGAGTGTGTTGAATTA 690  
 Db 705 cacagttctccagcttggcagcagcagctgttctcacttggcggaggtgttgaatta 764  
 Qy 691 CAAGCTGTGCTTCTGCTTTGTTCAACGTGACTGAGCAAGCCCAAGTGTATCCACAGATT 750  
 Db 765 caagctgtgtctctgttctgacagtgactgactgaagcaagccaagtgatccacagatt 824  
 Qy 751 GCCTTCTCATCTTTGGCTTACTCAAACTCTGA 783  
 Db 825 ggcctctcatcttttggcttactcaaaactctga 857

RESULT 13

AAQ63959  
 ID AAQ63959 standard; cDNA to mRNA; 786 BP.  
 XX AC AAQ63959;  
 XX DT 11-JAN-1995 (first entry)  
 DE Human CD40-L type II transmembrane protein coding sequence.  
 KW Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;  
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;  
 KW soluble CD40-L; tumour necrosis factor family; ss.  
 XX OS Homo sapiens.  
 XX FH Location/Qualifiers  
 FT CDS 1..786  
 FT /\*tag= a  
 FT /product= human\_CD40-L  
 FT /note= "nucleotides 148-783 code for the  
 FT extracellular region (amino acids 50-261)."  
 XX W09410308-A.  
 XX 11-MAY-1994.  
 XX 20-OCT-1993; 93WO-US10034.  
 XX 23-OCT-1992; 92US-0969703.  
 XX 13-AUG-1993; 93US-0107353.  
 XX (IMMUNEX CORP.  
 XX Spriggs MK, Srinivasan S;  
 XX WPI; 1994-167465/20.  
 XX P-PSDB; AAR53969.  
 XX Prepn. of soluble oligomeric mammalian proteins - using host  
 XX cells to express a fusion protein comprising a leucine zipper  
 XX domain and a heterologous mammalian protein

XX Example 1; Page 22-23; 35pp; English.  
 PS A DNA fragment encoding the extracellular (soluble) region of human  
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding  
 CC for a leader peptide, a 33 amino acid leucine zipper sequence  
 CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the  
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L  
 CC in the supernatant. The leucine zipper sequence spontaneously  
 CC trimerises in solution and fusion proteins comprising  
 CC the sequence fused to a heterologous mammalian protein, also form  
 CC oligomers.

XX Sequence 786 BP; 250 A; 168 C; 200 T; 0 other;

Query Match 75.7%; Score 592.4; DB 15; Length 786;

Best Local Similarity 85.5%; Pred. No. 1.5e-156;

Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGCACTGGAGCTGCCATCAGC 60  
 Db 1 atgatcgaacatacaacaaacttctcccgatctgcgccactggactgccatcagc 60  
 Qy 61 ATGAAATTTTATGTATTTACTTTACTGTTTCTTTATACCCAGATGATGGGTACGA 120  
 Db 61 atgaaaattttatgtatttacttactgttttcttaccaccagatgattgggtcagca 120  
 Qy 121 CTTTGTGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGAGAGTAACCTTCAT 180  
 Db 121 ctttgtgctgtatcttcataagaaggttgacaagatagaagatgaagaagatcttc 180  
 Qy 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAAGAGAGAGAGATCTTTATCC 240  
 Db 181 gaagattttgtattcatgaaacacacacacacacacacacacacacacacacacac 240  
 Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAGACCTTGTCAAGGATATACGTTA 300  
 Db 241 ttactgaactgtgaggagattaaagccagtttgaaggttgaaggtataatgta 300  
 Qy 301 AACAAAGAGA---GAAAGAGAGAGAGAGTTCGAAAGAGAGAGAGAGATCCT 357  
 Db 301 aacaaagagagacagaaagaaacacagcttgaaatgcaaaaggtgatcagaatcct 360  
 Qy 358 CAATTTGACGACACGCTTGTAAAGCAACACATANTGACGATCCGTTCTACAGTGG 417  
 Db 361 caaattgcgcacatgtcataagtgaggccagcagtaaaacacacacacacacacac 420  
 Qy 418 GCCAAGAAAGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAAGTGGGAACAG 477  
 Db 421 gctgaaagagatactac 480  
 Qy 478 CTGACGGTTAAAGAGAGAGGACTCTATTATGCTACACTCAAGTCACTTCGCTCTAAT 537  
 Db 481 ctgaccgttaaaagacaaggtctattatctatgcccagtcacacctctctgtcccat 540  
 Qy 538 CGGAGCCTTCGAGTCAACGCCCATTCATCGTTCGCCCTCTGGCTGAAGCCAGCATTTGA 597  
 Db 541 cggaagcttcagtcagtcacacacacacacacacacacacacacacacacacacac 600  
 Qy 598 TCTGAGAGAAATCTTACTCAAGCGGCAATATCCACAGTTCCTCCACGCTTTGCCAGCAG 657  
 Db 601 ttcgagagaatcttactcagagctgcaataccacacacacacacacacacacacacac 660  
 Qy 658 CAGTCTGTTCACTTGGCGGAGTGTGTAATATACAGTGGTGTCTGTCTTCTCAAC 717  
 Db 661 caatccattcacttgggagagattattgaattgcaacacaggtgtctgtgttgcacat 720  
 Qy 718 GTGACTGAAGCAAGCAAGTGTATCCACAGTGTGCTTCTCATCTTTTGGCTTACTCAA 777  
 Db 721 gtgactgatcccaagccaagtgagccatggcactggcttcaagctctcttggcttactcaaa 780  
 Qy 778 CTCTCA 783



PR 13-AUG-1993; 93US-0107353.

XX (IMM ) IMMUNEX CORP.

XX Spriggs MK, Srinivasan S;

PI WPI; 1998-144799/13.

DR P-PSDB; AAW41178.

XX Soluble oligomeric fusion proteins - comprising leucine zipper fused  
PT to extracellular region of transmembrane protein

XX Example 1; column 19-20; 21pp; English.

This sequence is the coding sequence for the human CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the method of the invention. The method is for preparing soluble oligomeric protein by culturing a host cell transfected with a vector for the fusion protein. The soluble oligomeric proteins comprise a leucine zipper fused to the N terminus of the extracellular region of a heterologous mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane protein, where the leucine zipper is a peptide comprising at least part of AAW41171 or AAW41172, optionally with conservative amino acid substitutions, provided that the peptide trimerizes in solution. A soluble fusion protein comprising the leucine zipper of AAW41171 linked to the extracellular region of CD40-L (a type II transmembrane protein that is found on activated T cells and acts as a ligand for the B-cell antigen CD40) stimulates B-cell proliferation and antibody production in a similar manner to membrane-bound CD40-L. A soluble fusion protein comprising the leucine zipper of AAW41172 linked to the extracellular region of CD27-L (a type II transmembrane protein that binds to the lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein comprising the extracellular region of CD27 and a human IgG1 Fc region) to EBV-transformed B cells expressing CD27-L.

XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 75.7%; Score 592.4; DB 19; Length 786;  
Best Local Similarity 85.5%; Pred. No. 1.5e-156;  
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

QY 1 ATGATCGAACAATACAAACACTTCTCCCGACTGCGCCACTGGACTGCCCATCAGC 60  
DB 1 atgacgaaacatacaacaaactctcccgactgctgcccactggactgccatcagc 60

QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCATCCACAGATGATTGGGTCAGCA 120  
DB 61 atgaaattttatgtatttacttactgttttcttattcattcaccacagatgattgggtcagca 120

QY 121 CTTTTCGTCTGCTATCTTCATAGAGATTGGATAAGGTGCAAGAGAGAACTTTCAT 180  
DB 121 cttttcgtctgctatcttcatagaagggttggaacagatagaagatgaaaggaaatcttc 180

QY 181 GAAGATTTTGTATCATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
DB 181 gaagattttgtattcatgaacacgatacagatgcaacacagagagaaagatccctatcc 240

QY 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAGACCTTGTCAAGGATATACGTTA 300  
DB 241 ttactgaactgtgagagattaaagccagtttgaaggcttctgtgaaggatataatgtta 300

QY 301 AACAAAGAAGA--GAAAGAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCCT 357  
DB 301 acaaaagagagacgaagaagaagaacacagctttgaaatgcaaaaaggtgatcagaatcct 360

QY 358 CAAATTCAGCAGCAGCTTGAAGCGAAGCAACAGTAATGACAGATCCCTTCTACAGTG 417  
DB 361 caaattgcgacatgtcataagtgagggccagcagtaaaacacatctgtgttacagtgg 420

QY 418 GCCAAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTTGAAATGGAAACAG 477  
DB 418 gccaagaaaggatattataccatgaaagcaacttgggttaattgctttgaaatggaaacag 477

DB 421 gctgaaaaggatatactacaccatgagcaacaacttggtaacctggaaaaatgggaaacag 480  
QY 478 CTGACGGTTAAAGAGAGAGAGGACTCTATTATGCTACACTCAAGTCACTTCTGCTCTAAT 537  
DB 481 ctgaccgttaaaagacaaggactctattatctatgcaccaagtcacacctctctgttccaat 540  
QY 538 CGGAGACCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCAGCATTTGA 597  
DB 541 cgggaagcttcagagtcaggctccatttatagcagcctctgctaaagtcctcccccggtaga 600  
QY 598 TCTGAGAGAACTTACTCAAGGCGGCAATACCCACAGTTCCTCCAGGTTTGGCAGAGCAG 657  
DB 601 ttcgagagaatcttactcagagctgcaaataccacagttccgccaacaccttgcgggcaa 660  
QY 658 CAGTCTGTTCACCTGGGCGGAGTGTGTAATTACAGCTGGTCTCTCTGTTCTGTCACAC 717  
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QY 718 GTGACTGAAGCAAGCAAGTGTATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAA 777  
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QY 778 CTCTGA 783  
DB 781 ctctga 786

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Job time: 11236 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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72:	/cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
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74:	/cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
75:	/cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	783	100.0	783	13	US-08-982-272-3
2	773.4	98.8	783	13	US-08-982-272-5
3	751	95.9	783	3	US-07-969-703B-1
4	751	95.9	783	13	US-08-982-272-2
5	751	95.9	818	6	US-08-234-580-1
6	749.4	95.7	783	3	US-07-969-703A-1
7	749.4	95.7	783	5	US-08-107-353-5
8	749.4	95.7	783	8	US-08-477-733A-1
9	749.4	95.7	783	8	US-08-484-624-1
10	749.4	95.7	783	11	US-08-770-981-1
11	749.4	95.7	783	14	US-09-088-913-1
12	749.4	95.7	783	17	US-09-322-021-1
13	749.4	95.7	783	17	US-09-322-021A-1
14	749.4	95.7	783	17	US-09-365-940-1
15	749.4	95.7	783	17	US-09-365-940A-1
16	749.4	95.7	783	17	US-09-392-618-1
17	749.4	95.7	783	17	US-09-399-106-1
18	749.4	95.7	1209	75	US-60-360-207-9611
19	749.4	95.7	1250	37	US-10-090-238-3
20	748	95.5	780	3	US-07-783-707A-1
21	748	95.5	780	3	US-07-805-723-1
22	648.6	82.8	783	13	US-08-982-272-20
23	645.2	82.4	1477	18	US-09-454-223-5
24	631.4	80.6	878	8	US-08-477-733A-22
25	631.4	80.6	878	8	US-08-484-624-22
26	631.4	80.6	878	11	US-08-770-981-22
27	631.4	80.6	878	14	US-09-088-913-22
28	631.4	80.6	878	17	US-09-322-021-22
29	631.4	80.6	878	17	US-09-322-021A-22
30	631.4	80.6	878	17	US-09-365-940-22
31	631.4	80.6	878	17	US-09-365-940A-22

## ALIGNMENTS

CORRESPONDENCE ADDRESS:

```

:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: 3.5" Diskette,
: MEDIUM TYPE: 1.44 Mb storage
:
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Fastseq version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/982,272
: FILING DATE:
:

```

CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96

ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs  
TYPE: nucleic acid

```

STRANDEDNESS: single
TOPOLOGY: linear

```

US-08-982-272-3

Query Match 100.0%; Score 783; DB 13

Best Local Similarity 100.0%; Pred. No. 3.6e-18

```

RESULT      2
US-08-982-272-5
; Sequence 5, Application US/08982272
; GENERAL INFORMATION:
; APPLICANT: Kipps, Thomas J.
; APPLICANT: Sharma, Sanjai
; APPLICANT: Cantwell, Mark
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING ACCESSORY
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-
; TITLE OF INVENTION: MODULATION AND TREATMENT OF
; TITLE OF INVENTION: MALIGNANCIES
; NUMBER OF SEQUENCES: 44

```









	Query Match	95.7%	Score 749.4;	DB 8;	Length 783;
	Best Local Similarity	97.3%;	Pred. No. le-177;		
	Matches 762;	Conservative	0; Mismatches	21; Indels	0; Gaps
Qy	1	ATGTCGAACCATACAACAAACTTCTCCCGAGTCTGGCGCACTGGACTGCCCATCAGC	60		
Dd	1	ATGATAGAACCATACAGCCAACCTTCCCCAGATCCGTGGCACTGGACTTCCAGCGAGC	60		
Ov	61	ATGAATATTTTTTATGTATTTACTTACTCTTTTTTCTTATCACCCAGATGATTGGGTCAGCA	120		











Db 781 TGA 783

111

RESULT 12

US-09-322-021-1

Sequence 1, Application US/09322021

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/322,021

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/249,189

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEetical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: MOUSE

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783

US-09-322-021-1

Query Match 95.78; Score 749.4; DB 17; Length 783;

Best Local Similarity 97.38; Pred. No. 1e-177;

Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCAAAACATACAAACAACTTCTCCCGATCTCGGCCACTGCACTGCCCATCAGC 60

Db 1 ATGATCAAAACATACAAACAACTTCTCCCGATCTCGGCCACTGCACTGCCCATCAGC 60

QY 61 ATGAAAAATTTTATGTATTTTACTTCTTCTTCTTATCAACCCAGATGATTTGGTCTAGCA 120

Db 61 ATGAAAAATTTTATGTATTTTACTTCTTCTTCTTATCAACCCAGATGATTTGGTCTAGCA 120

QY 121 CTTTCTCTGTGTATCTTATAGAGATTTGGATAGGTCGGAAGGAGGAGTAACCTTCAT 180

Db 121 CTTTCTCTGTGTATCTTATAGAGATTTGGATAGGTCGGAAGGAGGAGTAACCTTCAT 180

QY 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATTC 240

Db 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATTC 240

QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300

Db 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300

QY 301 AACAAAGAAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCAA 360

Db 301 AACAAAGAAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCAA 360

QY 361 ATTCAGCACACGTTGTAAGCGAAGCAACAGTAATGCAGATCCGTTCTACAGTGGGCC 420

Db 361 ATTCAGCACACGTTGTAAGCGAAGCAACAGTAATGCAGATCCGTTCTACAGTGGGCC 420

QY 421 AAGAAAGATATTTATACCATGAAAGCAACTTGTATGCTTGAATGCTGGAATGGAAACAGCTG 480

Db 421 AAGAAAGATATTTATACCATGAAAGCAACTTGTATGCTTGAATGCTGGAATGGAAACAGCTG 480

QY 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTCTTAATCGG 540

Db 481 ACGTTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTCTTAATCGG 540

QY 541 GAGCCTTCGAGTCAAGCGGCAATTCATGTCGGCCCTCTGGCTGAGAGCCAGCATGGATCT 600

Db 541 GAGCCTTCGAGTCAAGCGGCAATTCATGTCGGCCCTCTGGCTGAGAGCCAGCATGGATCT 600

QY 601 GAGAGATCTTACTCAAGCGGCAATTCATGTCGGCCCTCTGGCTGAGAGCCAGCATGGATCT 660

Db 601 GAGAGATCTTACTCAAGCGGCAATTCATGTCGGCCCTCTGGCTGAGAGCCAGCATGGATCT 660

QY 661 TCTGTTTCACTTGGCGGAGTGTGTAATTAACAAGTGGTGTCTCTGTTTGTCAACGTG 720

Db 661 TCTGTTTCACTTGGCGGAGTGTGTAATTAACAAGTGGTGTCTCTGTTTGTCAACGTG 720

QY 721 ACTGAAGCAAGCAAGTGTATCCAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780

Db 721 ACTGAAGCAAGCAAGTGTATCCAGAGTGGCTTCTCATCTTTGGCTTACTCAAACTC 780

QY 781 TGA 783

Db 781 TGA 783

RESULT 13

US-09-322-021A-1

Sequence 1, Application US/09322021A

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON





Thu May 30 05:46:03 2002

```

|||||
Db 181 gaagatttctgtattataaaagtaagagatgcaaaagagagagatttattcc 240
QY 241 TTGCTGAACGTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAGGATATAACGTTA 300
Db 241 ttgctgaactgtgagagatgagaaggcaatttgaagaccttgtcaaggaataacgtta 300
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 acaaaagagagagagagagagagagagagagagagagagagagagagagagagag 360
QY 361 ATTGCAGCACACGTTGTAAAGCGAAGCCACAGTAATGCGAGCATCCGTTCTACAGTGGCC 420
Db 361 attgcagcacacgttgtaaagcgaagcgaacagtaatgcagcatccgtttctacagtggcc 420
QY 421 AAGAAAGGATATATACCATGAAAGCAACTTGTTAAATGCTTGAATAATGGGAAACAGCTG 480
Db 421 aagaagagatattataccatgaaagcaacttggtaattgcttgaataatgggaacagctg 480
QY 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 acggttaaagagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCTCTGGCTGAAGCCAGCATTTGGATCT 600
Db 541 gagccttcgagtcaacgcccaattcatcgtcggctctggctgaagccagcagtgatct. 600
QY 601 GAGAGAACTTTACTCAAGCGCGCAAAATACCCACAGTTCTCCAGCTTCCGAGCAGCAG 660
Db 601 gagagaactcttactcaaggcggcaaataccacagttctccagcttgcgagcagcag 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGTGCTTCTGTTGTTGTCACAGTG 720
Db 661 tctgttcaacttggcgagggtgttgtaattacaagctgtgcttctgttgcacacgtg 720
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 actgaagcaagcgaagtgtatccacagagttggcttctcatcttttggcttactcaactc 780
QY 781 TGA 783
Db 781 tga 783

```

Search completed: May 30, 2002, 05:22:46  
Job time: 18645 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:26 ; Search time 627.19 Seconds  
(without alignments)  
1310.273 Million cell updates/sec

Title: US-08-982-272-3  
Perfect score: 783  
Sequence: 1 ATGATCGAATACATACACCA.....TTGGCTTACTCAACTCTGA 783

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	749.4	95.7	1250	5	US-09-053-375B-821
2	592.4	75.7	1816	5	US-09-053-375B-226
3	592.4	75.7	1816	5	US-09-442-384B-457
4	315	40.2	508	5	US-09-911-904-131
5	155.8	19.9	2395	5	US-09-875-453A-9
6	41.6	5.3	2865	6	US-10-027-632-111808
7	39.2	5.0	123157	6	US-10-027-632-179264
8	38.4	4.9	45698	6	US-10-105-299-12515
9	38.4	4.9	68566	5	US-09-830-706B-37
10	38	4.9	476	6	US-10-027-632-187249
11	38	4.9	476	6	US-10-027-632-187250
12	38	4.9	685	6	US-10-027-632-35082
13	37.6	4.8	349	5	US-09-721-544-11180
14	37	4.7	1758	6	US-10-071-192-29
15	36.6	4.7	341	5	US-09-789-189-555
16	36.6	4.7	57649	6	US-10-105-299-9151
17	36.6	4.7	57649	6	US-10-105-299-10646
18	36.6	4.7	57649	6	US-10-105-299-14274
19	36.2	4.6	2430	6	US-10-105-694-1
20	36.2	4.6	2430	6	US-10-105-695-1
21	36.2	4.6	2430	6	US-10-106-014-1
22	36.2	4.6	3321	5	US-09-919-002-413
23	36	4.6	1379	6	US-10-027-632-199307
24	35.8	4.6	598	6	US-10-027-632-207524
25	35.8	4.6	2580	6	US-10-027-632-258659
26	35.6	4.5	626	6	US-10-027-632-239684

Sequence 1404, Ap  
Sequence 499, App  
Sequence 8655, Ap  
Sequence 219364,  
Sequence 219365,  
Sequence 233265,  
Sequence 233265,  
Sequence 141134,  
Sequence 380, App  
Sequence 270, App  
Sequence 362, App  
Sequence 362, App  
Sequence 85186, A  
Sequence 85187, A  
Sequence 46525, A  
Sequence 46526, A  
Sequence 210428,  
Sequence 200394,  
Sequence 228875,  
Sequence 233425,

## ALIGNMENTS

RESULT 1  
US-09-053-375B-821  
; Sequence 821, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; CURRENT APPLICATION NUMBER: US/09/053.375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 821  
; LENGTH: 1250  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-053-375B-821

Query Match 95.7%; Score 749.4; DB 5; Length 1250;

Best Local Similarity 97.3%; Pred. No. 7.9e-183;

Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGATCGAATACATACACCAACTTCTCCCGATCTGGCGCACTGGAGTGGCCATCAGC 60  
Db 13 atgataaatacagcaaccttccccagatccgtggcaactggacttccagcgagc 72  
Qy 61 ATGAAATTTTATCTATTACTTACTTCTTTTCTTATCACCAGATGATTGGTGCAGCA 120  
Db 73 atgaagattttatgtattacttactgttttcttattaccaccaaatgatgactgtg 132  
Qy 121 CTTTTGCTGTGATCTTCATAGAGATGGATAGGTCGAAGAGAGAACTTCAAT 180  
Db 133 ctttttgcgtgtatcttctcctagaaagattgataaggctcgaaggaggaataaaccttcat 192  
Qy 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAGAGAGAGAGATCTTTATCC 240  
Db 193 gaagattttgtattcataaaaaagctaaagagatgcaacaaggagagatctttatccc 252  
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300  
Db 253 ttgctgaactgtgagagatgagaaggcaatttgagaccttgtcgaagataaagttta 312  
Qy 301 ACAAAG 360  
Db 313 acaagaag 372  
Qy 361 ATTGCAGCACAGTGTGTAAAGCAAGCAACAGTATGAGCATCGTCTACAGTGGGCC 420  
Db 361 ATTGCAGCACAGTGTGTAAAGCAAGCAACAGTATGAGCATCGTCTACAGTGGGCC 420

Db 373 attgcagcacacgttgaagcgaagcccaacagtaatgcagcatccgtttctacagtgggcc 432  
Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTTGAAATGGGAACAGCTG 480  
Db 433 aagaagagataattataccatgaaagcaactggtaagtcttgaaaaaggaacagctg 492  
Qy 481 ACGTTAAAGAGAGGACTCTATTATGTCTACACTCAAGTCACCTTCTGCTCTAATCGG 540  
Db 493 acggttaaaagagaagactattatgtctacactcaagtccacttctgctctaactcg 552  
Qy 541 GAGCCTTCGAGTCAACGCCATTCATCGTCGGCCTCTGCTGAAAGCCAGCAATTCGATCT 600  
Db 553 ggccttcagtgcaacgcgccattcatcgtcgccctgctgctgaagcagctggatct 612  
Qy 601 GAGAGAATCTTACTCAAGCGGCAATACCCACAGTTCCTCCAGCTTTCAGGAGCAGCAG 660  
Db 613 gagagaatcttactcaaggcggcaaataccacagttctccacagcttgcgagcagcag 672  
Qy 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTACAAGCTGGTGTCTTCTGTTGTCAACGTG 720  
Db 673 tctgttcaacttggcgagtggtttgaattacaagctgggtctctgtgttgcacagtg 732  
Qy 721 ACTGAAGCAAGCAAGTGATGCCACAGAGTGGCTTCTCAATCTTTGGCTTACTCAAACTC 780  
Db 733 actgaagcaagccaagtgatccacagagttggcttctcatctttgtggttactcaaatc 792  
Qy 781 TGA 783  
Db 793 tga 795  
RESULT 2  
US-09-053-375B-226  
; Sequence 226, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-226

Query Match 75.7%; Score 592.4; DB 5; Length 1816;  
Best Local Similarity 85.5%; Pred. No. 1.8e-142;  
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;  
Qy 1 ATGATCGAAACATACCAACCAACTCTCCCGCATCTGGCGCACTGACGATGCCCATCAGC 60  
Db 40 atgatcgaaacatacaacaaactctcccgcatctg9gccaactgactg9cccatcagc 99  
Qy 61 ATGAAATTTTATGTAATTTACTTCTTTTCTTATCATCCAGATGATGGGTGACGA 120  
Db 100 atgaataattttatgtatttacttactgtttttcttatccacagagattggtgacga 159  
Qy 121 CTTTTTGTGTATCTTATAGATGATGATAGGTGCGAAGAGAGATTAACCTTCAT 180  
Db 160 ctttttgtgtatcttctcagaaggttggacaagaLagaagatgaaaggaatcttcat 219  
Qy 181 GAAGATTTTGTATTTATTAAGCAAGTCAACCAAGGAGAGAGATCTTTATCC 240  
Db 220 gaagatttttattcatgaaacagacagagatgcaacagagagaaagatccctatcc 279  
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGGTA 300  
Db 280 ttactgaactgtgagagagattaaagccagtttgaagcgttggagagataataatgta 339

Qy 301 AACAAAGAAGA---GAAAAAGAAACACAGCTTTGAAATGAAAGAGGTGATGAGATCCT 357  
Db 340 aacaaagagagacgagaaagaaacacagctttgaaatgcaaaagtgatcagaatcct 399  
Qy 358 CAATTCGACACACAGCTTGTAAAGCAAGCCAAACAGTAATGAGCATCCGTTCTACAGTG 417  
Db 400 caattggcgacatgtcataagtgaaggcagcagtaaaacaacatctgtttacagtgg 459  
Qy 418 GCCAAGAAAGATATTATACCATGAAAGCAACTTGTGTAATGCTTTGAAATGGGAACAG 477  
Db 460 gctgaaagagataactacacatgagcaacacttgtaacccttg9aaatg9gaaacag 519  
Qy 478 CTGACGGTTAAAGAGAGAGAGACTCTATTATGCTTACACTCAAGTCAACCTTCTGCTCTAAT 537  
Db 520 ctgaccgttaaaagacaagagactattatatactatgcccgaagtcacactctgttccaat 579  
Qy 538 CGGAGACCTTCGAGTCAACGCCCTTCATCGTCGGCCTCTGCTGAAAGCCAGCATTGGA 597  
Db 580 cgggaagcttcgagtcgaagctccatttatagccagcctctcctaaagtcccccggtaga 639  
Qy 598 TCTGAGAAATCTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTTGGAGAGCAG 657  
Db 640 ttcgagagaatcttactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699  
Qy 658 CAGTCTGTTCACCTTGGCGGAGTGTGTTGAATTAACAGCTGGTCTGCTGTTGTCTAAC 717  
Db 700 caatccattcacttgggagagatttgaattgcaaccaggtgcttcggtctgttccaat 759  
Qy 718 GTGACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGTCTTACTCAA 777  
Db 760 gtgactgatccaaagcgaagtgcacatgagccatggaactggttcaactgttcttactcaaa 819  
Qy 778 CTCTGA 783  
Db 820 ctctga 825  
RESULT 3  
US-09-442-384B-457  
; Sequence 457, Application US/09442384B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashev, Matvey  
; TITLE OF INVENTION: Hematology/Immunology Array  
; FILE REFERENCE: CLON-006CIP15  
; CURRENT APPLICATION NUMBER: US/09/442,384B  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 830  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-442-384B-457

Query Match 75.7%; Score 592.4; DB 5; Length 1816;  
Best Local Similarity 85.5%; Pred. No. 1.8e-142;  
Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;  
Qy 1 ATGATCGAAACATACCAACCAACTCTCTCCCGCATCTGGCGCACTGACGATGCCCATCAGC 60  
Db 40 atgatcgaaacatacaacaaactctcccgcatcttcccgcatctg9gccaactgactg9cccatcagc 99  
Qy 61 ATGAAATTTTATGTAATTTACTTCTTTTCTTATCATCCAGATGATGGGTGACGA 120  
Db 100 atgaataattttatgtatttacttactgtttttcttatccacagagattggtgacga 159  
Qy 121 CTTTTTGTGTATCTTATAGATGATGATAGGTGCGAAGAGAGATTAACCTTCAT 180



Db 160 ctttttgcgtgtatcttcataagaaggttggaagaagatagaagatgaaggaatcttcac 219  
Qy 181 GAAGATTTGTATTCAAAAAGCTAAAGAGATCCACAAGAGGAGAGATCTTTATCC 240  
Db 220 gaagattttgtattcatgaacagatagacagagatgcaacacagagagaagatccctatcc 279  
Qy 241 TTGCTGAATGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300  
Db 280 ttactgaactgtgaggagattaaagccagtttggaagctttgtgaagataataatgta 339  
Qy 301 RACAAAGAGA--CAAAAAGAAACACCTTTGAAATGCAAGAGAGGATGATCAGATCCT 357  
Db 340 acaaaagaggagacgaagaagaaacagctttgaaatgcataaaaggtgatcagaatcc 399  
Qy 358 CAATTTGACGACACAGCTTTGTAAGCGAAGCCACACAGTAATGACGACATCCGTTTACAGTGG 417  
Db 400 caaatgcgacatgtcataagtgaggcgagcagtaaaacaacatctgtgtacagtg 459  
Qy 418 GCCAAGAAAGGATATATACCATGAAGCAACTTTGGTAATGCTTGAANAATGGGAACAG 477  
Db 460 gctgaaaagagatactacacatgagcaacaacttggtaacctggaataatgggaacag 519  
Qy 478 CTGACGGTTAAAGAGAAGGACTCTATTATGCTACACTCAAGTCAAGTCTGCTCTAAT 537  
Db 520 ctgacccgttaaaagacaaggactcatatatactatgcccagtcacacctctgttccaa 579  
Qy 538 CGGAGCCTTCAGTCAACGCCATTCATCGTCGCCCTCGCTGAAGCCACAGCATTTGA 597  
Db 580 cgggaagcttgagtcagctcattatagccagccctctgctaaagtcctcccggtaga 639  
Qy 598 TCTGAGAACTTTACTCAAGCGCGCAATATCCACAGTTCCTCCAGCTTTCCGAGCAG 657  
Db 640 ttcgagagaatttactcagagctgcaaatcccaagcttcgcgaacaccttgcgggcaa 699  
Qy 658 CAGTCTGTCTACTTGGCGGAGCTTTGTAATTAAGCTGGTCTGCTGCTTGTGTCAC 717  
Db 700 caatccatctctggaggagatttgaattgcaccaggtgcttcggtgttgtaaat 759  
Qy 718 GTGACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAA 777  
Db 760 gtgactgatccaaagcgaagtgaagcactggcactgcttcacgtctcttggcttaactaaa 819  
Qy 778 CTCTGA 783  
Db 820 ctctga 825

RESULT 4  
US-09-911-904-131  
; Sequence 131, Application US/09911904  
; GENERAL INFORMATION:  
; APPLICANT: Parr, Spencer B.  
; APPLICANT: Pickett, Gavin G.  
; APPLICANT: Neft, Robin Eileen  
; APPLICANT: Dunn, II, Robert Thomas  
; TITLE OF INVENTION: CANINE TOXICITY GENES  
; FILE REFERENCE: 400742000200  
; CURRENT APPLICATION NUMBER: US/09/911,904  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US 60/220,057  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 386  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 131  
; LENGTH: 508  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-911-904-131

Query Match 40.2%; Score 315; DB 5; Length 508;  
Best Local Similarity 76.3%; Pred. No. 1.9e-71;  
Matches 387; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

Qy 268 CAATTTGAAGACCTTGTCAAGCATATACGTTAAACAAGAGAGAGAGAGAGAGAGAGAG 327  
Db 2 caatttgaagcccttctcaagagagataatgcataaacacgaatgaagaagaagaac 61  
Qy 328 TTTGAAATGCAAGAGGATGATGAGGATCCTCAAAATTCAGACACAGCTTTGTAAGCGAAGCC 387  
Db 62 attgcaatgcataaaggtgatcagagatcctcgaattgcagcccatgcatgaagtgaagct 121  
Qy 388 AACACTAATGACGATCCGTTCTACAGTGGCGCAAGAGAGGATATATACCATGAAGAGC 447  
Db 122 agtagtaaccccgctccggtctctcgttgcggcgcaaaaggttactcacaccataagcagc 181  
Qy 448 AACTTTGGTAATGCTGAAATGGAAACAGCTTGACGGTTTAAAGAGAGAGGACTCTATTAT 507  
Db 182 aacctgggtgagcctcgagaatggaaacagttggccgtgaaagacagaagactctattac 241  
Qy 508 GTCTACACTCAAGTCAAGTCTGCTCTAATCGGGAGCCTTCGAGTCAAGCGCCATTCATC 567  
Db 242 gtctatgcccagtcacctctctcctcaatcgggcagcttcgagtcagctccgcttcgc 301  
Qy 568 GTCGCGCTCTGCTGAAGCCACAGATTGATCTGAGAGATCTTACTCAAGCGCGCAANT 627  
Db 302 gccagccctatgctccattcccccgagtggaacggagagagtgcttactccgcccgcgagc 361  
Qy 628 ACCCAGATTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTTGAA 687  
Db 362 tcccgggctcgtccaaaccttgcggccaaacagtcacatccacttggaggagattattgaa 421  
Qy 688 TTACAAGCTGTGCTGCTGCTGTTGTTCAAGCTGATCAAGCAAGCAAGCAAGTGTCCACAGA 747  
Db 422 ttgatccaggtgctcgtggttcgtcgaacgtgactgatcccaagccaagtgcacacggg 481  
Qy 748 GTTGGCTTCTCATCTTTTGGCTTACTC 774  
Db 482 accggttccacgtctcttgggttactc 508

RESULT 5  
US-09-875-453A-9  
; Sequence 9, Application US/09875453A  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jungsuh P.  
; APPLICANT: Starr, Douglas B.  
; APPLICANT: Tam, Albert W.  
; APPLICANT: Laurence, Megan E.  
; APPLICANT: Michelotti, Emil F.  
; APPLICANT: Velligan, Mark D.  
; APPLICANT: Latour, Derek R.  
; APPLICANT: Thomas, Rita L.  
; APPLICANT: Kongpachith, Ana  
; APPLICANT: Sheppard, Liana T.  
; APPLICANT: Lim, Moon Young  
; APPLICANT: Bruce, Thomas W.  
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION  
; FILE REFERENCE: 54600-8135.US00  
; CURRENT APPLICATION NUMBER: US/09/875,453A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: US 60/209,549  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2395  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-453A-9

Query Match 19.9%; Score 155.8; DB 5; Length 2395;  
Best Local Similarity 90.7%; Pred. No. 2.3e-30;  
Matches 166; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```

RESULT 6
; SS-10-027-632-111808/c
; Sequence 111808, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111808
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Human
; SS-10-027-632-111808

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Query Match	5.3%;	Score	41.6;	DB	6;	Length	2865;	
Best Local Similarity	46.8%;	Pred. No.	0.51;					
Matches 131;	Conservative	0;	Mismatches	149;	Indels	0;	Gaps	0;
QY	61	ATGAAAATTTTATGTATTACTTGTCTTACCTGTTTTCTTATCACCCAGATGATGGGTACGCA	120					
Db	2158	AGATAGGTTATATAGATTTCATCTGTTTATTACTAAGCAGAGAAATGGCAATAC	2099					
QY	121	CTTTTTGCTGTATCTTCATAGAAAGATTGGATAAGTCCGAGCAGGAAGCTAAACCTTCAT	180					
Db	2098	ATTTTGAAGGATTTCCTATAGAAGGGATTGCACAGCTTTTCTTAATAGAAAATATTA	2039					
QY	181	GAAGATTTTGTATTTCATAAAAAGCTAAAGAGATGCAACAAAGCAGGAAGGATCTTTATCC	240					
Db	2038	TATATAATCTTCCTAAAAACATTACTATATCATTTCCAAACAATAAATCCATATAGA	1979					
QY	241	TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTCAGGATATAAAGCTTA	300					
Db	1978	TTCCCATACAGTGAGATTAGATAAATAATATCTCTCACCTTTAGTATTTTATAACTTA	1919					
QY	301	AACAAAGACAGAAAAGAAAAGAACAGCTTTGAAATGCAAA	340					
Db	1918	AGAAGATCAATACAAACAAAGCCCTGGTTATTATTAAGATGTTAA	1879					

RESULT. 7  
US-10-027-632-179264/C  
; Sequence 179264, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027.632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows: Version 4.0  
; SEQ ID NO 179264  
; LENGTH: 1223197  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(1223197)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-179264

Query Match 5.0%; Score 39.2; DB 6; Length 1223197;  
Best Local Similarity 48.1%; Pred. No. 14;  
Matches 101; Conservative 3; Mismatches 106; Indels 0; Gaps 0;

QY 92 TTTCTTATCACCACGAGATGTCGGTCAGACATTTTTCGTCTGTATCTTCATAGAAATGG 151  
Db 759351 TCCTGTTAAAGCAGATTAATATGGTCCTCAGPATTTACTATCAAGTATCGTAGAACCCTGAG 759292  
QY 152 ATAAAGTCGACAGAGAAGTAACCTTCATGAAGATTTTGTATTCATAAAAAGCTAAAGA 211  
Db 759291 TTGAATATCTATTCTCGACAGACATTTCTGAGTGTATTTGGGTGATTTCTCTGATCAC 759232  
QY 212 GATGCAACAAAGGAGAAGATCTTTATTCCTTTGCTGAACCTGTGAGGAGATGAGAGGCAAT 271  
Db 759231 TCCGTTGCAATGGGAGTGACGTTTATCCCTTCCTCTATPAGGAGGCAAAATTTTGGGTCA 759172  
QY 272 TTGAAGACCTTGTCAAGGATATAACGTTAA 301  
Db 759171 TTCCAGCAATAGTTATAGAAAAAAGTCA 759142

```

RESULT      8
US-10-105-299-12515/c
; Sequence 12515; Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosgen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P3950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12515

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QY	269	AATTTGAAGACCTTGTCAAGATATACGTTAAACAAGAGAAAAAGAAAACAGT	328
Matches	98	Conservative	0
Mismatches	0	Mismatches	100
Indels	0	Indels	0
Gaps	0	Gaps	0

269 AATTGAGACCTTGTCAAGGATATTAACGTTAAACAAGAGAGAAAAAGAAACAGCT 322

[illegible]

Db 193 ggtgaccaggcattgttgaaagaaactaatggaagatgatccacgcaggcgcaaaagagct 252  
 Oy 376 GTAA 379  
 Db 253 gaaa 256

RESULT 14

US-10-071-192-29  
 ; Sequence 29, Application US/10071192  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hunter, Shirley Wu  
 ; Sim, Gek-kee  
 ; Weber, Eric R.  
 ; TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND  
 ; APPARATUS TO COLLECT SUCH PROTEINS  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SHERIDAN ROSS P.C.  
 ; STREET: 1560 BROADWAY, SUITE 1200  
 ; CITY: DENVER  
 ; STATE: CO  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80202

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/071.192  
 ; FILING DATE: 07-Feb-2002  
 ; CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/171.156  
 ; FILING DATE: 1998-10-09  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Connell, Gary J.  
 ; REGISTRATION NUMBER: 32,020  
 ; REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS

TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 303/863-9700  
 ; TELEFAX: 303/863-0223  
 ; INFORMATION FOR SEQ ID NO: 29:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1758 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:

NAME/KEY: CDS  
 LOCATION: 1...1758

FEATURE:  
 NAME/KEY: W - A or T  
 LOCATION: 1136

SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
 US-10-071-192-29

Query Match 4.7%; Score 37; DB 6; Length 1758;  
 Best Local Similarity 47.2%; Pred. No. 6.6;  
 Matches 109; Conservative 1; Mismatches 121; Indels 0; Gaps 0;

Oy 155 AGTCTGAGAGAGAGAACTTTCATGAGATTTTGTATTATTAATAAGCTTAAAGAGAT 214  
 Db 1043 AAGATGTAGAGAAATTGAAGAAGCATAGTTCGCTGAGAAACCAAGAGATGAGATAA 1102  
 Oy 215 GCAACAAGGAGAGAGATTTTATCTTCTGCACTGTGAGGAGATGAGAACGCAATTG 274  
 Db 1103 AAGAACTAAAGGAGCTCAACGATTGTTGAAGAGGGTTAAACAAGATGATAACGAAATGG 1162

Oy 275 AAGACCTTGTCAAGATATACGTTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334  
 Db 1163 ATACTGTTGTACAGAAATTGAAAGCAAAAGATCTTGAGAGAGAGAGAGAGAGAGAGAG 1222  
 Oy 335 TGCAAGAGAGGTGATGAGGATCTCAAAATTCGACGACACAGCTTGTAAAGCGAAG 385  
 Db 1223 TTGAAGCTCCTAGGAGCGCTACTGAACTCAAGATTAGATGTAAGGAAG 1273

RESULT 15

US-09-789-189-555/c  
 ; Sequence 555, Application US/09789189  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lelias, Jean-Michel  
 ; TITLE OF INVENTION: Human Polynucleotides and Polypeptides  
 ; FILE REFERENCE: 25436/1720  
 ; CURRENT APPLICATION NUMBER: US/09/789.189  
 ; CURRENT FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/183452  
 ; PRIOR FILING DATE: 2000-02-18  
 ; NUMBER OF SEQ ID NOS: 2005  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 555  
 ; LENGTH: 341  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-789-189-555

Query Match 4.7%; Score 36.6; DB 5; Length 341;  
 Best Local Similarity 53.1%; Pred. No. 5;  
 Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Oy 203 ACCTAAAGAGATGCCAAAGAGAGAGATCTTTATCTTCTGCTGAAGAGAGATGA 262  
 Db 278 AGGTGAGGGGTGGATATGAGGAGGAGGAGATTTGTAATGGAAGGGGAGGTTAAGTGAAGA 219  
 Oy 263 GAAGGCAATTTGAAGACCTTGTCAAGGATATAACCTTAAACAAGAGAGAGAGAGAGAGAG 322  
 Db 218 TATTGCTGATTGATAGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159  
 Oy 323 ACAGCTTTGAATGCAAGAGAGCTGATG 349  
 Db 158 AGGTGTCGAAAAATAAAGATGTAATG 132

Search completed: May 30, 2002, 05:38:54  
 Job time: 16708 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 23:38:16 ; Search time 139.75 Seconds  
(without alignments)  
1376.251 Million cell updates/sec

Title: US-08-982-272-3  
Perfect score: 783  
Sequence: 1 ATGATCGAACAATACAAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	751	95.9	818	1	US-08-431-055-1
2	751	95.9	818	4	US-08-858-137-1
3	749.4	95.7	783	1	US-08-446-922-5
4	749.4	95.7	783	2	US-08-249-189-1
5	749.4	95.7	783	2	US-08-484-624A-1
6	749.4	95.7	783	2	US-08-477-733B-1
7	749.4	95.7	783	3	US-09-088-913A-1
8	749.4	95.7	783	4	US-08-769-819-1
9	749.4	95.7	783	4	US-08-770-974-1
10	749.4	95.7	783	5	PCT-US93-10034-5
11	631.4	80.6	878	2	US-08-249-189-22
12	631.4	80.6	878	2	US-08-484-624A-22
13	631.4	80.6	878	2	US-08-477-733B-22
14	631.4	80.6	878	3	US-09-088-913A-22
15	631.4	80.6	878	4	US-08-769-819-22
16	631.4	80.6	878	4	US-08-770-974-22
17	592.4	75.7	786	1	US-08-446-922-3
18	592.4	75.7	786	5	PCT-US93-10034-3
19	592.4	75.7	840	1	US-07-940-605A-1
20	592.4	75.7	840	1	US-08-184-422-7
21	592.4	75.7	840	1	US-08-360-923A-1
22	592.4	75.7	840	1	US-08-431-055-3
23	592.4	75.7	840	2	US-08-690-096-1
24	592.4	75.7	840	2	US-08-249-189-11
25	592.4	75.7	840	2	US-08-484-624A-11
26	592.4	75.7	840	2	US-08-477-733B-11
27	592.4	75.7	840	3	US-08-763-995-1

28	592.4	75.7	840	3	US-09-088-913A-11	Sequence 11, Appl
29	592.4	75.7	840	3	US-08-589-771B-7	Sequence 7, Appl
30	592.4	75.7	840	4	US-08-769-819-11	Sequence 11, Appl
31	592.4	75.7	840	4	US-08-770-974-11	Sequence 11, Appl
32	592.4	75.7	840	4	US-08-858-197-3	Sequence 3, Appl
33	446.2	57.0	1425	2	US-08-249-189-15	Sequence 15, Appl
34	446.2	57.0	1425	2	US-08-484-624A-15	Sequence 15, Appl
35	446.2	57.0	1425	2	US-08-477-733B-15	Sequence 15, Appl
36	446.2	57.0	1425	3	US-09-088-913A-15	Sequence 15, Appl
37	446.2	57.0	1425	4	US-08-769-819-15	Sequence 15, Appl
38	446.2	56.9	929	1	US-08-446-922-10	Sequence 10, Appl
39	445.2	56.9	929	2	US-08-249-189-20	Sequence 20, Appl
40	445.2	56.9	929	2	US-08-484-624A-20	Sequence 20, Appl
41	445.2	56.9	929	2	US-08-477-733B-20	Sequence 20, Appl
42	445.2	56.9	929	3	US-09-088-913A-20	Sequence 20, Appl
43	445.2	56.9	929	4	US-08-769-819-20	Sequence 20, Appl
44	445.2	56.9	929	4	US-08-770-974-20	Sequence 20, Appl
45	445.2	56.9	929	4	US-08-770-974-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-08-431-055-1  
; Sequence 1, Application US/08431055  
; Patent No. 5817516  
; GENERAL INFORMATION:  
; APPLICANT: KEHRY, MERILYN R  
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 100 NEW YORK AVE. N.W. SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,055  
; FILING DATE: 28-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/234,580  
; FILING DATE: 28-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 1011.10300000/RAM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..795  
US-08-431-055-1

Query Match 95.9%; Score 751; DB 1; Length 818;  
Best Local Similarity 97.4%; Pred. No. 1.3e-212;

Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGAGTCCCATCAGC 60  
DB 13 ATGATGAAACATACAGCAACCTTCCCGCAGATCGGCACTGGACCTTCCACGGAGC 72  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGCA 120  
DB 73 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGC 132  
QY 121 CTTTCTGCTGATCTTCTATAGAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 180  
DB 133 CTTTCTGCTGATCTTCTATAGAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 192  
QY 181 GAAGATTTTGTATTCATATAAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 240  
DB 193 GAAGATTTTGTATTCATATAAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 252  
QY 241 TTGCTGAACCTGAGGAGATGAGAGCAATTTCAAGACCTTCTCAAGGATTAACGTTA 300  
DB 253 TTGCTGAACCTGAGGAGATGAGAGCAATTTCAAGACCTTCTCAAGGATTAACGTTA 312  
QY 301 AACAAAGAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 360  
DB 313 AACAAAGAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 372  
QY 361 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATCCAGATCCGTTTACAGTGGCC 420  
DB 373 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATCCAGATCCGTTTACAGTGGCC 432  
QY 421 AAGAAAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 480  
DB 433 AAGAAAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 492  
QY 481 ACGGTTAAAGAGAGAGACTTATATGCTTACACTCAAGTCAAGTCAAGTCAAGTCA 540  
DB 493 ACGGTTAAAGAGAGAGACTTATATGCTTACACTCAAGTCAAGTCAAGTCAAGTCA 552  
QY 541 GAGCCTTCGAGTCAACGCCATTCATCGTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 600  
DB 553 GAGCCTTCGAGTCAACGCCATTCATCGTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 612  
QY 601 GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660  
DB 613 GAGAGATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTGGAGCAGCAG 672  
QY 661 TCTGTTCACTTGGCGGAGTGTGAAATACAGCTGCTTCTGCTGCTTGTCAAGCTG 720  
DB 673 TCTGTTCACTTGGCGGAGTGTGAAATACAGCTGCTTCTGCTGCTTGTCAAGCTG 732  
QY 721 ACTGAAGCAAGCAAGTATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
DB 733 ACTGAAGCAAGCAAGTATCCACAGATTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 792  
QY 781 TGA 783  
DB 793 TGA 795

RESULT 2  
us-08-858-197-1  
Sequence 1, Application US/08858197  
Patent No. 6297052  
GENERAL INFORMATION:  
APPLICANT: KEHRY, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON

STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/858,197  
APPLICATION NUMBER: US/08/858,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US/08/234,580  
APPLICATION NUMBER: US/08/234,580  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 818 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..795  
US-08-858-197-1

Query Match 95.9%; Score 751; DB 4; Length 818;  
Best Local Similarity 97.4%; Pred. No. 1.3e-212;  
Matches 763; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCGGGCCACTGGAGTCCCATCAGC 60  
DB 13 ATGATGAAACATACAGCAACCTTCCCGCAGATCGGCACTGGACCTTCCACGGAGC 72  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGCA 120  
DB 73 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGC 132  
QY 121 CTTTCTGCTGATCTTCTATAGAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 180  
DB 133 CTTTCTGCTGATCTTCTATAGAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 192  
QY 181 GAAGATTTTGTATTCATATAAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 240  
DB 193 GAAGATTTTGTATTCATATAAGATTTGATTAAGGTCGAGAGAGATTAACCTTCA 252  
QY 241 TTGCTGAACCTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATTAACGTTA 300  
DB 253 TTGCTGAACCTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATTAACGTTA 312  
QY 301 AACAAAGAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 360  
DB 313 AACAAAGAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 372  
QY 361 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATCCAGATCCGTTTACAGTGGCC 420  
DB 373 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATCCAGATCCGTTTACAGTGGCC 432  
QY 421 AAGAAAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 480  
DB 433 AAGAAAGATTAATACATCAAAAGCACTTGAATGCAAGAGATGATGAGGATCCTCA 492  
QY 481 ACGGTTAAAGAGAGAGACTTATATGCTTACACTCAAGTCAAGTCAAGTCAAGTCA 540  
DB 493 ACGGTTAAAGAGAGAGACTTATATGCTTACACTCAAGTCAAGTCAAGTCAAGTCA 552



QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600  
DB 553 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 612  
QY 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCCCTCCAGCTTTCGGAGCAGCAG 660  
DB 613 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCCCTCCAGCTTTCGGAGCAGCAG 672  
QY 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 720  
DB 673 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 732  
QY 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
DB 733 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 792  
QY 781 TGA 783  
DB 793 TGA 795

RESULT 3  
US-08-446-922-5  
; Sequence 5, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A  
; REGISTRATION NUMBER: 34,693  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 783 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; STRAIN: CD40-L  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: 1..780  
US-08-446-922-5

Query Match 95.7%; Score 749.4; DB 1; Length 783;  
Best Local Similarity 97.3%; Pred. No. 3.9e-212;  
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTCGCGCACTGCGCACTGCCATCAGC 60  
DB 1 ATGATGAAGACATACAGCCCACTTCCCGGATCTCGCGCACTGCCATCAGC 60  
QY 61 ATGAATAATTTTATGATTTACTTACTTCTTATFACCCAGATGATTTGGTGCAGCA 120  
DB 61 ATGAAGATTTTATGATTTACTTACTTCTTATFACCCAGATGATTTGGTGCAGCA 120  
QY 121 CTTTTTCTGTGATCTTCATAGAAGATTCGATAGGTCGAGAGGAGTAACCTTCAT 180  
DB 121 CTTTTTCTGTGATCTTCATAGAAGATTCGATAGGTCGAGAGGAGTAACCTTCAT 180  
QY 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240  
DB 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300  
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300  
QY 301 AACAAAGAAGAGAAAAGAAAAGCAAGCTTTGAAATGCAAGAGCTGATGAGATCCCTCAA 360  
DB 301 AACAAAGAAGAGAAAAGAAAAGCAAGCTTTGAAATGCAAGAGCTGATGAGATCCCTCAA 360  
QY 361 ATTGCAGCACACGTTTGAAGCGAAGCCCAACAGTAATGACAGCATCCGTTTCTACAGTGGCC 420  
DB 361 ATTGCAGCACACGTTTGAAGCGAAGCCCAACAGTAATGACAGCATCCGTTTCTACAGTGGCC 420  
QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAAGAGGAAACAGCTG 480  
DB 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAAGAGGAAACAGCTG 480  
QY 481 ACGGTTAAAGAGAGGAGCTCTATTATGCTTACACTCAAGTCAAGTCTCTCTAATCGG 540  
DB 481 ACGGTTAAAGAGAGGAGCTCTATTATGCTTACACTCAAGTCAAGTCTCTCTAATCGG 540  
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600  
DB 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600  
QY 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCTCCAGCTTTCGGAGCAGCAG 660  
DB 601 GAGAGAATCTTACTCAAGGGCGGCAAAATACCCACAGTTTCTCCAGCTTTCGGAGCAGCAG 660  
QY 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 720  
DB 661 TCTGTTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTTCTGTTTGTCAAGCTG 720  
QY 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
DB 721 ACTGAAGCAAGCAAGTGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
QY 781 TGA 783  
DB 781 TGA 783

RESULT 4  
US-08-249-189-1  
; Sequence 1, Application US/08249189  
; Patent No. 5961974  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE

QY	181	GAAGATTTTGTATTATCATAAAAAGCTTAACAGAGATGCAACAAAGAGAGAGATCTTATCC	240
Db	181	GAAGATTTTGTATTATCATAAAAAGCTTAACAGAGATGCAACAAAGAGAGATCTTATCC	240
QY	241	TTGCCTGAACCTGTGAGGAGATGAGAAAGCAATTTCAGACCTCTGCAAGGATATAACGTTA	300
Db	241	TTGCCTGAACCTGTGAGGAGATGAGAAAGCAATTTCAGACCTCTGCAAGGATATAACGTTA	300
QY	301	AACAAGAGAGAAAAAGAAAAACAGCTTTGAAATGCAAGAGAGTGATGAGGATCCTCAA	360
Db	301	AACAAGAGAGAAAAAGAAAAACAGCTTTGAAATGCAAGAGAGTGATGAGGATCCTCAA	360
QY	361	ATTGCAGCACAGTTGTAAAGCGAAGCCACAGTAATGCAGCATCGTTCTACAGTGGGCC	420
Db	361	ATTGCAGCACAGTTGTAAAGCGAAGCCACAGTAATGCAGCATCGTTCTACAGTGGGCC	420
QY	421	AAGAAAGGATATTATACCATGAAAAAGCAACTGGTAATGCTTGAATGGGAACAGCTG	480
Db	421	AAGAAAGGATATTATACCATGAAAAAGCAACTGGTAATGCTTGAATGGGAACAGCTG	480
QY	481	ACGGTTAAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTCTCGTCTTAATCGG	540
Db	481	ACGGTTAAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTCTCGTCTTAATCGG	540
QY	541	GAGCCTTCGAGTCAAGGCCCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATTTGGATCT	600
Db	541	GAGCCTTCGAGTCAAGGCCCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATTTGGATCT	600
QY	601	GAGAGATCTTTACTCAGGCGGCAAAATCCACAGTTCCTCCAGCTTTGCGAGCAGCAG	660
Db	601	GAGAGATCTTTACTCAGGCGGCAAAATCCACAGTTCCTCCAGCTTTGCGAGCAGCAG	660
QY	661	TCTGTTCACTTTGGCGGAGTGTTTGAATTAACAAGCTGGTGCTCTGTTTGTCTCAACG	720
Db	661	TCTGTTCACTTTGGCGGAGTGTTTGAATTAACAAGCTGGTGCTCTGTTTGTCTCAACG	720
QY	721	ACTGAAGCAAGCAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
Db	721	ACTGAAGCAAGCAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC	780
QY	781	TGA 783	
Db	781	TGA 783	

RESULT 5  
US-08-484-C24A-1  
Sequence 1, Application US/08484624A;  
Patent No. 5962406  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLow, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
Zip: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, ver 5.0  
CURRENT APPLICATION DATA:

[illegible]



FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-477-733B-1

Query Match 95.7%; Score 749.4; DB 2; Length 783;  
Best Local Similarity 97.3%; Pred. No. 3.9e-212;  
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAACCTTCCCGGATCTCCGGCCACTGGACTGCCATCAGC 60  
Db 1 ATGATGAACATACAGCAACCTTCCCGGATCTCCGGCCACTGGACTGCCATCAGC 60  
QY 61 ATGAAATTTTATGTTTACTTACTTCTTCTTATCATCCAGATGATGGTGCAGCA 120  
Db 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCATCCAGATGATGGTGCAGC 120  
QY 121 CTTTTCGTGTATCTCTATGAGATGTGATAGTTCGAGAGGAGTAACCTTCAT 180  
Db 121 CTTTTCGTGTATCTCTATGAGATGTGATAGTTCGAGAGGAGTAACCTTCAT 180  
QY 181 GAAGATTTTGTATCATAAAAAGCTTAAGAGATGCAACAGAGAGAGATCTTTATCC 240  
Db 181 GAAGATTTTGTATTCATAAAAAGCTTAAGAGATGCAACAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAAGTGTGAGGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
Db 241 TTGCTGAAGTGTGAGGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
QY 301 AACAAAGAGAGAAAAAGAACAGCTTTGAAATGCAAGAGAGTGTAGGATCCTCAA 360  
Db 301 AACAAAGAGAGAAAAAGAACAGCTTTGAAATGCAAGAGAGTGTAGGATCCTCAA 360  
QY 361 ATTGCAGCAGCTTGTAGGAGAGCAACAGATGATGAGATCCGTTCTACATGGGCC 420  
Db 361 ATTGCAGCAGCTTGTAGGAGAGCAACAGATGATGAGATCCGTTCTACATGGGCC 420  
QY 421 AAGAAAGATATATACATGAAAGCAACTTGTGTAATGCTTGAATGGGAAACAGCTG 480  
Db 421 AAGAAAGATATATACATGAAAGCAACTTGTGTAATGCTTGAATGGGAAACAGCTG 480  
QY 481 ACGGTTAAAGAGAGGACTCTATTATGCTACATCAAGTCACCTTCGCTCTAATCGG 540  
Db 481 ACGGTTAAAGAGAGGACTCTATTATGCTACATCAAGTCACCTTCGCTCTAATCGG 540  
QY 541 GAGCCTTCGATCAAGGCCCATTCATCGTGGCCTCTCGCTGAAGCCAGCATTTGATCT 600

Db 541 GAGCCTTCGATCAAGGCCCATTCATCGTGGCCTCTCGCTGAAGCCAGCATTTGATCT 600  
QY 601 GAGAGATCTTACTCAAGGGGCAATACCCACAGTTTCTCCAGCTTTGGAGCAGCAG 660  
Db 601 GAGAGATCTTACTCAAGGGGCAATACCCACAGTTTCTCCAGCTTTGGAGCAGCAG 660  
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCTGCTTCTGTTGTTCAAGCTG 720  
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCTGCTTCTGTTGTTCAAGCTG 720  
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
QY 781 TGA 783  
Db 781 TGA 783

RESULT 7  
US-09-088-913A-1  
; Sequence 1, Application US/09088913A  
; Patent No. 6087329  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,913A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-09-088-913A-1

Query Match 95.78; Score 749.4; DB 3; Length 783;  
Best Local Similarity 97.3%; Pred. No. 3.9e-212;  
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGATGAACACATCAACCAACCTTCCTCCGATCTCGGCCACTGGACTGCCCATCAGC 60  
Db 1 ATGATGAACACATCAACCAACCTTCCTCCGATCTCGGCCACTGGACTGCCCATCAGC 60

Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTTCTTATCACCCAGATGATGGGTTCAGCA 120  
Db 61 ATGAAATTTTATGTATTTACTTACTTCTTTCTTATCACCCAAATGATGGATCTGTG 120

Qy 121 CTTTTCGTGTATCTTCATAGAGATTTGGATAGGTTCGAGAGGAAGTAACCTTCAT 180  
Db 121 CTTTTCGTGTATCTTCATAGAGATTTGGATAGGTTCGAGAGGAAGTAACCTTCAT 180

Qy 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTATCC 240  
Db 181 GAAGATTTTGTATTCATAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTATCC 240

Qy 241 TTGCTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
Db 241 TTGCTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

Qy 301 AACAAAG 360  
Db 301 AACAAAG 360

Qy 361 ATTCAGCACAGCTGTGAAGCGAGCCCAACAGTAATGAGAGATCGCTTCTACAGTGGCC 420  
Db 361 ATTCAGCACAGCTGTGAAGCGAGCCCAACAGTAATGAGAGATCGCTTCTACAGTGGCC 420

Qy 421 AAGAAAGATATTATACCATGAAAGCAACTTTGGTAATGCTTGAATAATGGGAAACAGCTG 480  
Db 421 AAGAAAGATATTATACCATGAAAGCAACTTTGGTAATGCTTGAATAATGGGAAACAGCTG 480

Qy 481 ACGGTAAAG 540  
Db 481 ACGGTAAAG 540

Qy 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGCCCTCTGGCTGAAGCCAGCAGATTGGATCT 600  
Db 541 GAGCCTTCAGTCAACGCCCATTCATCGTCGCCCTCTGGCTGAAGCCAGCAGATTGGATCT 600

Qy 601 GAGAGATCTTACTCAAGCGGCGGCAATACCCACAGTTCCTCCAGCTTTGGGAGCAGCAG 660  
Db 601 GAGAGATCTTACTCAAGCGGCGGCAATACCCACAGTTCCTCCAGCTTTGGGAGCAGCAG 660

Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAGCTGTGCTCTGCTGTTTGTCAACGTG 720  
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAGCTGTGCTCTGCTGTTTGTCAACGTG 720

Qy 721 ACTGAAGCAAGCAAGTCAACAGAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTCAACAGAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780

Qy 781 TGA 783  
Db 781 TGA 783

RESULT 8  
US-08-769-819-1  
Sequence 1, Application US/08769819  
Patent No. 6264951  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08769,819  
FILING DATE: 19-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-769-819-1

Query Match	95.7%	Score 749.4	DB 4	Length 783
Best Local Similarity	97.3%	Pred. No. 3.9e-212		
Matches 762	Conservative	0	Mismatches 21	Indels 0
Gaps				
1	ATGATCGAAACATACAAACAACTTCCTCCCGATCTGCGGCCACTGGACATGCCCATCGC 60			
1	ATGATGAAACATACAGCAACCTTCCTCCCGAGATCCGCGAACTGGACTTCACGGAGC 60			
61	ATGAAATATTTTATGTATTTACTTTACTTTCTTATACCCAGATGATGGGTACGCA 120			
61	ATGAAGATTTTATGTATTTACTTTACTTTCTTATACCCAAATGATGGATCTGTG 120			
121	CTTTTGTGCTATCTTCATAGAAAGATTTGATTAAGTTCGAAGAGNAGTAAACCTTCAT 180			
121	CTTTTGTGCTATCTTCATAGAAAGATTTGATTAAGTTCGAAGAGNAGTAAACCTTCAT 180			
181	GAAGATTTTGTATTCATTAAGAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240			
181	GAAGATTTTGTATTCATTAAGAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240			
241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACCTTA 300			
241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACCTTA 300			
301	AACAAG 360			
301	AACAAG 360			
361	ATTGACGACACGCTTGTAGCGNAGCCACAGTAAATGACAGATCCGTTCTACAGTGGGCC 420			
361	ATTGACGACACGCTTGTAGCGNAGCCACAGTAAATGACAGATCCGTTCTACAGTGGGCC 420			
421	AAGAAAGATATTATACCATGAAAGCAACTTGGTAACTGCTTCAAAATGGGAACAGCTG 480			
421	AAGAAAGATATTATACCATGAAAGCAACTTGGTAACTGCTTCAAAATGGGAACAGCTG 480			
481	ACGGTTAAAG 540			
481	ACGGTTAAAG 540			
541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCTTGGCTGAAGCCACAGCATTTGGATCT 600			
541	GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCTTGGCTGAAGCCACAGCATTTGGATCT 600			
601	GAGAGATTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTTGCGAGAGAGAG 660			
601	GAGAGATTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTTGCGAGAGAGAGAG 660			
661	TCGTGTTCACTTGGCGGAGTGTTCATTAAGTACAGCTGGTCTGTGTGTGTGTCAACGCTG 720			
661	TCGTGTTCACTTGGCGGAGTGTTCATTAAGTACAGCTGGTCTGTGTGTGTGTCAACGCTG 720			
721	ACTGAG 780			
721	ACTGAG 780			
781	TGA 783			
781	TGA 783			

RESULT 9  
US-08-770-974-1  
; Sequence 1, Application US/08770974  
; Patent No. 6290972  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,974  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PS-08-770-974-1

Query Match	95.7%	Score	749.4	DB.4	Length	783
Best Local Similarity	97.3%	Pred. NO.	3.9e-212			
Matches	762	Conservative	-0	Mismatches	0	Gaps
QY	1	ATGATCGAAACATACAACCAACTCTCCCGGATCTGGCGCACCTGGACTGCCCATCAGC	60			
Dd	1	ATGATAGAACAATACAGCGCAACCTTTCGCCAGATCCCTGGCAACTTCGCAGCGAC	60			
QY	61	ATGAATAAATTTTATGTATTTACTTACTGTGTTTTCTTATCATCCACAGATGTTGGTGACGA	120			
Dd	61	ATGAAGATTTTATGTATTATTTACTTGTGTTTTCTTATCATCCCAATATGTTGCATCTGG	120			
QY	121	CTTTTTTCCTGTCTATCTTCATAGAAGATTTGGTAAGTTCGAAGAGGGAAGTAAACCTTCAT	180			
Dd	121	CTTTTTGCCTGTGTAUCTTCATAGAAGATTTGGTAAGGTCGAAGAGGGAAGTAAACCTTCAT	180			
Ov	181	GAAGATTTTGTATTTCAATAAAAAGCTAAAGATCCAAAGCAGAAGGATCTTTATACC	240			

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Db 181 GAAGATTTTGTATTATCAAAAAAGCTAAAGAGATGCAAAAGGAGAGATCTTTATCC 240
Qy 241 TTGCTGAAGTGTGAGGAGTGAAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAAGTGTGAGGAGTGAAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Qy 301 ACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCCTCAA 360
Db 301 ACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGATCCTCAA 360
Qy 361 ATTGAGCAGACGTTGTAAGCGAAGCCACAGATGATGAGATCGGTTCTACAGTGGGCC 420
Db 361 ATTGAGCAGACGTTGTAAGCGAAGCCACAGATGATGAGATCGGTTCTACAGTGGGCC 420
Qy 421 AAGAAAGGATATTATACCATGAAAAAGCAACTTGGTAATGCTTGAATGGAAGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAAAGCAACTTGGTAATGCTTGAATGGAAGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Db 481 ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Qy 541 GAGCCTTCGAGTCAAGGCCATTCATGCTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAAGGCCATTCATGCTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 600
Qy 601 GAGAGAATCTTACTCAAGCGGCAATACCCACAGTTCTCCACGTTTGGCAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGCGGCAATACCCACAGTTCTCCACGTTTGGCAGCAGCAG 660
Qy 661 TCTGTTCACTTTGGCGGAGTGTGAATTAACAAGCTGGTCTTCTGTTGTCAACGTC 720
Db 661 TCTGTTCACTTTGGCGGAGTGTGAATTAACAAGCTGGTCTTCTGTTGTCAACGTC 720
Qy 721 ACTGAAGCAAGCAAGTATCAACAGCTGCTGCTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTATCAACAGCTGCTGCTCTCATCTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783
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RESULT 10
PCT-US93-10034-5
; Sequence 5, Application PC/TUS9310034
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10034
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..780
PCT-US93-10034-5
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Query Match 95.7%; Score 749.4; DB 5; Length 783;
Best Local Similarity 97.3%; Pred. No. 3.9e-212;
Matches 762; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ATGATCGAAACATACAAACCACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60
Db 1 ATGATGAAACATACAGCCAACTTCCCGCAGATCGGTGGCAACTGGACTTCCACGGAGC 60
Qy 61 ATGAAATTTTATGATTTACTTACTTCTTATATACCCACCATGATTTGGTTCAGCA 120
Db 61 ATGAAATTTTATGATTTACTTACTTCTTATATACCCAAATGATTTGGATCTGTG 120
Qy 121 CTTTTTGTGCTATCTTATAGAAAGATTTGATAAGTTCGAAGAGTGAAGTAAACCTTAT 180
Db 121 CTTTTTGTGCTATCTTATAGAAAGATTTGATAAGTTCGAAGAGTGAAGTAAACCTTAT 180
Qy 181 GAAGATTTTGTATTTATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTTATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Qy 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAAAGAGTGTGATGAGATCCTCAA 360
Db 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAAAGAGTGTGATGAGATCCTCAA 360
Qy 361 ATTGAGCAGACGTTGTAAGCGAAGCCACAGTATGATGAGATCGGTTCTACAGTGGGCC 420
Db 361 ATTGAGCAGACGTTGTAAGCGAAGCCACAGTATGATGAGATCGGTTCTACAGTGGGCC 420
Qy 421 AAGAAAGGATATTATACCATGAAAAAGCAACTTGGTAATGCTTGAATGGAAGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAAAGCAACTTGGTAATGCTTGAATGGAAGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Db 481 ACGGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540
Qy 541 GAGCCTTCGAGTCAAGGCCATTTCAATGCTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 600
Db 541 GAGCCTTCGAGTCAAGGCCATTTCAATGCTGGCCCTTGGCTGAAGCCAGCATTTGGATCT 600
Qy 601 GAGAGAATCTTACTCAAGCGGCAATACCCACAGTTCTCCACGTTTGGCAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGCGGCAATACCCACAGTTCTCCACGTTTGGCAGCAGCAG 660
Qy 661 TCTGTTCACTTTGGCGGAGTGTGAATTAACAAGCTGGTCTTCTGTTGTCAACGTC 720
Db 661 TCTGTTCACTTTGGCGGAGTGTGAATTAACAAGCTGGTCTTCTGTTGTCAACGTC 720
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Thu May 30 05:46:02 2002

QY 721 ACTGAAGCAAGCAAGTATGATCAGAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780  
 Db 721 ACTGAAGCAAGCAAGTATGATCAGAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780  
 QY 781 TGA 783  
 Db 781 TGA 783

RESULT 11  
 US-08-249-189-22 Application US/08249189  
 ; Sequence 22, Patent No. 5961974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; APPLICANT: SRINIVASAN, SUBHASHINI  
 ; APPLICANT: GIBSON, MARYLOU  
 ; TITLE OF INVENTION: NOVEL CYTOKINE  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.1  
 ; SOFTWARE: Microsoft Word for Apple, version 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/249,189  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/969,703  
 ; FILING DATE: October 23, 1992  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/805,723  
 ; FILING DATE: December 5, 1991  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/783,707  
 ; FILING DATE: October 25, 1991  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2802-C  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 2065870430  
 ; TELEFAX: 2065870606  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 878 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cdna  
 ; ORIGINAL SOURCE:  
 ; STRAIN: Murine CD40-L trimer  
 ; FEATURE:  
 ; NAME/KEY: sig\_peptide  
 ; LOCATION: 15...92  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 15...857  
 ; FEATURE:  
 ; NAME/KEY: mat\_peptide

LOCATION: 93...857  
 US-08-249-189-22  
 Query Match 80.6%; Score 631.4; DB 2; Length 878;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-177; Indels 0; Gaps 0;  
 Matches 632; Conservative 0; Mismatches 1;  
 QY 151 GATAAGGTCGAAGAGCAAGTAAACCTTCAATGAAGATTTTGTATTCATATAAAAGCTAAAG 210  
 Db 225 GATAAGGTCGAAGAGCAAGTAAACCTTCAATGAAGATTTTGTATTCATATAAAAGCTAAAG 284  
 QY 211 AGATGCAACAAAGAGGAGAGATCTTTATCTTCTGCTGACTGTGAGGAGATCAGAAGCA 270  
 Db 285 AGATGCAACAAAGAGGAGAGATCTTTATCTTCTGCTGACTGTGAGGAGATCAGAAGCA 344  
 QY 271 TTGGAAGCCTTGTCAAGGATATACGTTTAAACAAAGAGAGAGAGAGAGAGAGAGAGCTTT 330  
 Db 345 TTGGAAGCCTTGTCAAGGATATACGTTTAAACAAAGAGAGAGAGAGAGAGAGAGCTTT 404  
 QY 331 GAAATGCAAAAGAGGTGATGAGGATCTCAAAATGTCAGCACACGTTGTAAAGCGAAGCCAA 390  
 Db 405 GAAATGCAAAAGAGGTGATGAGGATCTCAAAATGTCAGCACACGTTGTAAAGCGAAGCCAA 464  
 QY 391 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGAGATATATACCATGAAAAGCAAC 450  
 Db 465 AGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGAGATATATACCATGAAAAGCAAC 524  
 QY 451 TTGTAATGCTTGAATGGAATGGGAACACAGCTACCGTTTAAAGAGAGAGAGAGAGAGAG 510  
 Db 525 TTGTAATGCTTGAATGGAATGGGAACACAGCTACCGTTTAAAGAGAGAGAGAGAGAGAG 584  
 QY 511 TACACTCAAGTCACCTTCTCTTAATCGGAGAGCTTCGAGTCAACGCCCATTCATCGTC 570  
 Db 585 TACACTCAAGTCACCTTCTCTTAATCGGAGAGCTTCGAGTCAACGCCCATTCATCGTC 644  
 QY 571 GGCCTCTGGCTGAAGCCAGCATTTGGATCTGAGAGATCTTACTCAAGCGCGCAATATACC 630  
 Db 645 GGCCTCTGGCTGAAGCCAGCATTTGGATCTGAGAGATCTTACTCAAGCGCGCAATATACC 704  
 QY 631 CACAGTTCCTCCAGCTTTGGAGAGCAGCTCTGTTCATCTTGGCGGAGTGTGTAATTA 690  
 Db 705 CACAGTTCCTCCAGCTTTGGAGAGCAGCTCTGTTCATCTTGGCGGAGTGTGTAATTA 764  
 QY 691 CAAGCTGGTGTCTGTGTTTGTCAACGTGACTGAAGCAAGCAAGTATCCACAGAGTT 750  
 Db 765 CAAGCTGGTGTCTGTGTTTGTCAACGTGACTGAAGCAAGCAAGTATCCACAGAGTT 824  
 QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783  
 Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 12  
 US-08-484-624A-22  
 ; Sequence 22, Patent No. 5962406  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; APPLICANT: SRINIVASAN, SUBHASHINI  
 ; APPLICANT: GIBSON, MARYLOU  
 ; APPLICANT: MORRIS, ARVIA E.  
 ; APPLICANT: MCGREW, JEFFERY  
 ; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA





Thu May 30 05:46:02 2002

APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: Murine CD40-L trimer  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 15..92  
NAME/KEY: CDS  
LOCATION: 15..857  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 93..857  
US-08-477-733B-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;  
Best Local Similarity 99.8%; Pred. No. 3.1e-177;  
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAAGGTCGAAGAGGAAGTAACCTTCATGAAGATTTTGTATTTCATTAATAAAAGCTAAAG 210  
DB 225 GATAAGGTCGAAGAGGAAGTAACCTTCATGAAGATTTTGTATTTCATTAATAAAAGCTAAAG 284  
QY 211 AGATGCAACAAAGGAGGAAGTCTTTATCTTCTGCTGAACCTGTGAGGAGATGAGAAGGCAA 270  
DB 285 AGATGCAACAAAGGAGGAAGTCTTTATCTTCTGCTGAACCTGTGAGGAGATGAGAAGGCAA 344  
QY 271 TTGTAAGACCTTCTCAAGGATATTAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330  
DB 345 TTTGAAGACCTTCTCAAGGATATTAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 404  
QY 331 GAAATGCAAGAGGTGATGAGGATCTCAAAATGTCAGCACACGTTGTAAAGGAGAGCCCAAC 390  
DB 405 GAAATGCAAGAGGTGATGAGGATCTCAAAATGTCAGCACACGTTGTAAAGGAGAGCCCAAC 464  
QY 391 AGTAATGCAGATCCGTTCTACAGTGGGCCAAGAAAGGATATTATACCATGAAAGAGCAAC 450  
DB 465 AGTAATGCAGATCCGTTCTACAGTGGGCCAAGAAAGGATATTATACCATGAAAGAGCAAC 524  
QY 451 TTGTAATGCTTGAATATGGAACAGCTCACGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510  
DB 525 TTGTAATGCTTGAATATGGAACAGCTCACGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 584  
QY 511 TACACTCAAGTCACCTTCTGCTCTTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570  
DB 585 TACACTCAAGTCACCTTCTGCTCTTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644  
QY 571 GGCCTCTGGCTGAGAGCCAGCATTTGGATCTCAGAGATCTTACTCAAGGCGCAATATACC 630  
DB 645 GGCCTCTGGCTGAGAGCCAGCATTTGGATCTCAGAGATCTTACTCAAGGCGCAATATACC 704  
QY 631 CACAGTCTCTCCAGCTTTGGAGCAGCAGTCTCTTCACTTGGCGGAGTGTTTGAATTA 690  
DB 705 CACAGTCTCTCCAGCTTTGGAGCAGCAGTCTCTTCACTTGGCGGAGTGTTTGAATTA 764  
QY 691 CAAGCTGGTGTCTGTCTTGTCTCAACGTGACTGAGCAAGCCCAAGTGATCCACAGAGTT 750

DB 765 CAAGCTGGTGTCTGTCTTGTCTCAACGTGACTGAGCAAGCCCAAGTGATCCACAGAGTT 824  
QY 751 GGCTTCTCATCTTTTGGCTTTACTCAAACTCTGA 783  
DB 825 GGCTTCTCATCTTTTGGCTTTACTCAAACTCTGA 857

RESULT 14  
US-09-088-913A-22  
Sequence 22, Application US/09088913A  
Patent No. 6087329  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARVLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088.913A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: Murine CD40-L trimer  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 15..92  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..857

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 93..857  
US-09-088-913A-22

Query Match 80.6%; Score 631.4; DB 3; Length 878;

Best Local Similarity 99.8%; Pred. No. 3.1e-177;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 210  
DB 225 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 284  
QY 211 AGATCAACAAGAGAGAGTCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 270  
DB 285 AGATCAACAAGAGAGAGTCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 344  
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 330  
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 404  
QY 331 GAAATGCAAGAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 390  
DB 405 GAAATGCAAGAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 464  
QY 391 AGTAATGCAAGAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 450  
DB 465 AGTAATGCAAGAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 524  
QY 451 TTGGTAATGCTTGAAGTGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510  
DB 525 TTGGTAATGCTTGAAGTGGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 584  
QY 511 TACACTCAAGTCACTTCTGCTCTAATCGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 570  
DB 585 TACACTCAAGTCACTTCTGCTCTAATCGGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 644  
QY 571 GGCCTCTGGCTGAAGCCAGAGATGGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630  
DB 645 GGCCTCTGGCTGAAGCCAGAGATGGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 704  
QY 631 CACAGTCTCTCCAGCTTGGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690  
DB 705 CACAGTCTCTCCAGCTTGGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 764  
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DB 765 CAAGCTGTGCTGTCTGTTGTCTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 824  
QY 751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783  
DB 825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 15

US-08-769-819-22  
Sequence 22, Application US/08769819  
Patent No. 6264951

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSHLOW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA

ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08769,819  
FILING DATE: 19-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: Murine CD40-L trimer  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 15..92  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..857  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 93..857  
US-08-769-819-22

Query Match 80.6%; Score 631.4; DB 4; Length 878;

Best Local Similarity 99.8%; Pred. No. 3.1e-177;

Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 210  
DB 225 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATAAAGCTAAAG 284  
QY 211 AGATCAACAAGAGAGAGATCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 270  
DB 285 AGATCAACAAGAGAGAGATCTTTATCTTCTGCTGAAGTGTGAGAGATGAGAAGGCAA 344  
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 330  
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGAGAGAG 404  
QY 331 GAAATGCAAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 390  
DB 405 GAAATGCAAGAGTGTGAGAGATCTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 464  
QY 391 AGTAATGCAAGATCCGTTCTACAGTGGGCGCAAGAGAGATATATACCATGAAAGCAAC 450

us-08-982-272-3.rni

Thu May 30 05:46:02 2002

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Db 465 AGTAATGCAGATCCGTTCTACAGTGGCCAAAGAAAGGATATTATACCATGAAAAGCAAC 524
QY 451 TTGGTAATGCTTGAAATGGGAAACAGCTGACGGTTAAAGAGAGGAGTCTATTATGTC 510
Db 525 TTGGTAATGCTTGAAATGGGAAACAGCTGACGGTTAAAGAGAGGAGTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570
Db 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644
QY 571 GGCTCTGGCTGAAGCCCAAGCATTGGATCTGAGAGAACTTACTCAAGCGCGCAATACC 630
Db 645 GGCTCTGGCTGAAGCCCAAGCATTGGATCTGAGAGAACTTACTCAAGCGCGCAATACC 704
QY 631 CACAGTTCTCCAGCTTTCCGAGCAGCTCTGTTCACTTGGGGGAGTGTGTTGAATTA 690
Db 705 CACAGTTCTCCAGCTTTCCGAGCAGCTCTGTTCACTTGGGGGAGTGTGTTGAATTA 764
QY 691 CAAGCTGGTGTCTCTGTTTGTCAAGCTGACTGAAGCAAGCCCAAGTATCCACAGATT 750
Db 765 CAAGCTGGTGTCTCTGTTTGTCAAGCTGACTGAAGCAAGCCCAAGTATCCACAGATT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857

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Search completed: May 30, 2002, 02:51:25  
Job time: 11589 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:45 ; Search time 6499.83 Seconds  
(without alignments)  
2530.567 Million cell updates/sec

Title: US-08-982-272-4  
Perfect score: 786  
Sequence: 1 ATGATCGAACAATACACCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_ov.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
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- 19: em\_mu.\*
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- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	776.4	98.8	786	6	I87864	I87864 Sequence 3
2	776.4	98.8	840	6	AR044779	AR044779 Sequence
3	776.4	98.8	840	6	AR076926	AR076926 Sequence
4	776.4	98.8	840	6	AR078316	AR078316 Sequence
5	776.4	98.8	840	6	AR085419	AR085419 Sequence
6	776.4	98.8	840	6	AR103375	AR103375 Sequence
7	776.4	98.8	840	6	AR106246	AR106246 Sequence
8	776.4	98.8	840	6	AR169232	AR169232 Sequence
9	776.4	98.8	840	6	AR171647	AR171647 Sequence
10	776.4	98.8	840	6	I23893	I23893 Sequence 1
11	776.4	98.8	840	6	I27345	I27345 Sequence 7
12	776.4	98.8	840	6	I67828	I67828 Sequence 1
13	776.4	98.8	879	6	AX090039	AX090039 Sequence
14	776.4	98.8	879	9	HSGP39MR	Z15017 H.sapiens m
15	776.4	98.8	1803	9	HSCD40	X67878 H.sapiens m
16	776.4	98.8	1816	9	HUMCD40L	L07414 Human CD40-
17	774.8	98.8	1822	9	HSTRAPA	X58550 H.sapiens T
18	761.2	96.8	839	9	HACD40L	X96710 H.sapiens m
19	760.4	96.7	1058	9	AF344841	AF344841 Cercocaba
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21	739.6	94.1	974	9	AF344860	AF344860 Aotus tri
22	739.6	94.1	975	9	AF344844	AF344844 Callithri
23	638.8	81.3	864	4	BTCD40LIG	Z48469 B.taurus mR
24	638.2	81.2	1425	6	AR076929	AR076929 Sequence
25	638.2	81.2	1425	6	AR078319	AR078319 Sequence
26	638.2	81.2	1425	6	AR085422	AR085422 Sequence
27	638.2	81.2	1425	6	AR103378	AR103378 Sequence
28	638.2	81.2	1425	6	AR169235	AR169235 Sequence
29	637.2	81.1	929	6	AR076932	AR076932 Sequence
30	637.2	81.1	929	6	AR078322	AR078322 Sequence
31	637.2	81.1	929	6	AR085425	AR085425 Sequence
32	637.2	81.1	929	6	AR103381	AR103381 Sequence
33	637.2	81.1	929	6	AR169238	AR169238 Sequence
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36	608.4	77.4	788	4	AF079105	AF079105 Felis cat
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39	571.6	72.7	783	6	AR076918	AR076918 Sequence
40	571.6	72.7	783	6	AR078308	AR078308 Sequence
41	571.6	72.7	783	6	AR085411	AR085411 Sequence
42	571.6	72.7	783	6	AR103367	AR103367 Sequence
43	571.6	72.7	783	6	AR169224	AR169224 Sequence
44	571.6	72.7	783	6	I87865	I87865 Sequence 5
45	571.6	72.7	1250	10	MMCD40	X65453 M.musculus

## ALIGNMENTS

RESULT 1	I87864	Sequence 3 from patent US 5716805.	786 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	I87864					
DEFINITION	I87864					
ACCESSION	I87864					
VERSION	I87864.1	GI:3407804				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 786)					
AUTHORS	Srinivasan,S. and Spriggs,M.K.					
TITLE	Methods of preparing soluble, oligomeric proteins					
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;					
FEATURES	Location/Qualifiers					
source	1..786					
BASE COUNT	250 a 168 c 168 g 200 t					
ORIGIN						

Query Match 98.8%; Score 776.4; DB 6; Length 786;  
Best Local Similarity 99.2%; Pred. No. 1.7e-191;



ACCESSION	AR076926	GI:10003672
VERSION	AR076926.1	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 840)	
TITLE	Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.	
JOURNAL	Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same	
FEATURES	Patent: US 5961974-A 11 05-OCT-1999;	
source	Location/Qualifiers	
BASE COUNT	1..840	
ORIGIN	/organism="unknown"	
	266 a 185 c 175 g 214 t	
Query Match	98.88;	Score 776.4; DB 6; Length 840;
Best Local Similarity	99.28;	Pred. No. 1.7e-191;
Matches 780;	Conservative 0;	Mismatches 6; Indels 0; Gaps 0;
QY	1	ATGATCGAAACATACAACCAACCTCTCCCGATCTGCGGCACCTGGACTGCCCATCAGC 60
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QY	61	ATGAAATTTTATGTATTTACTTACTGTTCCTTTATCACCCAAATGATTGGATCTGTG 120
Db	106	ATGAAATTTTATGTATTTACTTACTGTTCCTTTATCACCCAGATGATTGGGTACGA 165
QY	121	CTTTTGTGCTGTATCTTCATAGAAGTGTGACAAGATAGAAGATGAAGAAATCTTCAT 180
Db	166	CTTTTGTGCTGTATCTTCATAGAAGTGTGACAAGATAGAAGATGAAGAAATCTTCAT 225
QY	181	GAAGATTTGTATTCATGAACACCATACAGAGATGCACACAGGAGAAGATCCTTATCC 240
Db	226	GAAGATTTGTATTCATGAACACCATACAGAGATGCACACAGGAGAAGATCCTTATCC 285
QY	241	TTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db	286	TTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
QY	301	AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 360
Db	346	AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 405
QY	361	CAAAATTCGGGCACATGTCATAAGTCAGGCCAGCAGTAAACAACATCTGCTTACAGTGG 420
Db	406	CAAAATTCGGGCACATGTCATAAGTCAGGCCAGCAGTAAACAACATCTGCTTACAGTGG 465
QY	421	GCTGAAAGAGATACTACACCATGAGCAACACTTGGTAAACCTCGGAAATGGGAAACAG 480
Db	466	GCTGAAAGAGATACTACACCATGAGCAACACTTGGTAAACCTCGGAAATGGGAAACAG 525
QY	481	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAAT 540
Db	526	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCAAT 585
QY	541	CGGGAAGCTTCGAGTCAAGCTCAATTTATACCGAGCCCTCGCCTAAAGTCCCCCGGTAGA 600
Db	586	CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCCTCGCCTAAAGTCCCCCGGTAGA 645
QY	601	TTCCAGAGAATCTTACTCAGAGCTGCAAAATACCACACAGTTCCGGCAAAACCTTGGGGCAA 660
Db	646	TTCCAGAGAATCTTACTCAGAGCTGCAAAATACCACACAGTTCCGGCAAAACCTTGGGGCAA 705
QY	661	CAATCCCATTCCTACTTGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTTCCTCAAT 720
Db	706	CAATCCCATTCCTACTTGGGAGGAGTATTTGAATTGCAACACAGGTGCTTCGGTGTTCCTCAAT 765
QY	721	GTGACTGATCCAGCCAGTGAGGCATGGCACTGGCTTTCAGCTCTTTGGCTTACTCAAA 780
Db	766	GTGACTGATCCAGCCAGTGAGGCATGGCACTGGCTTTCAGCTCTTTGGCTTACTCAAA 825

[illegible]

Thu May 30 05:46:05 2002

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601  TTTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCCGCAAAACCTTGGGGCAA 660
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646  TTTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCCGCAAAACCTTGGGGCAA 705
      |||||||
661  CAATCCATTACATTTGGAGAGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT 720
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706  CAATCCATTACATTTGGAGAGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT 765
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721  GTGACTGATCCAGCCAAAGTGGAGAGTGGCTTCCAGCTTCCCTTTGGCTTACTCAA 780
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766  GTGACTGATCCAGCCAAAGTGGAGAGTGGCTTCCAGCTTCCCTTTGGCTTACTCAA 825
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QY 781  CTCTGA 786
Db 826  CTCTGA 831

RESULT 5
LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5981724.
ACCESSION AR085419
VERSION AR085419.1 GI:10012188
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
  1 (bases 1 to 840)
  Unclassified.
  Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,
  Gibson, M.G., Morris, A.E. and McGrew, J.T.
  CD40 ligand, a cytokine that binds CD40
  DNA encoding CD40 ligand, a cytokine that binds CD40
  Patent: US 5981724-A 11 09-NOV-1999;
  JOURNAL
  FEATURES
    LOCATION/Qualifiers
    1..840
    /organism="unknown"
  SOURCE
    266 a 185 c 175 g 214 t

BASE COUNT. 266 a 185 c 175 g 214 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGAGTCCCATCAGC 60
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Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGAGTCCCATCAGC 105
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QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 120
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Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 165
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QY 121 CTTTGTGCTGTATCTTCATAGAGGTGGACAAGATGAAGATGAAAGGATCTTCAT 180
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Db 166 CTTTGTGCTGTATCTTCATAGAGGTGGACAAGATGAAGATGAAAGGATCTTCAT 225
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QY 181 GAAGATTTTGTATTTATGTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 240
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Db 226 GAAGATTTTGTATTTATGTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 285
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QY 241 TTACTGAATCTGTAGAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 300
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Db 286 TTACTGAATCTGTAGAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
      |||||||
QY 301 AACAAGAGGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAACTCT 360
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Db 346 AACAAGAGGAGACGAAAGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGAACTCT 405
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QY 361 CAAATTTGGCGACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTTACATGG 420
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Db 406 CAAATTTGGCGACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTTACATGG 465
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QY 421 GCTTAAAGAGGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAACAG 480
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466  GCTGAAAAGGATACTACACCATGAGCAACAACTTGTAAACCTTGGAAATGGAAACAG 525
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526  CTGACCGTTAAAGACAAGGACTCTATTATATCTATGATGATGATGATGATGATGATGAT 585
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541  CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGCGGTAGA 600
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586  CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGCGGTAGA 645
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601  TTTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCCGCAAAACCTTGGGGCAA 660
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646  TTTGAGAGAAATCTTACTAGAGCTGCAATATACCCACAGTTCCGCAAAACCTTGGGGCAA 705
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661  CAATCCATTACATTTGGAGAGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT 720
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706  CAATCCATTACATTTGGAGAGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCAT 765
      |||||||
721  GTGACTGATCCAGCCAAAGTGGAGAGTGGCTTCCAGCTTCCCTTTGGCTTACTCAA 780
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766  GTGACTGATCCAGCCAAAGTGGAGAGTGGCTTCCAGCTTCCCTTTGGCTTACTCAA 825
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QY 781  CTCTGA 786
Db 826  CTCTGA 831

RESULT 6
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6087329.
ACCESSION AR103375
VERSION AR103375.1 GI:12814963
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
  1 (bases 1 to 840)
  Unclassified.
  Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.
  CD40 ligand polypeptide
  Patent: US 6087329-A 11 11-JUL-2000;
  JOURNAL
  FEATURES
    LOCATION/Qualifiers
    1..840
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    266 a 185 c 175 g 214 t

BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN
Query Match 98.8%; Score 776.4; DB 6; Length 840;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGAGTCCCATCAGC 60
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QY 121 CTTTGTGCTGTATCTTCATAGAGGTGGACAAGATGAAGATGAAAGGATCTTCAT 180
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QY 181 GAAGATTTTGTATTTATGTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 240
      |||||||
Db 226 GAAGATTTTGTATTTATGTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG 285
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QY 241 TTACTGAATCTGTAGAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 300
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Db 286 TTACTGAATCTGTAGAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
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QY 301 ACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
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Thu May 30 05:46:05 2002

us-08-982-272-4.rge

BASE COUNT 263 a 182 c 214 t  
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Query Match 98.8%; Score 776.4; DB 6; Length 840;  
Best Local Similarity 99.2%; Pred. No. 1.7e-191;  
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QY 181 GAAGATTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
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QY 361 CAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420  
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RESULT 10  
LOCUS I23893 840 bp DNA linear PAT 07-OCT-1996.  
DEFINITION Sequence 1 from patent US 540926.  
ACCESSION I23893  
VERSION I23893.1 GI:1603763  
KEYWORDS

RESULT 9  
LOCUS AR171647 840 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 3 from patent US 6297052.  
ACCESSION AR171647  
VERSION AR171647.1 GI:17910597  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Kehry,M. and Castile,B.  
TITLE B cell culture system comprising high density membrane bound CD40 ligand  
JOURNAL Patent: US 6297052-A 3 02-OCT-2001;  
FEATURES Location/Qualifiers  
1. 840 source

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A.  
TITLE Soluble and its use in B cell stimulation  
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;  
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source  
BASE COUNT 263 a 182 c 181 g 214 t  
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;  
Best Local Similarity 99.2%; Pred. No. 1.7e-191;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 60  
DB 22 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTCGGCGCACTGGACTGCCCATCAGC 81

QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
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QY 121 CTTTCTGCTGTATCTTCATAGAGGTTGGACAAGATGAAAGATGAAAGGAATCTTCAT 180  
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QY 241 TTACTGAACGTGAGGAGATTAAGCCAGTTTGAAGCCTTTGCAAGGATATAATGTTA 300  
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QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 360  
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QY 781 CTCTGA 786  
DB 802 CTCTGA 807

RESULT 11  
LOCUS I27345  
DEFINITION Sequence 7 from patent US 5565321.  
ACCESSION I27345  
VERSION I27345.1 GI:1818121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs, M. K., Armitage, R. J. and Fanslow, W. C. III.  
TITLE Detection of mutations in a CD40 ligand gene  
JOURNAL Patent: US 5565321-A 7 15-OCT-1996;  
FEATURES Location/Qualifiers  
source  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 98.8%; Score 776.4; DB 6; Length 840;  
Best Local Similarity 99.2%; Pred. No. 1.7e-191;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCGCACTGGACTGCCCATCAGC 60  
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QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
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 LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998  
 DEFINITION Sequence 1 from patent US 5674492.  
 ACCESSION 167828  
 VERSION 167828.1 GI:2829950  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 840)  
 AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.  
 TITLE Method of preventing or treating disease characterized by neoplastic cells expressing CD40  
 JOURNAL Patent: US 5674492-A 1 07-OCT-1997;  
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 LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001  
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 ACCESSION AX090039  
 VERSION AX090039.1 GI:13444004  
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 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 879)  
 AUTHORS Ahuja, S.U. and Bonewald, L.U.  
 TITLE Cd40 agonist compositions and methods of use  
 JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;  
 BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)  
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 Best Local Similarity 99.2%; Pred. No. 1.7e-191;  
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 QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGAGTGCCTCATCAGC 60  
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Db 802 CTCTGA 807
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DEFINITION     H. sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION      215017.1
VERSION        215017.1 GI:38483
KEYWORDS       glycoprotein 39.
SOURCE         human.
ORGANISM       Homo sapiens
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REFERENCE      1 (bases 1 to 879)
AUTHORS        Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
               Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
               and Aruffo, A.
TITLE          The human T cell antigen gp39, a member of the TNF gene family, is
               a ligand for the CD40 receptor: expression of a soluble form of
               gp39 with B cell co-stimulatory activity
               EMBO J. 11 (12), 4313-4321 (1992)
JOURNAL        93049181
MEDLINE        2 (bases 1 to 879)
REFERENCE      Hollenbaugh, D.L.
AUTHORS        Direct Submission
TITLE          Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
JOURNAL        PRI, Seattle, WA, 98121
REFERENCE      3 (bases 1 to 879)
AUTHORS        Hollenbaugh, D.
TITLE          Direct Submission
JOURNAL        PRI, Seattle, WA, 98121
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BASE COUNT    274 a 193 c 190 g 222 t
ORIGIN

Query Match      98.8%; Score 776.4; DB 9; Length 879;
Best Local Similarity 99.2%; Pred. No. 1.7e-191;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGAGCTGCCCATCAGC 60
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QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGGCCTTTCAGCTGCTTGGCTTACTCAAA 780
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Db 742 GTGACTGATCCAAAGCAAGTGAGCCATGGCCTTTCAGCTGCTTGGCTTACTCAAA 801
|||||
QY 781 CTCTGA 786
|||||
Db 802 CTCTGA 807
|||||

RESULT 15
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HSCD40 LOCUS HSCD40 1803 bp mRNA linear PRI 06-JUN-1997  
DEFINITION H.sapiens mRNA for CD40 ligand.  
ACCESSION X67878 S50586  
VERSION X67878.1 GI:38411  
KEYWORDS glycoprotein.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1803)  
Spriggs, M.  
Direct Submission  
Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development  
Corporation, 51 University Street, Seattle WA 98101, USA  
REFERENCE 2 (bases 1 to 1803)  
Spriggs, M.K., Amittage, R.J., Strockbine, L., Clifford, K.N.,  
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.,  
Recombinant human CD40 ligand stimulates B cell proliferation and  
immunoglobulin E secretion  
J. Exp. Med. 176 (6), 1543-1550 (1992)  
93094757  
FEATURES  
source  
CDS  
sig\_peptide  
BASE COUNT 510 a 456 c 344 g 493 t  
ORIGIN  
Query Match 98.8%; Score 776.4; DB 9; Length 1803;  
Best Local Similarity 99.2%; Pred. No. 1.6e-191;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGTATTTACTTACTTGTCTTCTTATACCCCAATGATGGATCTGTG 120  
DB 106 ATGAAATTTTATGTATTTACTTACTTGTCTTCTTATACCCCAATGATGGATCTGTG 165  
QY 121 CTTTGTCTGTATCTTCTATAGAGGTGGACAAGATAGAAGATGAAGAAATCTTCAT 180  
DB 166 CTTTGTCTGTATCTTCTATAGAGGTGGACAAGATAGAAGATGAAGAAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATCAAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTCATCAAAACCATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACCTGTAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACCTGTAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGGACCAACAAACAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 360  
DB 346 AACAAAGAGGACCAACAAACAAACAGCTTTGAATGCAAAAGGTGATCAGAAATCCT 405  
QY 361 CAAATTCGGCCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTCTACATGG 420

DB 406 CAAATTCGGCCACATGTCTAATAGTGAGGCCAGCAGTAAACAAACATCTGTCTACATGG 465  
QY 421 GCTGAAAAAGGATACTTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGAAACAG 480  
DB 466 GCTGAAAAAGGATACTTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGAAACAG 525  
QY 481 CTGACCGTTAAAGACAAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 540  
DB 526 CTGACCGTTAAAGACAAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGAAATCTTACTTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCAA 660  
DB 646 TTCGAGAGAAATCTTACTTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCAA 705  
QY 661 CAATCCATTCACTTGGGAGGAGTATTGTAATTCGAACCCAGTCTTCGGTGTGTGTCAAT 720  
DB 706 CAATCCATTCACTTGGGAGGAGTATTGTAATTCGAACCCAGTCTTCGGTGTGTGTCAAT 765  
QY 721 GTGACTCATCCAGCCCAAGTGAGCCATGGCCTTTCACGCTCCTTTGGCTTACTCAAA 780  
DB 766 GTGACTCATCCAGCCCAAGTGAGCCATGGCCTTTCACGCTCCTTTGGCTTACTCAAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

Search completed: May 30, 2002, 02:48:52  
Job time: 22011 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:01 : Search time 5112.58 Seconds  
(without alignments)  
2075.001 Million cell updates/sec

Title: US-08-982-272-4  
Perfect score: 786  
Sequence: 1 ATGATCGAATACATACACCA.....TTGGCTTACTCAACTCTGA 786

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pln: \*  
16: em\_gss\_vrt: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	355.8	45.3	492	10	BF599437 263218 MA
2	280.4	35.7	398	9	AM486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.p007
4	50.2	6.4	1027	12	A2166561
5	48.8	6.2	997	12	CNS005TE
6	48.4	6.2	1043	12	CNS0145P
7	47.2	6.0	396	10	BF820152
8	47.2	6.0	486	9	AV714252
9	47.2	6.0	578	9	AV724813
10	47.2	6.0	583	9	AV724813
11	47.2	6.0	586	10	BF791160 602251255
12	47.2	6.0	797	9	AL534423
13	47.2	6.0	845	10	BF715238 602676117
14	47.2	6.0	845	10	BF715238 602676117
15	47.2	6.0	861	10	BF573761 602077072
16	47.2	6.0	873	10	BF616023 602643466
17	47.2	6.0	874	10	BF715241 602676120

C	18	47	6.0	423	12	A2438784
C	19	46.8	6.0	553	9	AA312300
C	20	46.6	5.9	458	9	AL514085
C	21	46.4	5.9	562	9	AL564525
C	22	46.2	5.9	433	9	AA115682
C	23	46.2	5.9	772	10	BF763299
C	24	46.2	5.9	777	10	BF1598192
C	25	46	5.9	432	10	BE888601
C	26	46	5.9	636	10	BF717854
C	27	46	5.9	1101	12	CNS00396
C	28	45.8	5.8	382	9	AA352023
C	29	45.6	5.8	302	9	AA852210
C	30	45.6	5.8	385	10	T08274
C	31	45.6	5.8	389	9	AV704993
C	32	45.6	5.8	434	9	AA081760
C	33	45.6	5.8	437	9	AV729112
C	34	45.6	5.8	460	10	BF598293
C	35	45.6	5.8	494	10	BF983924
C	36	45.6	5.8	508	9	AA408255
C	37	45.6	5.8	512	9	AA372979
C	38	45.6	5.8	515	10	BE895474
C	39	45.6	5.8	523	10	BE397964
C	40	45.6	5.8	560	10	BF539029
C	41	45.6	5.8	565	9	AI929671
C	42	45.6	5.8	575	9	AA605905
C	43	45.6	5.8	602	9	AV713776
C	44	45.6	5.8	607	10	BF720477
C	45	45.6	5.8	610	10	BE398061

## ALIGNMENTS

RESULT 1  
LOCUS BF599437 492 bp mRNA linear EST 25-APR-2001  
DEFINITION 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF599437  
VERSION BF599437.1 GI:11695919

KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 492)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Perteira,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
Keele,J.W.

REFERENCE

Sequence evaluation of four pooled-tissue normalized bovine CDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@maill.marc.usda.gov

TITLE

Journal MEDLINE  
COMMENT  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGTATGACCAT  
BACKWARD: GTTCCACAGTACGACG  
Plate: 33 row: N column: 5  
Seq primer: ATTGAGTGACACTATAG.

FEATURES

source  
1..492  
/organism="Bos taurus"  
/db\_xref="taxon:9913"



/clone.lib="MARC.3BOV"  
/tissue.type="pooled"  
/lab.host="DH10B"  
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."  
BASE COUNT 163 a 103 c 104 g 122 t  
ORIGIN

Query Match 45.3%; Score 355.8; DB 10; Length 492;  
Best Local Similarity 87.2%; Pred. No. 4.7e-70;  
Matches 390; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

1 ATGATGGAACATACCAACCAACTCTCCCGGATGCGGCGCAGTGCATGCATCAGC 60  
|||||  
46 ATGATGGAACATACCAACCAACTCTCCCGGATGCGGCGCAGTGCATGCATCAGT 105  
|||||  
61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 120  
|||||  
106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATGAGCG 165  
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121 CTTTTCCTGTATCTTCTATAGAGGTGGACAGATAGATGAAGATCTTCAT 180  
|||||  
166 CTTTTCCTGTATCTTCTATAGAGGTGGACAGATAGATGAAGATGAAGATCTTCAT 225  
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181 GAAGATTTTGTATTCATGAAAGATACAGATGACACAGAGAGAAATGCTTATCC 240  
|||||  
226 GAAGATTTTGTATTCATGAAAGATACAGATGACACAGAGAGAGAGAGAGAGAGAG 285  
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241 TTACTGAACGTGAGGATTAAGAGCAGTTGAAGCTTTTGAAGATTAATGTTA 300  
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286 TTACTGAACGTGAGGATTAAGAGCAGTTGAAGCTTTTGAAGATTAATGTTA 345  
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301 AACAAAG 360  
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346 AACAAAG 405  
|||||  
361 CAATTCGGGACATGTCATAGTCAGAGCGCAGAGATTAACATCTGTTGATGATG 420  
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406 CAGATATGCGGACATGTCATAGTCAGAGCGCAGAGATTAACATCTGTTGATGATG 465  
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421 GCTGAAAGAGATACCATGAGC 447  
|||||  
466 GCCCCCAAGATTAACCATGAGC 492

RESULT 2  
AM486605 398 bp mRNA linear EST 25-Apr-2001

LOCUS AM486605  
DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION AM486605  
VERSION AM486605.1 GI:7056711  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 398)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Cassas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.M., Kohrer,G.A., Chalko-McKown,C.G.,  
Perteira,G., Holt,I., Karameycheva,S., Liang,F., Quakenbush,J. and  
Keeler,J.W.

AUTHORS

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA

tel: 402 762 4366  
fax: 402 762 4390  
Email: smitht@mail.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.960904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTGCTGACGACG  
Plate: 34 Row: F Column: 23  
Seq primer: ATTAGCTGACACTATAG.  
Location/Qualifiers  
1. 398  
/organism="Bos taurus"  
/db.xref="taxon:9913"  
/clone.lib="MARC.1BOV"  
/tissue.type="pooled"  
/lab.host="DH10B"  
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;  
Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."  
BASE COUNT 134 a 77 c 82 g 105 t  
ORIGIN

Query Match 35.7%; Score 280.4; DB 9; Length 398;  
Best Local Similarity 88.2%; Pred. No. 4.5e-53;  
Matches 305; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 ATGATGGAACATACCAACCAACTCTCCCGGATGCGGCGCAGTGCATGCATCAGC 60  
|||||  
53 ATGATGGAACATACCAACCAACTCTCCCGGATGCGGCGCAGTGCATGCATCAGT 112  
|||||  
61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 120  
|||||  
113 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCCAATGATGATGATGAGCG 172  
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121 CTTTTCCTGTATCTTCTATAGAGGTGGACAGATAGATGAAGATCTTCAT 180  
|||||  
173 CTTTTCCTGTATCTTCTATAGAGGTGGACAGATAGATGAAGATGAAGATCTTCAT 232  
|||||  
181 GAAGATTTTGTATTCATGAAAGATACAGATGACAGATGACAGAGAGAGAGAGAGAG 240  
|||||  
233 GAAGATTTTGTATTCATGAAAGATACAGATGACAGATGACAGAGAGAGAGAGAGAG 292  
|||||  
241 TTACTGAACGTGAGGATTAAGAGCAGTTGAAGCTTTTGAAGATTAATGTTA 300  
|||||  
293 TTACTGAACGTGAGGATTAAGAGCAGTTGAAGCTTTTGAAGATTAATGTTA 352  
|||||  
301 AACAAAG 346  
|||||  
353 AACAAAG 398  
|||||

RESULT 3  
A1982044 638 bp mRNA linear EST 07-MAY-2001

LOCUS A1982044  
DEFINITION pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus  
Clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.

ACCESSION A1982044  
VERSION A1982044.1 GI:5885072  
KEYWORDS EST.  
SOURCE CHICKEN.  
ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 638)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.

AUTHORS Tirmegary,V.G., Sofer,L., Cui,J. and Burnside,J.

TITLE An expressed sequence tag database of T-cell-enriched activated  
chicken splenocytes: sequence analysis of 5251 clones  
JOURNAL Genomics 66 (2), 144-151 (2000)  
MEDLINE 20318616





Location/Qualifiers

### Source

## ORIGIN

Matches	39;	conservative	143;	misinformation	100;	and	of	and
---------	-----	--------------	------	----------------	------	-----	----	-----

[illegible]

D5 790 KAKGAKKKKGGKKKGKKKNKNAAGHVVV.....

[illegible][illegible][illegible]

DD

DD 450 RN 407

CNS0145P/C	1043 bp	DNA.	linear	GSS 26-JU
CNS0145P				
10000				

ILY), genomic survey sequence.  
 M102725

SOURCE : FRUIT FLY.

Muscomorpha; Ephyraeidae, Diophridae, Protopharyngidae

JOURNAL  
Submitted (23-JUL-1999) Genoscope  
20101 01006 ENVY codex - FRANCE (E-mail): secref@genoscope.c

LOCALIZATION OF THE  
1 1043

## Source

100

120

190

240

**ՀԱՅԿԱՍՏԱՆԻ ՀԱՆՐԱՊԵՏՈՒԹՅԱՆ ՎՃԱՌԱՋԱՆԳԱԾ**

ՀԱՅԱՍՏԱՆԻ ՀԱՆՐԱՊԵՏՈՒԹՅԱՆ ԱՆՏՀԱՆՈՒԹՅԱՆ ԱՊՐԱՆՈՒԹՅԱՆ ԿԵՆՏՐՈՆԻ ՎԵՐԱԿԱՆԱԿՈՒՄԸ 369

303

LOCUS : BF820152 396 bp ILIKWA LINEAL  
 177100-003-006 BT0025 HOMO SAPIENS CDNA, mRNA sequence.

**KEYWORDS** EST.

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Balda, G.S., Simpson, D.H.

TITLE Shotgun sequencing of the human transcriptome with one expressed

COMMENT Contact: Simpson A.J.G.





Inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 198 a 107 c 163 g 118 t

Query Match 6.0%; Score 47.2; DB 10; Length 586;  
Best Local Similarity 50.0%; Pred. No. 1.5;  
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAAGTGGAGGACATTTAAAGCCATTGAGCTTTGAGAGATTAATG 297  
Db 144 TTCTATGATTCAGAGTGGTGAATAAAACGTGATGATGCTCCAGAGCAGAGTA 203  
QY 298 TTAACAAG 357  
Db 204 CTCAATATGCTGAGACACCAATTTGCAGAAACAGAGAGAGAGAGAGAGAGAG 263  
QY 358 CCTCAATATGCTGAGACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 417  
Db 264 CAGATATGAG 323  
QY 418 TGGGCTGAG 473  
Db 324 CAGAAAG 379

RESULT 12  
LOCUS AL534423 797 bp mRNA linear EST 13-FEB-2001  
DEFINITION AL534423 LTL\_FL013\_FBRn1 Homo sapiens cDNA clone CS0DF004YD24 5 prime, mRNA sequence.  
VERSION AL534423  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 797)  
AUTHORS L.W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers

FEATURES  
SOURCE  
1. 797  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DF004YD24"  
/clone\_id="LTL\_FL013\_FBRn1"  
/dev\_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"  
/lab\_host="DH10B"  
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Notti-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others

ORIGIN

Query Match 6.0%; Score 47.2; DB 9; Length 797;  
Best Local Similarity 39.6%; Pred. No. 1.6;

Matches 168; Conservative 37; Mismatches 215; Indels 4; Gaps 1;

QY 151 GACAGATGAGAGATGAGAGAGATCTTCATGATTTTGTATTCATGAGAGATGAG 210  
Db 244 GAAAG 303  
QY 211 AGATGCAACAGAGAGAGAGAGATCTTCATGAGAGATGAGAGATGAGAGAGAG 270  
Db 304 AAATGTAAG 363  
QY 271 TTGAGAGCTTTGAGAGAGAT---ATATGTTAAACAGAGAGAGAGAGAGAGAG 326  
Db 364 WAAG 423  
QY 327 CAGCTTGAATGCAAG 386  
Db 424 AAGTGAAG 483  
QY 387 GCGCAGAGTAAACACATCTGTGTACGTGAGAGAGAGAGAGAGAGAGAGAGAG 446  
Db 484 AATGAGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543  
QY 447 CACAACTGTTAACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506  
Db 544 AAAATTAAG 603  
QY 507 TTATATCTATGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566  
Db 604 TTGTTTMT 663  
QY 567 TATA 570  
Db 664 MMTA 667

RESULT 13  
LOCUS BG715238 845 bp mRNA linear EST 08-MAY-2001  
DEFINITION 602676117F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4798372 5', mRNA sequence.  
VERSION BG715238  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 845)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: ggapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1AM10686 row: b column: 05  
High quality sequence stop: 830.  
Location/Qualifiers

FEATURES  
SOURCE  
1. 845  
/organism="Homo sapiens"  
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/clone="IMAGE:4798372"  
/clone\_id="NIH\_MGC\_96"  
/clone\_lib="NIH\_MGC\_96"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptPR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROF 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, In preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 284 a 151 c 228 g 182 t  
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 845;  
Best Local Similarity 50.0%; Pred. No. 1.6;  
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 238 TCCTTACTGACTGTGAGGAGATTAAAGCCAGTTTGAGCGCTTGTGAGGATTAATG 297  
DB 177 TTCTATCATTTACAGTGTGGAATAAAAATCGGGATGMAATGGGTCCGGAGACAGAGTA 236  
OY 298 TTTAACAAG 357  
DB 237 CTCGAATACGTGACACCAATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296  
OY 358 CCTCAATTCGGCAGATGTCATTAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417  
DB 297 CAGATGACAG 356  
OY 418 TGGGCTGAAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473  
DB 357 CAGAAAAATGTTGAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412

RESULT 14 845 bp mRNA linear EST 07-SEP-2001  
LOCUS B1601432  
DEFINITION 603249012F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5300787 5', mRNA sequence.  
ACCESSION B1601432  
VERSION B1601432.1 GI:15494371  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE 1 (bases 1 to 845)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshikuni and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
Plate: LLM11761 row: h column: 04  
High quality sequence stop: 740.

FEATURES  
source  
Location/Qualifiers  
1. 845

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/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
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for full-length clones and constructed using the Cap-trapper method (Carninci, In preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 279 a 145 c 243 g 178 t  
ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 845;  
Best Local Similarity 50.0%; Pred. No. 1.6;  
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 238 TCCTTACTGACTGTGAGGAGATTAAAGCCAGTTTGAGCGCTTGTGAGGATTAATG 297  
DB 209 TTCTATCATTTACAGTGTGGAATAAAAATCGGGATGMAATGGGTCCGGAGAGAGTA 268  
OY 298 TTTAACAAG 357  
DB 269 CTCGAATACGTGACACCAATTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 328  
OY 358 CCTCAATTCGGCAGATGTCATTAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417  
DB 329 CAGATGACAG 388  
OY 418 TGGGCTGAAAAAGAGATCTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473  
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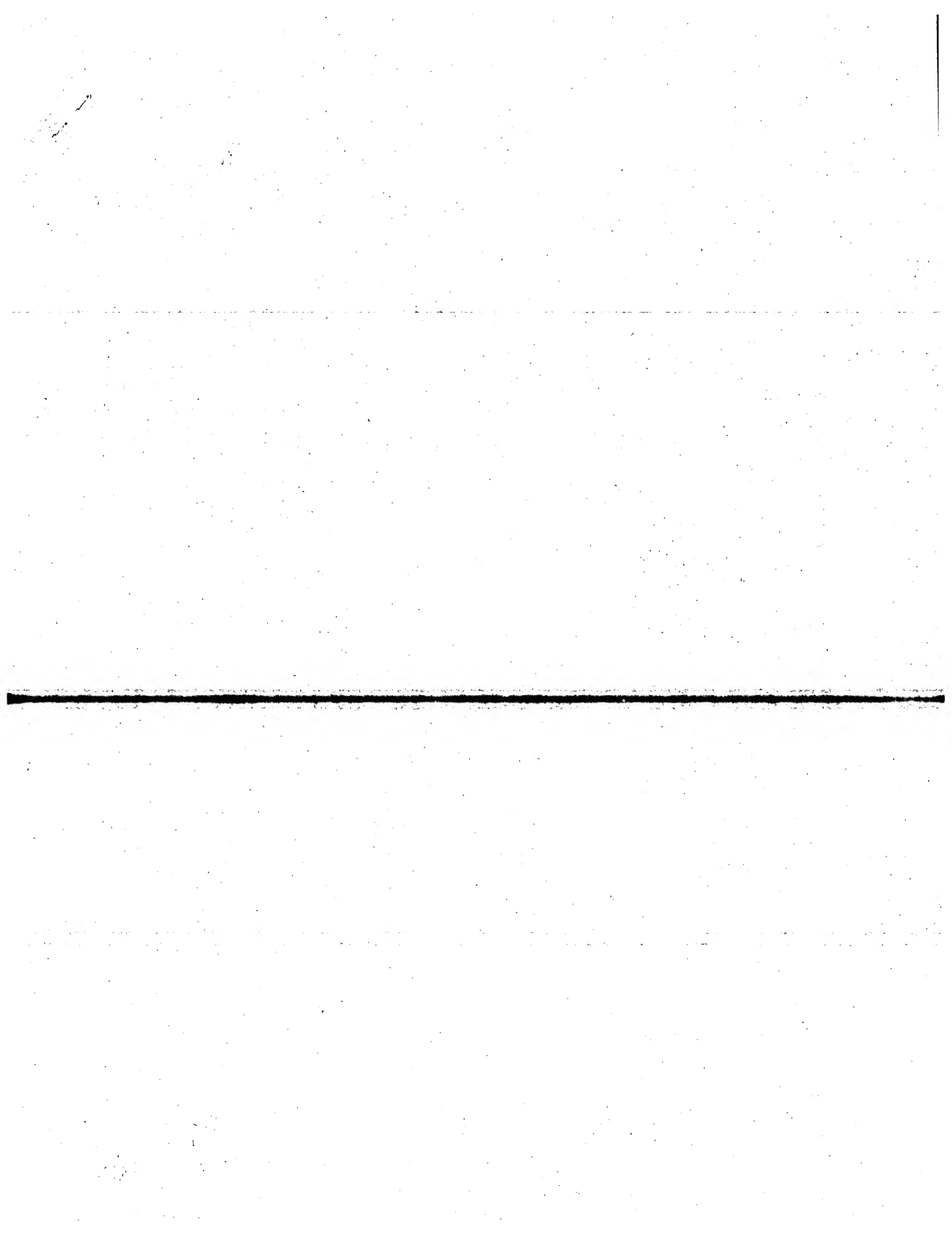
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DEFINITION 602077072F2 NIH\_MGC\_62 Homo sapiens cDNA clone IMAGE:4251880 5', mRNA sequence.  
ACCESSION BF573761  
VERSION BF573761.1 GI:11647473  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE 1 (bases 1 to 861)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: ATCC/DC/DTP  
CDNA Library Preparation: CLOVETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
Plate: LLM1075 row: o column: 17  
High quality sequence stop: 590.

FEATURES  
source  
Location/Qualifiers  
1. 861

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/clone="IMAGE:4251880"  
/clone\_1lb="NIH\_MGC\_62"  
/tissue\_type="melanotic melanoma, high MDR"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccgctggc); Site 2: SfiI (ggccatattg); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGCGCGAGCGCGAGATG-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGAGCGCGAGATG-3' (30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:07 ; Search time 680.87 Seconds

(Without alignments)  
1982.015 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786  
Sequence: 1 ATGATCGAAGACTACACCA.....TTGGCTTACTCAACTCTCA 786

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query length	ID	Description
1	786	100.0	786 19 AAV39000	Exemplary CD40 lig
2	776.4	98.8	786 15 AA063959	Human CD40-L type
3	776.4	98.8	786 19 AAV38997	CD40 ligand gene u
4	776.4	98.8	786 19 AAV12852	CD40 ligand coding
5	776.4	98.8	840 14 AA041506	CD40-L DNA. Homo
6	776.4	98.8	840 15 AA067123	CD40 ligand gene.
7	776.4	98.8	840 16 AAT05763	Human CD40 ligand
8	776.4	98.8	840 18 AAT93782	CDNA of CD40L, a n
9	776.4	98.8	840 19 AAV61063	Human CD40 ligand

10	776.4	98.8	840 20 AA27525	Human CD40-L codin
11	776.4	98.8	879 22 AAF55539	Nucleotide sequenc
12	776.4	98.8	1816 21 AA51745	Human CD40 ligand
13	776.4	98.8	1816 23 AAS86571	DNA encoding novel
14	773.4	98.4	840 18 AAT58122	Human CD40L mutein
15	773.2	98.4	840 15 AA057984	Genomic sequence o
16	771.6	98.2	840 16 AA094091	Human CD40-L cDNA.
17	763.6	97.2	786 19 AAV39003	Exemplary CD40 lig
18	754	95.9	786 19 AAV39002	Exemplary CD40 lig
19	717.2	91.2	783 19 AAV42184	Exemplary nucleoti
20	648.2	82.5	1552 22 AAH25525	Nucleotide sequenc
21	642.8	81.8	865 22 AAF82933	HIV-1 gp120 V3 loo
22	642.8	81.8	906 22 AAF82932	HIV-1 gp120-human
23	642.8	81.8	2209 22 AAF82929	HIV-1 gp120-human
24	642.8	81.8	2252 22 AAF82928	CD40 ligand gene u
25	638.8	81.3	864 19 AAV39004	Human CD40-L/Fc fu
26	638.2	81.2	1425 14 AA041516	Human CD40-L/Fc fu
27	638.2	81.2	1425 20 AA27534	CDNA encoding Yeas
28	637.2	81.1	929 18 AAT58123	Human trimeric CD4
29	637.2	81.1	929 20 AA27537	Feline CD154 cDNA.
30	606.8	77.2	885 21 AA255540	Feline CD154 cDNA.
31	606.8	77.2	885 21 AA255541	Feline CD154 cDNA.
32	603.8	76.8	780 21 AA255542	Feline CD154 cDNA
33	603.8	76.8	780 21 AA255543	Feline CD154 cDNA
34	592.4	75.4	783 19 AAV39001	Exemplary CD40 lig
35	587.6	74.8	1878 21 AA255534	Canine CD154 cDNA.
36	587.6	74.8	1878 21 AA255535	Canine CD154 cDNA
37	584.6	74.4	780 21 AA255536	Canine CD154 cDNA
38	582.8	74.1	783 19 AA255537	Canine CD154 cDNA
39	582.8	74.1	783 19 AAV38999	Exemplary CD40 lig
40	571.6	72.7	783 15 AA063960	Mouse CD40-L type
41	571.6	72.7	783 19 AAV12853	CD40 ligand coding
42	571.6	72.7	783 20 AA275524	Mouse CD40-L codin
43	570	72.5	783 19 AAV38998	CD40 ligand gene u
44	570	72.5	818 19 AAV61062	Murine CD40 ligand
45	567.4	72.2	782 14 AA041507	Murine CD40-L DNA.

# ALIGNMENTS

RESULT 1	AAV39000 standard; DNA; 786 BP.
XX	AAV39000;
XX	23-SEP-1998 (first entry)
XX	Exemplary CD40 ligand gene used in the course of the invention.
DE	CD40 ligand; alteration; immunoreactivity; human cell;
XX	accessory molecule ligand; AM; gene therapy; treatment; neoplasia;
KW	autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.
XX	Chimeric - Mus sp.
OS	Chimeric - Homo sapiens.
XX	WO9826061-A2.
XX	18-JUN-1998.
XX	08-DEC-1997; 97WO-US22740.
XX	01-DEC-1997; 97US-0982272.
PR	09-DEC-1996; 96US-0032145.
XX	(REGC) UNIV CALIFORNIA.
PA	Cantwell M, Kipps TJ, Sharma S;
XX	WPI; 1998-348521/30.
XX	

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QY	661	CAATCCATTACTCTGGGAGAGATTTGAATTGCAACACAGTGCCTTCGCTTTGTCAAT	720

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Matches	780	Mismatches	6
Conservative	0	Indels	0

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Db 361 caaatctgcgacatgtcatagtaagtgagccagcagtaaaacaatctgtgtacagtg 420
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QY 781 CTCTGA 786
Db 781 ctctga 786

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## RESULT 3

AAV38997 ID AAV38997 standard; DNA: 786 BP.

AC AAV38997;

DT 23-SEP-1998 (first entry)

DE CD40 ligand gene used in the course of the invention.

XX CD40 ligand; alteration; immunoreactivity; human cell;

KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

XX autoimmune disorder; rheumatoid arthritis; vaccine; ss.

OS Mus sp.

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XX PN MO9826061-A2.
XX PD 18-JUN-1998.
XX PF 08-DEC-1997; 97WO-US22740.
XX PR 01-DEC-1997; 97US-0982272.
XX PR 09-DEC-1996; 96US-0032145.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Cantwell M, Kipps TJ, Sharma S;
XX DR WPI; 1998-348521/30.
XX PT Vectors containing accessory molecule ligand genes - used for
XX PS altering immunoreactivity of cells, particularly for treatment of
XX PS neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
XX PS Disclosure; Page 104; 167pp; English.
XX CC The present sequence represents the CD40 ligand gene. The sequence is
XX CC used to exemplify the method of the invention. The specification
XX CC describes a method for altering the immunoreactivity of human cells
XX CC which comprises introducing a gene encoding an accessory molecule
XX CC ligand (AML) into the cells so that the AML is expressed on the surface
XX CC of the cells. Vectors containing the AML genes can be used in gene
XX CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
XX CC arthritis. They can also be used for vaccination to produce immunity
XX CC against a virus cell, bacteria, protein, fungus or neoplasia.
XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 98.8%; Score 776.4; DB 19; Length 786;
Best Local Similarity 99.2%; Pred. No. 6.2e-214;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 721 gtgactgaccgaagtgagccatgacgtgcttccacgtccttgccttactcaaa 780  
 OY 781 CTCGA 786  
 Db 781 ctcgca 786

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 AC AA041506  
 XX 12-AUG-1993 (first entry)  
 DE CD40-L DNA.  
 XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;  
 KM transmembrane; region; intracellular; soluble; activity; B cell;  
 KM proliferation; induction; antibody; secretion; IGE; agonist;  
 KM antagonist; binding assay; ss.  
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 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 46..831  
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 XX  
 PN W09308207-A.  
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 XX 29-APR-1993.  
 PD  
 PE 23-OCT-1992; 92WO-US08990.  
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 PR 25-OCT-1991; 91US-0783707.  
 PR 05-DEC-1991; 91US-0805723.  
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 PA (IMMUNEX CORP.  
 PI Armitage RJ, Fanslow WC, Spriggs MK;  
 DR WPI; 1993-152417/18.  
 DR P-PSDB; AAR36701.  
 XX  
 XX New cytokine CD40-L as CD40 agonist and antagonist - is used for  
 PT treating allergies, lupus, rheumatoid arthritis, is used for  
 PT graft-versus-host disease and insulin-dependent diabetes mellitus  
 PT  
 XX Claim 1; Fig 2; 80pp; English.  
 PS  
 CC This sequence encodes a human CD40-L polypeptide which binds to CD40.  
 CC CD40-L is a type II membrane polypeptide which has an extracellular  
 CC region at its C-terminus, a transmembrane region and an  
 CC intracellular region at its N-terminus. A soluble form of CD40-L  
 CC lacks the transmembrane domain. CD40-L activity is mediated by  
 CC binding with CD40 an induces B cell proliferation and induction of  
 CC antibody secretion, including IGE. Membrane bound CD40-L acts as a  
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L  
 CC can be used in a binding assay to detect cells expressing CD40.  
 CC  
 XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;  
 SQ

Query Match 98.8%; Score 776.4; DB 14; Length 840;  
 Best Local Similarity 99.2%; Pred. NO. 6.4e-214;  
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 ATGATCGAAGATACCAACAACTCTCCCGATCGCGGCACATGACATCCATCAGC 60  
 |||||||  
 Db 46 atgacgataacatacaacaactctcccgatctgcgccacgactgacatccacgc 105  
 |||||||  
 OY 61 ATGAAATTTTATGATTAATTAATCTTCTTATACCAACAAATGATGATCTGTG 120

Db 106 atgaanaatttatgtattacttactctgtttcttctatccaccagatgattggtcagca 165  
 OY 121 CTTTGTGCTGTATCTTATCTTGAAGGTTTGCAAGATGAAAGTAATCTTAT 180  
 |||||||  
 Db 166 ctlttgcgtgtatcttcatatagaaggttgagcaagatagaagatgaagatcttcat 225  
 OY 181 GAAGATTTTGTATCATGAAACGATACGAGATGCAACACAGGAGAAAGATCTTATCC 240  
 |||||||  
 Db 226 gaagatttctgtatcatalgaanaacgatacagagatgacaagagaaatcttctatcc 285  
 OY 241 TTACTGAACTGTGAGAGATTAATAAGCCAGTTTGAAGGCTTTGTGAGAGATTAATGTTA 300  
 |||||||  
 Db 286 ttactgaaactgtgagagatlaaagccagtttgaagccttgtgaaagataatgtta 345  
 OY 301 AACAAAGAGAGAGACGAGAAAGAAACACCTTTGAATGCAAAAAGTGATCAAGATCT 360  
 |||||||  
 Db 346 aacaaagagagagcaaaagaaagaaacagcttgaatgcaaaagtgatcaagaatcct 405  
 OY 361 CAAATTGCGGCATGTCTAAGTGAGGCGACAGTAAACAAACATCTGTGTACAGTGG 420  
 |||||||  
 Db 406 caaattgcygcacatgctcataagtgagccagcaaglaaacaacatctgttacaagtgg 465  
 OY 421 GCTGAAAAAGATACTACACCATGAGCAACAACTTGTAACCTTGAAAAATGGAACAG 480  
 |||||||  
 Db 466 gctgaaaaagatatactacacccaatgagcaaacacttgtaaccctggaatggaacag 525  
 OY 481 CTGACCGTTTAAAGACAGGACTATTTATCTATGCCCAGTCAACCTTGTTCCAT 540  
 |||||||  
 Db 526 ctgaccgttlaaaagaaagagactcatalatctatgccaagtaaccttctgttccat 585  
 OY 541 CGGGAAGCTTCGAGTCAAGCTCATTTATAGCCAGCTTGCTTAAAGTCCCGGTAGA 600  
 |||||||  
 Db 586 cgggaagcttcgagtcacagctcattatagcagccttgcctiaaagctcccgtaga 645  
 OY 601 TTGAGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCCGCCAAACCTTGCGGCA 660  
 |||||||  
 Db 646 ttcgagagatcttactcagagctgcaaataccacagcttcgcgcaaaccttgcgagca 705  
 OY 661 CAATCATTCATCTGGGAGAGATTTTGAATGCAACGAGTGCTGGTGTGTCAT 720  
 |||||||  
 Db 706 caatccatcacttctggaagagatcttgaaatgcaacacagtgctggttctgcaat 765  
 OY 721 GTGATGATCAAGCCAAAGTGAAGGACGATGAGCTGCTTCACGCTTGTGCTTACTCAAA 780  
 |||||||  
 Db 766 gtgactgaccgaagtgagccatgacgtgcttccacgttcccttgccttactcaaa 825  
 OY 781 CTCGA 786  
 |||||||  
 Db 826 ctcgca 831

RESULT 6  
 AA067123 standard; DNA; 840 BP.  
 ID AA067123  
 AC AA067123  
 XX 23-MAR-1995 (first entry)  
 DE CD40 ligand gene.  
 XX  
 DE Probe; primer; PCR; amplify; polymerase chain reaction; detection;  
 KM mutation; CD40 ligand gene; IGM; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 46..831  
 FT /tag= a  
 FT /product= CD40 ligand  
 XX  
 PN W09417196-A.

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XX 04-AUG-1994.
PD 21-JAN-1994; 94WO-US00786.
XX 22-JAN-1993; 93US-0009258.
PR 20-JAN-1994; 94US-0184422.
XX (IMMV) IMMUNEX CORP.
XX Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;
PI Spriggs MK, Widmer MB;
XX WPI: 1994-264109/32.
DR P-PSDB; AAR57469.
XX Method for detecting mutation in CD 40 ligand gene - comprises
PT amplification of nucleic acid, and mutational analysis
PS Disclosure; Page 22-24; 38pp; English.
XX This sequence represents the CD40 ligand gene. Mutations within
CC this gene were identified by the method of the invention. The
CC method comprises isolating DNA from an individual and selectively
CC amplifying the isolated DNA derived from the CD40 ligand gene. The
CC amplification product is then analysed to determine if there is a
CC mutation present and determining if a protein expressed from the
CC ligand gene will bind CD40. The detection of mutations in the CD40
CC ligand gene allows subsequent treatment of a syndrome resulting in
CC elevated levels of serum IgM and diminished levels of other Ig
CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked
CC hyperIgM syndrome.
XX
XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other:
SQ
Query Match 98.8%; Score 776.4; DB 15; Length 840;
Best Local Similarity 99.2%; Pred. No. 6.4e-214;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 ATGATCGAAGCATACMACCAACTTCTCCGATCTGCGGCACATGCACTGCCATCAGC 60
DB 46 atgacgaaacatacaacaaactctcccgatctgcygcacgacgacgacatccgc 105
OY 61 ATGAAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 120
DB 106 atgaaattttatatttatttatttatttatttatttatttatttatttatttattt 165
OY 121 CTTTGTGCTGTATCTTATGAGAGTTTGACAGATGAGAGATGAGAGATGAGATGAT 180
DB 166 ctttgcgtgtatcttcatatagaaggttgacaagatagaagatagaagatcttcat 225
OY 181 GAAGATTTGTATTCATGAAACGATACAGAGATGATCAACACAGAGAGAGATCTTATCC 240
DB 226 gaagatttctatctatcaagaaacgatacagagatgacaacagagagaaagatccctatcc 285
OY 241 TTACTGAAGCTGTAGAGATTTAAAGCCAGTTGAGGCTTTGTGAAGATATATGTTA 300
DB 286 ttactgaactgtgagaggttaaaagccagtttgaagcttgtgaagatataatgtta 345
OY 301 AACCAAGAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCCT 360
DB 346 aacaagaagagagacgagaagaagaagaacagcttgaatgcaaaaggtgatacagaatcc 405
OY 361 CAATATTCGGGCATCTCTAAGTGTAGGCGCAGAGTAATAACATCTGTACAGTGG 420
DB 406 caaatctgcgcacatgctatgaagtgagccagagaaacacatctgtgtacagtg 465
OY 421 GGTGAAAAGAGATATACACCATGACCAACACTTGTATACCTGGAAGAGGGAAGACG 480
DB 466 gctgaaaagagatctacacacatgagcaaacctgttaacctggaatggaagacag 525
OY 481 CTGACCGCTTAAAGACAGACTCTATATCTATATGCCCCAATGACCTCTCTCCAAAT 540

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DB 526 ctgacgctlaaagaagaagactatattatctatgcccacagctctgtccaat 585
OY 541 CGGAGAGCTTGTAGTCAAGCTCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGAG 600
DB 586 cgggaagcttcgaagcaagctccattatagccagctctgcttcaaaagtcgccgtaga 645
OY 601 TTGCAAGAGATCTTATCTAGAGAGTGAAGTACCAAGTTCGCGCAACCTTGGGCGCA 660
DB 646 ttcgagagaaactctatctcagagctgcaaatataccacagcttcgcgaacttgcgca 705
OY 661 CAATCATTTCACTTGGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 720
DB 706 caatcattcacttggagagagatttgaattgaacacagctctgctgtgtgta 765
OY 721 GTGACTGATTCAGCAAGCAGTGCATGACATGCACTGCTTACGCTTGTGCTTACTCAA 780
DB 766 gtgactgatacagaagcagagtgacatgacatgacatgacatgacatgacatgac 825
OY 781 CTCTGA 786
DB 826 ctctga 831

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RESULT 7  
AAT05763  
ID AAT05763 standard; DNA; 840 BP.

XX AAT05763;

DT 18-MAR-1996 (first entry)

XX Human CD40 ligand DNA.

XX High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;  
KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;  
KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 22..807  
FT /tag= a

XX W09529935-A1.

XX 09-NOV-1995.

XX 28-APR-1995; 95WO-US05448.

XX 28-APR-1994; 94US-0234580.

XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX Castle BE, Kehry M;

XX WPI: 1995-393038/50.

XX P-PSDB; AAR5486.

XX High density membrane bound CD40 ligand - for stimulating the  
PT proliferation of B cells in vitro or in vivo, partic. for producing  
PT differentiated cells

XX Disclosure; Fig 1; 74pp; English.

XX The nucleotide sequence given in AAT05763 encodes a human high-density,  
CC membrane-bound (hdmB) CD40 ligand (AAR5486) that induces long-term  
CC proliferation of B-cells in culture. These proliferating B-cells  
CC can be induced to differentiate into antibody-prod. cells. The  
CC nucleotide sequence is incorporated into a baculovirus vector that  
CC is used to transfect Sf9 insect cells for prodn. of recombinant  
CC hdmB-CD40.

XX	Cytokine: activated CD4+ T cell; CD40L; monoclonal antibody; neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS; melanoma; carcinoma; ss.	XX	Homo sapiens.	XX	Key CDS	XX	Location/Qualifiers
XX		XX		XX		XX	46..831
XX		XX		XX		XX	/tag= a
XX	US674492-A.	XX		XX		XX	
XX	07-OCT-1997.	XX		XX		XX	
XX	21-DEC-1994;	XX		XX		XX	
XX	94US-0360923.	XX		XX		XX	
XX	23-DEC-1993;	XX		XX		XX	
XX	93US-0172664.	XX		XX		XX	
XX	(IMMUNEX CORP.	XX		XX		XX	
XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	XX		XX		XX	
XX	Armltage RJ, Fanslow WC, Longo DL, Murphy MJ;	XX		XX		XX	
XX	WPI: 1997-502273/46.	XX		XX		XX	
XX	P-PSDB; AAW34669.	XX		XX		XX	
XX	Treating or preventing neoplastic disease associated with CD40-expressing cells - particularly B-cell lymphoma, by administration of CD40-binding protein, preferably antibody or soluble CD40-ligand	XX		XX		XX	
XX	Claim 3; Columns 19-22; 21pp; English.	XX		XX		XX	
XX	The present sequence represents the cDNA sequence of a novel cytokine ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide, which is expressed by activated CD4+ T cells, and causes B cell proliferation and induction of antibody secretion. The protein can be used to produce monoclonal antibodies, which in turn bind to CD40-expressing cells. This inhibits binding of soluble CD40 to its ligand CD40L. The monoclonal antibody against CD40L is used to inhibit proliferation of neoplastic cells, and is particularly useful in treating B-cell lymphoma (e.g. where induced after transplants or in other cases of immune deficiency such as AIDS), and also melanoma or carcinoma. Since the monoclonal antibodies inhibit neoplastic cells directly, they may not need to be coupled to a toxin or radioisotope, avoiding toxic effects on normal B cells.	XX		XX		XX	
XX	Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;	XX		XX		XX	
XX	Query Match	XX		XX		XX	
XX	Best Local Similarity 98.8%; Score 776.4; DB 18; Length 840;	XX		XX		XX	
XX	Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	XX		XX		XX	
XX	1 ATGATCGAAGCAATACCAACCTCCCGCATGTGGCGGCACGTGCGCCATCAGC 60	XX		XX		XX	
XX	46 atgacgcgaacacaaacaaactctcccgatctgcggccacgcgcgcacgcgc 105	XX		XX		XX	
XX	61 ATGAAATTTTATGATTTACTTACTGCTGTTTCTTATCACCACCAATGATGGATCTG 120	XX		XX		XX	
XX	106 atgaatatttatgtattacttactactgttttcttatacaccagatgattggtcagca 165	XX		XX		XX	
XX	121 CTTTTCCTGCTGATATCTTCATAGAGGTTGCAAGATGAGATGAAGGAAATCTTAT 180	XX		XX		XX	
XX	166 ctttctgtctgtatcttcatacagaaggttgacaagatagaagatgaaagaaatcttcat 225	XX		XX		XX	
XX	181 GAAGATTTTGTATTCATCAAAAAAGTATACAGAGATCAACACAGAGAAAGATCTTATCC 240	XX		XX		XX	
XX	226 gaagatttctgtatcattatgaaaaagatacagatgcaacacacaggaagaaatccttacc 285	XX		XX		XX	
XX	241 TTACTGAACGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTAGAGATTAATGTTTA 300	XX		XX		XX	









XX 08-MAR-2001.  
 XX 24-AUG-2000; 2000WO-US23276;  
 XX 27-AUG-1999; 99US-0151250.  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 XX Ahuja SS, Bonewald LF;  
 XX  
 XX WPI: 2001-169007/17.  
 XX P-PSDB; AAB67612.  
 XX  
 XX CD40 agonist containing composition, used to reduce bone cell death or  
 XX apoptosis associated with osteoporosis, osteonecrosis and inflammatory  
 XX arthritis -  
 XX  
 XX Disclosure; Page 113; 118pp; English.  
 XX  
 XX The present sequence encodes a gp39 protein. It is a CD40 ligand.  
 XX CD40 ligands are used for reducing osteoblast cell death or apoptosis,  
 XX and for treating or preventing bone loss in animals, preferably humans,  
 XX at risk of, or undergoing, bone loss. The bone loss is associated with  
 XX osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal  
 XX oestrogen loss, estrogen loss due to ovariectomy, total hysterectomy,  
 XX lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,  
 XX anti-glomerular basement membrane nephritis, myositis, scleroderma,  
 XX idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive  
 XX lung disease, nephrotic/nephritic syndrome, or cancer. They may also be  
 XX used to treat or prevent bone loss in a subject undergoing, or scheduled  
 XX for, an organ or bone marrow transplant.  
 XX  
 XX Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;

Query Match 98.8%; Score 776.4; DB 22; Length 879;  
 Best. Local Similarity 99.2%; Pred. No. 6,5e-214;  
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATGGAATCATACACCAAACTTCTCCGATCGCGGCCACTGGACCTGCCATCAGC 60  
 DB 22 atgattgaatacatatacacaacttctccgattcgcggccactggacctgccatcagc 81  
 QY 61 ATGAAATTTTATGTAATTTACTTACTGTTTCTTATGACCCAAATGATGGATCTGTG 120  
 DB 82 atgaattttatgtatattacttactgttttcttattacaccagatgttggtagca 141  
 QY 121 CTTTTCGTGTGATCTTATAGAGGTTGGACAGATGAGATGAAGAATCTTCAT 180  
 DB 142 cttttgctgtatcttcatatagaaagttggacaagatgaagaagatcttcat 201  
 QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACAGACAGAGAAAGATCCTTATCC 240  
 DB 202 gaagatttgtattcatagaagaagatgacagagatgacaagaagaatcttcatcc 261  
 QY 241 TTAGTGAATGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAGATATATATGTTA 300  
 DB 262 ttactgaactgtgagagatgaagaagccagtttgaaggttttggatgaataatgta 321  
 QY 301 AACCAAGAGAGACGACGAAGAAAGAAACAGCTTTGAATTCACAAAGAGTATCAGAACTCT 360  
 DB 322 aacaaagagagacgacgaagaaagaaacagctttgaatgcaaaaagtgatcagaatcct 381  
 QY 361 CAAATTCGGGACATGCTCTAAGTGGGCGACAGTAAACAAACATCTGTGTACAGTGG 420  
 DB 382 caatttgggacatgtctaaagtgagggccacagtaaaacacatctgttaccagtg 441  
 QY 421 GGTGAAAAAGATACTACACCATGAGCAACAATTGTATACCTGTGAAATGGGAAACAG 480  
 DB 442 gctgaaaaagatactacacccatgagcaaaccttgttaacctgtgaaatggygaacag 501  
 QY 481 CTGACCGTTTAAAGACAGACTCTATTATATCTATGCCCCAAGTACCTTCTGTCCAAAT 540

DB 502 ctgaccgttaaaagacaagacacttatatatcatgaccgaagtcacacttctgttccaat 561  
 QY 541 CGGAGAGCTTTCGAGTCAGATCCATTTATAGCCAGGCTTCGCTTAAGTCCCGGTAG 600  
 DB 562 cgggaagcttgtagtcaagctcattatagaagcctctgcttaagaagtcgccgttaga 621  
 QY 601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATCCACAGATGTCGCCCAACCTTCGGGCA 660  
 DB 622 ttccgagagatcttactcagagctgcaataccacacagttccgcaaaccttgcgggca 681  
 QY 661 CAATCCATTCACCTTGGGAGAGATTTGAATTGCAACAGAGTCTTCGTTGTTCAT 720  
 DB 682 caatccatcacttggagagatattgaattgcaaccagtgcttcggtgttgcacat 741  
 QY 721 GTGACGTATCCAAAGCCAGAGCCATGCGACATGCGCTTACCTTCCTTGGCTTACCA 780  
 DB 742 gtgactgatccaaagccaagtgagcagatgacatgcttcaagcttctgttactcaaa 801  
 QY 781 CTCTGA 786  
 DB 802 ctctga 807

RESULT 12  
 ID AAA51745  
 AAA51745 standard; cDNA; 1816 BP.

AAA51745:  
 31-OCT-2000 (first entry)

Human CD40 ligand cDNA.

CD40 ligand: CD40; T cell; T cell receptor; rearrangement; maturation;  
 cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;  
 anti-inflammatory; anti-diabetic; anti-rheumatic; anti-naemic;  
 ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;  
 dermatological; cytostatic; ss.

Homo sapiens.

key Location/Qualifiers  
 CDS 40..825  
 /tag= a  
 /product= Human CD40\_ligand

MO200039283-A1.

06-JUL-2000.

22-DEC-1999; 99WO-US30930.

29-DEC-1998; 98US-0114106.

(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

Newell MK, Wagner D, Newell E;

WPI: 2000-452387/39.

P-PSDB; AAY96993.

Inducing T cell receptor gene rearrangement for treating autoimmune  
 diseases comprises contacting T cells with a CD40-binding agent

Disclosure; Page 46; 50pp; English.

CD40 engagement on T cells can be used to induce T cell receptor  
 rearrangement and enhance T cell affinity for a particular antigen. CD40  
 engagement can be bought about by contacting CD40 with a CD40-binding  
 agent, e.g. human CD40 ligand. The CD40-binding agents can also be used  
 in methods for promoting T cell maturation, inhibiting T cell receptor  
 rearrangement, inhibiting environmental stress-induced cell death,

altering the specificity of a T cell towards an antigen, inducing T cell reactivity towards an antigen or enhancing environmental stress-induced cell death (all claimed). T cell affinity maturation towards a specific antigen can be inhibited, especially for a self-antigen in an autoimmune disease, which includes rheumatoid arthritis, uveitis, insulin-dependent diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease, Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease, myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic lupus erythematosus. Inducing environmental stress-induced T cell death is carried out in a cancerous T cell or a self-reactive T cell where the environmental stress is a chemotherapeutic agent (claimed).

Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other:

Query Match 98.8%; Score 776.4; DB 21; Length 1816;  
Best Local Similarity 99.2%; Pred. No. 9e-214;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGATCGAAGATACACCAACTCTCCGATCGCGGACATGACCTGCCATCAGC 60  
40 atgacgaacatatacaacaaactctcccgatctgcyccactgagctgccatcagc 99  
61 ATGAAATTTTATTTATTTACTTCTGTTTCTTATCACCACCAATGATGATG 120  
100 atgaaattttatattacttacttacttcttcttcttaccacagatgattggtcagca 159  
121 CTTTTCCTGTATCTCATAGAGTTGCAAGTAGAAGTAGAAGTAGAAGTAGAAG 180  
160 cttttcgtgtatctctcatagaaagttggaagaatagaaagaaatcttcaat 219  
181 GAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240  
220 gaagatttctatctatcaataacagatgacacacaggaagaagatccctatcc 279  
241 TTACGAGCTGTGAGGAGATTAAGCCAGTTTGAGGCTTTGTGAAGATATATGTTA 300  
280 ttacgagctgtgagagattaaagcaggttggaagcttggtaagataatgttca 339  
301 AACAAAGGAGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360  
340 aacaaaggagagacgaagaagaagaagaagaagaagaagaagaagaagaagaatcc 399  
361 CAAATTTGGGACATGTCATAGTAGGCGCAGCAGTAAACAACTCTGTGTACAGTGG 420  
400 caaatitgggacatgtcatagtagagggcagcagtaaaacaactctgttcaatg 459  
421 GCTGAAAAAGATCTACACCATGAGCAACAACCTTGTAACCTTGAAAAATGGAACAG 480  
460 gctgaaaaagatctacacacatgagcaacaacttggtaacctgtgaaatggaacag 519  
481 CTGACCGTTAAAGACAGGACTCTATATATCTATGCGCAAGTCACTCTGTTCCAT 540  
520 ctgaccggttaaaagaagaagaagaagaagaagaagaagaagaagaagaagaatcc 579  
541 CGGGAAGCTTGAGTCAAGCTCCATTTATAGCAGCCTCTGCGCTTAAGTCCCGGTGA 600  
580 cgggaagcttgagtcagatccatattatagccagcctctgctaagaatcccccgt 639  
601 TTGAGGAATTTCTTCTAGAGCTGCAATATACCACTTCCGCAAACTTTGGGGGAA 660  
640 ttgaggaatttcttctagagctgcaaatatccacagltccgcaaaactctgggga 699  
661 CAATCCATTCACCTTGAGGAGATTTGAAATGCAACAGAGTCTCGTGTGTTTCAT 720  
700 caatccatctacttggggaggtattgtaattgcaacaagtgctgtgttgcataat 759  
721 GTGACTGATCCAAAGCAAGTGAAGCCATGACCTGCTTACGCTTGTGCTTACTCAA 780  
760 gtgactgattccaagcgaagtggcatgcaactggtcttcacgtcttgccttactcaa 819  
781 CTCTCA 786  
|||||

Db 820 ctctga 825

RESULT 13

ID AAS86571 standard; CDNA; 1816 BP.

XX AAS86571;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #22375.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

XX P-PSDB; ABG22384.

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

PS Claim 1; SEQ ID No 22375; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (III) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for creating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other:

Query Match 98.8%; Score 776.4; DB 23; Length 1816;  
Best Local Similarity 99.2%; Pred. No. 9e-214;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGATCGAAGATACACCAACTCTCCGATCGCGGACATGACCTGCCATCAGC 60  
40 atgacgaacatatacaacaaactctcccgatctgcyccactgagctgccatcagc 99  
|||||



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Db 346 aacaaagggagcagaagaagaacacgcttgaagaagaagaagtgatcacgaatct 405
OY 361 CAAATTCGGGACATGTCTATAAGTAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
Db 406 caattggagacatgcatatagtcgaagccagcagtaaaacaacatctgttaccagtg 465
OY 421 GCTGAAAAAGATCTACACATGATGACCAACAACTTGTGAACCCCTGGAAAAATGGGAACAG 480
Db 466 gctgaaaaagatactacacacatgagcaacaacttggtaaccctggaaaaatgggaaacag 525
OY 481 CTGACCCGTTAAAGACAGACGACTATATATATCTATATGCGCAAGTCACCTCTGTTCAT 540
Db 526 ctgacgcttaaaagacaagagctctatatactatctatgccaagtcacctctgttccaat 585
OY 541 CGGGAAGCTTGGAGTCAAGCTTCATTTATACCAAGCTCTCTCTAAAGTCCCCGGGTAGA 600
Db 586 cgggaagcttcgaagtcacacccatctatagccagcctcmmctaaagctcccccgtlaga 645
OY 601 TTCGAGAGATCTTACTGAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Db 646 ttggaaggaatcttactatcagcagtcgcaaatatccacagcttccgcaaaccttggggcaa 705
OY 661 CAATCCATTCCTTGGGAGAGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAAT 720
Db 706 caatccatcactctggagaggtatltgaaltgcaaccagtgctcggttgcacat 765
OY 721 GTGACTGATCCAGCAAGTAGGCGCATGGCAGCTGCTTACGCTTGTACTCAAA 780
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OY 781 CTCTGA 786
Db 826 ctctga 831

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## RESULT 15

AA057984

ID AA057984 standard; DNA: 840 BP.

AC AA057984:

XX 20-AUG-1994 (first entry)

XX Genomic sequence of human gp39.

XX gp39: T-cell antigen; CD40 ligand; B-cell proliferation;

XX B-cell differentiation; ss.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 22.807

XX CDS /\*tag- a

XX EP585943-A.

XX 09-MAR-1994.

XX 03-SEP-1993; 93EP-0114153.

XX 04-SEP-1992; 92US-0940605.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;

XX MPI: 1994-076264/10.

XX P-PSDB: AAR59548.

XX New nucleic acid encoding human gp39 T cell antigen - which is a  
 PT ligand for the CD40 receptor, causing proliferation and  
 PT differentiation of B cells and some cancer cells

```

XX PS Claim 1; Fig 1; 39pp; English.
XX CC The complete nucleic acid sequence of human gp39 (hgp39) protein
XX CC (corresp. to cDNA) and the complete AA sequence of hgp39 are
XX CC presented in AA057984 and AAR59548 respectively and confd. In plasmid
XX CC CD8-hgp39, deposited with the ATCC as E. coli, CD8h MCI1061/p3-hgp39
XX CC and assigned accession No. 69050. The human T cell antigen gp39 is a
XX CC ligand for the CD40 receptor. Soluble gp39 may be produced using the
XX CC expression vector CD8-gp39.
XX SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

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Query Match 98.4%; Score 773.2; DB 15; Length 840;
Best Local Similarity 99.0%; Pred. No. 5.3e-213;
Matches 778; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 361 CAAATTCGGGACATGTCTATAAGTAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420
Db 382 caattggagacatgcatatagtcgaagccagcagtaaaacaacatctgttaccagtg 441
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OY 781 CTCTGA 786
Db 802 ctctga 807

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Thu May 30 05:46:06 2002

Search completed: May 30, 2002, 03:03:15  
Job time: 11244 sec

us-08-982-272-4.rng

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:22:46 ; Search time 8356.06 Seconds  
(without alignments)  
2035.054 Million cell updates/sec

Title: US-08-982-272-4

Perfect score: 786

Sequence: 1 ATGATCGAACAATACACCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 1081749327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
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5	776.4	98.8	840	1	PCT-US94-14767-1
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16	776.4	98.8	840	8	US-08-484-624-11
17	776.4	98.8	840	9	US-08-589-771-7
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ALIGNMENTS

RESULT 1  
US-08-982-272-4  
Sequence 4, Application US/08982272  
GENERAL INFORMATION:  
APPLICANT: Kipps, Thomas J.  
APPLICANT: Sharma, Sanjai  
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
TITLE OF INVENTION: CONTAINING ACCESSORY  
TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
TITLE OF INVENTION: THEIR USE FOR IMMUNO-  
TITLE OF INVENTION: MODULATION AND TREATMENT OF  
TITLE OF INVENTION: MALIGNANCIES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette,  
MEDIUM TYPE: 1.44 Mb storage,  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA: US/08/982, 272  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Query Match 100.0%; Score 786; DB 13;  
Best Local Similarity 100.0%; Pred. No. 2e-199;  
US-08-982-272-4 Length 786;

Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 2  
US-08-107-353-3  
Sequence 3, Application US/08107353  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA



COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,353  
FILING DATE: 19930813  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
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FEATURE:  
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US-08-107-353-3

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Qy	421	GCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	480
Db	421	GCTGAAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	480
Qy	481	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAAAT	540

Db	481	CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAAAT	540
Qy	541	CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGGTAGA	600
Db	541	CGGGAAGCTTCAGATCAAGCTCCATTTATAGCAGCCTCTGCCTAAAGTCCCGGGTAGA	600
Qy	601	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGGGCAA	660
Db	601	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGGGCAA	660
Qy	661	CAATCCATTTCATTTGGGAGGAGTATTTGAATTTGCAACAGGTCTTCGGTGTCTTCTCAAT	720
Db	661	CAATCCATTTCATTTGGGAGGAGTATTTGAATTTGCAACAGGTCTTCGGTGTCTTCTCAAT	720
Qy	721	GTGACTGATCCAAAGCAAGTCAGCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAA	780
Db	721	GTGACTGATCCAAAGCAAGTCAGCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAA	780
Qy	781	CTCTGA 786	
Db	781	CTCTGA 786	

RESULT 3  
US-08-982-272-1  
Sequence 1: Application US/08982272  
GENERAL INFORMATION:  
APPLICANT: Kipps, Thomas J.  
APPLICANT: Sharma, Sanjai  
APPLICANT: Cantwell, Mark  
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
TITLE OF INVENTION: CONTAINING ACCESSORY  
TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
TITLE OF INVENTION: THEIR USE FOR IMMUNO-  
TITLE OF INVENTION: MODULATION AND TREATMENT OF  
MALIGNANCIES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette,  
MEDIUM TYPE: 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,272  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-982-272-1

Query Match 98.8%; Score 776.4; DB 13; Length 786;  
Best Local Similarity 99.2%; Pred. No. 7.3e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGACTGCCCATCAGC 60
DB 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGACTGCCCATCAGC 60

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATCAGTCTGTG 120
DB 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCAGTCTGTG 120

QY 121 CTTTTCGTCTGTATCTTCATAGAAGTTGGACAAGATAGAAGATAGAAGATAGAAGATAGA 180
DB 121 CTTTTCGTCTGTATCTTCATAGAAGTTGGACAAGATAGAAGATAGAAGATAGAAGATAGA 180

QY 181 GAAGATTTTGTATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 240
DB 181 GAAGATTTTGTATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 240

QY 241 TTACTGAATCTGTGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGCTTTTGAAGGCTTT 300
DB 241 TTACTGAATCTGTGAGGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGCTTTTGAAGGCTTT 300

QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

QY 361 CAATTCGGGCACATGTCTAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CAATTCGGGCACATGTCTAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 421 GCTGAAAGAGAGATACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GCTGAAAGAGAGATACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 481 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 541 CGGAGAGAGATCGAGTCAAGTCTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CGGAGAGAGATCGAGTCAAGTCTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

QY 601 TTCGAGAGAGATCTTACTCAGAGCTGCAATATACCCAGAGTCCGCTTAAAGTCCCGGTCAG 660
DB 601 TTCGAGAGAGATCTTACTCAGAGCTGCAATATACCCAGAGTCCGCTTAAAGTCCCGGTCAG 660

QY 661 CAATCCATTCAGTTGGGAGGAGATTTGAATGCAACAGGAGTCTCGGTGTTTGTCAAT 720
DB 661 CAATCCATTCAGTTGGGAGGAGATTTGAATGCAACAGGAGTCTCGGTGTTTGTCAAT 720

QY 721 GTGACTGATCCCAAGCAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 GTGACTGATCCCAAGCAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

QY 781 CTCTGA 786
DB 781 CTCTGA 786
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RESULT 4  
PCT-US94-00786-7  
; Sequence 7; Application PC/TUS9400786  
; GENERAL INFORMATION:  
; APPLICANT: ASMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: RENSHAW, BLAIR  
; APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00786  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapiens  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
PCT-US94-00786-7

Query Match. 98.8%; Score 776.4; DB 13; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGACTGCCCATCAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCGACCTGGACTGCCCATCAGC 105

QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCAGTCTGTG 120
DB 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCAGTCTGTG 165

QY 121 CTTTTCGTCTGTATCTTCATAGAAGTTGGACAAGATAGAAGATAGAAGATAGAAGATAGA 180
DB 166 CTTTTCGTCTGTATCTTCATAGAAGTTGGACAAGATAGAAGATAGAAGATAGAAGATAGA 225

QY 181 GAAGATTTTGTATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 240
DB 226 GAAGATTTTGTATTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 285

QY 241 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGCTTTTGAAGGCTTT 300
DB 286 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGCTTTTGAAGGCTTT 345
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QY 721 GTGACTGATCCCAAGCAAGTGAGCCATGGCTTCAGCTGCTTCAGCTTACTCAAA 780  
Db 766 GTGACTGATCCCAAGCAAGTGAGCCATGGCTTCAGCTTACTCAAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831  
RESULT 6  
PCT-US97-11956-1  
; Sequence 1, Application PC/TUS9711956  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Power Macintosh 7200/90  
; OPERATING SYSTEM: Apple Operating System 7.6  
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/11956  
; FILING DATE: 09-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/677,762  
; FILING DATE: 10-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USN 08/763,995  
; FILING DATE: 12-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2845-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
; PCT-US97-11956-1

Query Match 98.8%; Score 776.4; DB 1; Length 840;  
Best Local Similarity 99.2%; Pred No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGATCGAACAATACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 60  
Db 46 ATGATCGAACAATACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105

QY 61 ATGAAAATTTTATGATTTACTTACTTCTTATCACCACCAAAATGATGGATCTGTG 120  
Db 106 ATGAAAATTTTATGATTTACTTACTTCTTATCACCACCAAGATTTGGTGCA 165  
QY 121 CTTTTCCTGTGTATCTTATAGAGGTTGGACAGATAGAGATCAAGAGGAATCTTCAT 180  
Db 166 CTTTTCCTGTGTATCTTATAGAGGTTGGACAGATAGAGATCAAGAGGAATCTTCAT 225  
QY 181 GAAGATTTTATGATTTATGAAAACGATACAGAGATGCAACACAGAGGAAAGATCCCTATCC 240  
Db 226 GAAGATTTTATGATTTATGAAAACGATACAGAGATGCAACACAGAGGAAAGATCCCTATCC 285  
QY 241 TTACTGAACGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTTGAATGCAAAAGAGTATCAGAAATCT 360  
Db 346 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTTGAATGCAAAAGAGTATCAGAAATCT 405  
QY 361 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGG 420  
Db 406 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACACATCTGTGTTACAGTGG 465  
QY 421 GCTGAAAAGAGATACACCATGAGCAACAACTTTGTAACCTTGGAAAAATGGGAACAG 480  
Db 466 GCTGAAAAGAGATACACCATGAGCAACAACTTTGTAACCTTGGAAAAATGGGAACAG 525  
QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCTCCCAAGTACCTTCTGTTCAT 540  
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCTCCCAAGTACCTTCTGTTCAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCCGCAAACTTGGGGCAA 660  
Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCCGCAAACTTGGGGCAA 705  
QY 661 CAATCCATTCAGTGGGAGGAGTATTCGAATGCAACAGGCTGCTCGTGTGTTGTCAT 720  
Db 706 CAATCCATTCAGTGGGAGGAGTATTCGAATGCAACAGGCTGCTCGTGTGTTGTCAT 765  
QY 721 GTGACTGATCCCAAGCAAGTGAGCCATGGCTTCAGCTGCTTTCAGCTTACTCAAA 780  
Db 766 GTGACTGATCCCAAGCAAGTGAGCCATGGCTTCAGCTGCTTTCAGCTTACTCAAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 7  
US-07-805-723-10  
; Sequence 10, Application US/07805723  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/805,723  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:

NAME: OSTER, JEFFREY B.  
REGISTRATION NUMBER: 32585  
REFERENCE/DOCKET NUMBER: 2802  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: CD40-L

US-07-805-723-10

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGATCGAAGACATCAACCAACTCTCCCGGATCTGGGCGACTGGAGTCCCATCAGC	60
Db	46	ATGATCGAAGACATCAACCAACTCTCCCGGATCTGGGCGACTGGAGTCCCATCAGC	105
Qy	61	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTCTG	120
Db	106	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTCTG	165
Qy	121	CTTTTCTGTTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT	180
Db	166	CTTTTCTGTTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT	225
Qy	181	GAAGATTTTGTATCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCTTATCC	240
Db	226	GAAGATTTTGTATCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCTTATCC	285
Qy	241	TTACTGAACTGTGAGGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA	300
Db	286	TTACTGAACTGTGAGGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA	345
Qy	301	AACAAAGAGGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGATCCT	360
Db	346	AACAAAGAGGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGATCCT	405
Qy	361	CAAAATTCGGGCACATGTATAGTGAGGCGCAGCAGTAAACAAACATCTGTCTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTATAGTGAGGCGCAGCAGTAAACAAACATCTGTCTACAGTGG	465
Qy	421	GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	480
Db	466	GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT	540
Db	526	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT	585
Qy	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	600
Db	586	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	645
Qy	601	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCCGCGCAAAACCTTGGCGGCA	660

Db	646	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCCGCCAARACCTTGGGGCAA	705
Qy	661	CAATCCATTCACTTGGGAGGAGTATTGAAATGGAACAGAGTGTTCGGTCTTTGTCAAT	720
Db	706	CAATCCATTCACTTGGGAGGAGTATTGAAATGGAACAGAGTGTTCGGTCTTTGTCAAT	765
Qy	721	GTGACTATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	780
Db	766	GTGACTATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	825
Qy	781	CTCTGA 786	
Db	826	CTCTGA 831	

#### RESULT 8

US-07-969-703A-11  
Sequence 11, Application US/07969703A  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,703A  
FILING DATE: 19921023  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46...831  
US-07-969-703A-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGATCGAAGACATCAACCAACTCTCCCGGATCTGGGCGACTGGAGTCCCATCAGC	60
Db	46	ATGATCGAAGACATCAACCAACTCTCCCGGATCTGGGCGACTGGAGTCCCATCAGC	105
Qy	61	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTCTG	120
Db	106	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTCTG	165
Qy	121	CTTTTCTGTTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT	180
Db	166	CTTTTCTGTTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGAAATCTTCAT	225
Qy	181	GAAGATTTTGTATCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCTTATCC	240
Db	226	GAAGATTTTGTATCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCTTATCC	285
Qy	241	TTACTGAACTGTGAGGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA	300
Db	286	TTACTGAACTGTGAGGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA	345
Qy	301	AACAAAGAGGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGATCCT	360
Db	346	AACAAAGAGGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTTGATCAGATCCT	405
Qy	361	CAAAATTCGGGCACATGTATAGTGAGGCGCAGCAGTAAACAAACATCTGTCTACAGTGG	420
Db	406	CAAAATTCGGGCACATGTATAGTGAGGCGCAGCAGTAAACAAACATCTGTCTACAGTGG	465
Qy	421	GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	480
Db	466	GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAAACCTGGGAAATGGGAAACAG	525
Qy	481	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT	540
Db	526	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACCTCTGTTCCTCAAT	585
Qy	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	600
Db	586	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	645
Qy	601	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTTCCGCGCAAAACCTTGGCGGCA	660

46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGCCACTGGACTGCCCATCAGC 105  
61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATTTGGATCTGTG 120  
106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAGATGATTTGGTTCAGCA 165  
121 CTTTTCGTGTGTATCTTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180  
166 CTTTTCGTGTGTATCTTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225  
181 GAAGATTTTGTATCTTCATGAAAGATACAGAGATGCAACAGGAGAAAGATCTTATCC 240  
226 GAAGATTTTGTATCTTCATGAAAGATACAGAGATGCAACAGGAGAAAGATCTTATCC 285  
241 TTACTGAATCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300  
286 TTACTGAATCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345  
301 AACAAAG 360  
346 AACAAAG 405  
361 CAAATTCGGCAGATCTTACATAGAGTTGAGGCGAGCAGTAAACACATCTGTGTACAGTG 420  
406 CAAATTCGGCAGATCTTACATAGAGTTGAGGCGAGCAGTAAACACATCTGTGTACAGTG 465  
421 GCTGAAAGAGATACATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
466 GCTGAAAGAGATACATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525  
481 CTGACCGTTTAAAG 540  
526 CTGACCGTTTAAAG 585  
541 CGGAGAGATCTGAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600  
586 CGGAGAGATCTGAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645  
601 TTCGAGAGAACTTACTACAGAGTGCAGATACCCACAGTTCGGCCCAACCTTGGGGCAA 660  
646 TTCGAGAGAACTTACTACAGAGTGCAGATACCCACAGTTCGGCCCAACCTTGGGGCAA 705  
661 CAATCCATCTACTGGGAGGAGATTTGAATTCGAACAGGTCTTGGGTGTGTCAAT 720  
706 CAATCCATCTACTGGGAGGAGATTTGAATTCGAACAGGTCTTGGGTGTGTCAAT 765  
721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTCAAGTCTTGGCTTACTCAA 780  
766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTCAAGTCTTGGCTTACTCAA 825  
781 CTCTGA 786  
826 CTCTGA 831

RESULT 9  
US-07-969-703B-11  
Sequence 11, Application US/07969703B  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANLOW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,703B  
FILING DATE: 19921023  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
NAME/KEY: CDS  
LOCATION: 46..831  
US-07-969-703B-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.9e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATTTGGATCTGTG 120  
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAGATGATTTGGTTCAGCA 165  
QY 121 CTTTTCGTGTGTATCTTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180  
DB 166 CTTTTCGTGTGTATCTTCATAGAGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATCTTCATGAAAGATACAGAGATGCAACAGGAGAAAGATCTTATCC 240  
DB 226 GAAGATTTTGTATCTTCATGAAAGATACAGAGATGCAACAGGAGAAAGATCTTATCC 285  
QY 241 TTACTGAATCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300  
DB 286 TTACTGAATCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345  
QY 301 AACAAAG 360  
DB 346 AACAAAG 405  
QY 361 CAAATTCGGCAGATCTTCATAGAGTTGAGGCGAGCAGTAAACACATCTGTGTACAGTG 420  
DB 406 CAAATTCGGCAGATCTTCATAGAGTTGAGGCGAGCAGTAAACACATCTGTGTACAGTG 465  
QY 421 GCTGAAAGAGATACATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 466 GCTGAAAGAGATACATACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525  
QY 481 CTGACCGTTTAAAG 540  
DB 526 CTGACCGTTTAAAG 585

Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600  
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 645  
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 705  
 Qy 661 CAATCCCATTTACTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTCTTTGTCAAT 720  
 Db 706 CAATCCCATTTACTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTCTTTGTCAAT 765  
 Qy 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAA 780  
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAA 825  
 Qy 781 CTCCTGA 786  
 Db 826 CTCCTGA 831

RESULT 10  
 US-08-009-258-7  
 ; Sequence 7, Application US/08009258  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; APPLICANT: WIDMER, MICHAEL  
 ; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
 ; TITLE OF INVENTION: IN A CD40 LIGAND GENE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/009,258  
 ; FILING DATE: 19930122  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: PERKINS, PATRICIA A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2802  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 2065870430  
 ; TELEFAX: 2065870606  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 840 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; IMMEDIATE SOURCE:  
 ; CLONE: CD40-L  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 46...831  
 ; US-08-009-258-7

Query Match 98.8%; Score 776.4; DB 4; Length 840;  
 Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 ATGATCGAAGCATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 60  
 Db 46 ATGATCGAAGCATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 105  
 Qy 61 ATGAAAATTTTATGTATTTTACTTACTTCTTCTTATCACCCTAAATGATTTGGATCTGTG 120  
 Db 106 ATGAAAATTTTATGTATTTTACTTACTTCTTCTTATCACCCTAAATGATTTGGGTGACGA 165  
 Qy 121 CTTTTCGTGTGTATCTTCATAGAAAGTTGGACAAGATAGAAAGATGAAGAATCTTCAT 180  
 Db 166 CTTTTCGTGTGTATCTTCATAGAAAGTTGGACAAGATAGAAAGATGAAGAATCTTCAT 225  
 Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATTCCTTATCC 240  
 Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAAAGATTCCTTATCC 285  
 Qy 241 TTACTGACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA 300  
 Db 286 TTACTGACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATATATGTTA 345  
 Qy 301 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 360  
 Db 346 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 405  
 Qy 361 CAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
 Db 406 CAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
 Qy 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGGAAATGGGAAACAG 480  
 Db 466 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGGAAATGGGAAACAG 525  
 Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAGCTCTGCTTAAAGTCCCGGTAGA 540  
 Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAGCTCTGCTTAAAGTCCCGGTAGA 585  
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 600  
 Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCCTAAAGTCCCGCGGTAGA 645  
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCCGCCCAACCTTGGCGGCAA 705  
 Qy 661 CAATCCCATTTACTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTCTTTGTCAAT 720  
 Db 706 CAATCCCATTTACTTGGGAGGAGTATTTGAATTGCAACACAGTGCTTCGGTCTTTGTCAAT 765  
 Qy 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAA 780  
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTCACGCTCTTTGGCTTACTCAA 825  
 Qy 781 CTCCTGA 786  
 Db 826 CTCCTGA 831

RESULT 11  
 US-08-172-664-1  
 ; Sequence 1, Application US/08172664  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: LONGO, DAN L.  
 ; APPLICANT: MURPHY, WILLIAM  
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
 ; TITLE OF INVENTION: EXPRESSING CD40



NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: IMMUNEX CORPORATION  
 STREET: 51 UNIVERSITY STREET  
 CITY: SEATTLE  
 STATE: WASHINGTON  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: Apple Macintosh System 7.1  
 SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/172,664  
 FILING DATE: December 23, 1993  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia A.  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2818  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 840 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORGANISM: Homo sapiens  
 IMMEDIATE SOURCE:  
 CLONE: CD40-L  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 46...831  
 US-08-172-664-1

RESULT 12  
 US-08-215-862-1  
 ; Sequence 1, Application US/08215862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gruss, Hans-J.rgen  
 ; TITLE OF INVENTION: Method of Diagnosing or Treating Hodgkin's  
 ; TITLE OF INVENTION: Disease  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Macintosh  
 ; OPERATING SYSTEM: Apple Macintosh System 7.1  
 ; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/215,862  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2820  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)233-0644  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 840 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens

Query Match 98.8%; Score 776.4; DB 5; Length 840;  
 Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
 Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGATCGAACAATACCAACCAACTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 60  
 DB 46 ATGATCGAACAATACCAACCAACTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 105  
 QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 120  
 DB 106 ATGAAATTTTATGTATTTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 165  
 QY 121 CTTTTGCTGTATCTATCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
 DB 166 CTTTTGCTGTATCTATCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 225  
 QY 181 GAAGATTTTGTATTATCATGAAACGATACAGATGCAACACAGGAGAAAGATCCCTATCC 240  
 DB 226 GAAGATTTTGTATTATCATGAAACGATACAGATGCAACACAGGAGAAAGATCCCTATCC 285  
 QY 241 TTACTGAATCTGAGGAGATTAAACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
 DB 286 TTACTGAATCTGAGGAGATTAAACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
 QY 301 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGAGGTGATCAGAAATCCT 360  
 DB 346 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGAGGTGATCAGAAATCCT 405  
 QY 361 CAAATTCGGCACATGTCTATTAAGTACAGGCGCAGCAGTAAACACATCTCTGTACAGTGG 420



IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46...831  
US-08-215-862-1

Query Match 98.8%; Score 776.4; DB 6; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 60  
DB 46 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTCTTATCACCCTTATGATGATGATGATG 120  
DB 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTCTTATCACCCTTATGATGATGATGATG 165  
QY 121 CTTTTTGTCTGATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180  
DB 166 CTTTTTGTCTGATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCATCC 285  
QY 241 TTACTGAATCTGAGGAGATTAAGACCGATTTGAAGCTTTTGTGAAGATATAATGTTA 300  
DB 286 TTACTGAATCTGAGGAGATTAAGACCGATTTGAAGCTTTTGTGAAGATATAATGTTA 345  
QY 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGGATCAGAAATCCT 360  
DB 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGGATCAGAAATCCT 405  
QY 361 CAAATTTGGCGGCACATGTCTAATAGTGAAGCCAGCAGTAAACAACTCTGTGTACAGTGG 420  
DB 406 CAAATTTGGCGGCACATGTCTAATAGTGAAGCCAGCAGTAAACAACTCTGTGTACAGTGG 465  
QY 421 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAACTCGGAAAGTGGAAACAG 480  
DB 466 GCTGAAAAGGATCTACACCATGAGCAACACTTTGGTAACTCGGAAAGTGGAAACAG 525  
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTCTCTGTTCAT 540  
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTCTCTGTTCAT 585  
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 600  
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 645  
QY 601 TTCGAGAGATCTTACTCAGAGCTCAATACCCACAGTTCGCCCAAACTTTGCGGGCAA 660  
DB 646 TTCGAGAGATCTTACTCAGAGCTCAATACCCACAGTTCGCCCAAACTTTGCGGGCAA 705  
QY 661 CAATCCATCTTCTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT 720  
DB 706 CAATCCATCTTCTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCCAAAGTGAAGCATGGCAGTGGCTTCACTCTCTGTGCTTACTCAA 780  
DB 766 GTGACTGATCCAAAGCCAAAGTGAAGCATGGCAGTGGCTTCACTCTCTGTGCTTACTCAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

RESULT 13  
US-08-234-580-3  
; Sequence 3, Application US/08234580  
; GENERAL INFORMATION:

APPLICANT: KEHRY, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,580  
FILING DATE: 28-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22...807  
US-08-234-580-3

Query Match 98.8%; Score 776.4; DB 6; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 60  
DB 22 ATGATCGAACAATCAACCAAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 81  
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 120  
DB 82 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATGATGATGATGATG 141  
QY 121 CTTTTTGTCTGATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180  
DB 142 CTTTTTGTCTGATCTTCTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 201  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCATCC 240  
DB 202 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTCATCC 261  
QY 241 TTACTGAATCTGTGAGGAGATTAAGACCGCTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 262 TTACTGAATCTGTGAGGAGATTAAGACCGCTTTGAAGGCTTTGTGAAGGATATAATGTTA 321  
QY 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 360  
DB 322 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGAAATCCT 381  
QY 361 CAAATTTGGCGGCACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 420  
DB 382 CAAATTTGGCGGCACATGTCTAATAGTGAAGGCGACAGTAAACAACTCTGTGTACAGTGG 441  
QY 421 GCTGAAAAGGATCTACTACCATGAGCAACAACTTTGGTAACTCGGAAAGTGGAAACAG 480

Db 442 GCTGAAAGGAGTACTACACCATGAGCAACAACTTGGTAACCCCTGGAAATGGGAACAG 501  
QY 481 CTGACCGTTAAAGAGCAAGAGCTATTATATCTATGCGCAAGTCACTCTCTGTTCCTCAAT 540  
Db 502 CTGACCGTTAAAGAGCAAGAGCTATTATATCTATGCGCAAGTCACTCTCTGTTCCTCAAT 561  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATATAGCCAGCTCTGCTAAAGTCCCGGTAGA 600  
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATATAGCCAGCTCTGCTAAAGTCCCGGTAGA 621  
QY 601 TTCAGAGATCTTACTCAGAGCTGCAATACCAAGTCCGCAAACTTGGCGGCAA 660  
Db 622 TTCAGAGATCTTACTCAGAGCTGCAATACCAAGTCCGCAAACTTGGCGGCAA 681  
QY 661 CAATCCATTTCAGTGGGAGGATTTGTAATTCGAACAGGTCTGCGTGTGTGTCAT 720  
Db 682 CAATCCATTTCAGTGGGAGGATTTGTAATTCGAACAGGTCTGCGTGTGTGTCAT 741  
QY 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 780  
Db 742 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 801  
QY 781 CTCCTGA 786  
Db 802 CTCCTGA 807

RESULT 14

US-08-396-230-1  
; Sequence 1, Application US/08396230  
; GENERAL INFORMATION:  
; APPLICANT: CAMPBELL, KIM A.  
; APPLICANT: KENNEDY, MARY K.  
; APPLICANT: MALISZEWSKI, CHARLES R.  
; TITLE OF INVENTION: METHOD FOR STIMULATING A CELL-MEDIATED  
; TITLE OF INVENTION: IMMUNE RESPONSE WITH A CD40 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: Apple Power Macintosh System 7.5.5  
; SOFTWARE: Microsoft Word for Macintosh, Version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/396,230  
; FILING DATE: March 1, 1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2830  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE-CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens

IMMEDIATE SOURCE:  
CLONE: CD40L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-396-230-1

Query Match 98.8%; Score 776.4; DB 7; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGGCCACTGGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGTATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 165  
QY 121 CTTTTCGTGTATCTTTCATAGAGTTGGACAGATGAAGATGAAGAAATCTTCAT 180  
Db 166 CTTTTCGTGTATCTTTCATAGAGTTGGACAGATGAAGATGAAGAAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285  
QY 241 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATGTTA 345  
QY 301 ACAAGAGGAGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 360  
Db 346 ACAAGAGGAGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 405  
QY 361 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACAACTCTGTTCAGTGG 420  
Db 406 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACAACTCTGTTCAGTGG 465  
QY 421 GCTGAAAGAGTACTTACACCATGAGCAACAACTTTGGTAACCCCTGGAAGAAACAG 480  
Db 466 GCTGAAAGAGTACTTACACCATGAGCAACAACTTTGGTAACCCCTGGAAGAAACAG 525  
QY 481 CTGACCGTTAAAGAGCAAGAGCTCTATTATATCTATGCGCAAGTCACTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGAGCAAGAGCTCTATTATATCTATGCGCAAGTCACTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645  
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCGCAAACTTTCGCGGCAA 660  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCGCAAACTTTCGCGGCAA 705  
QY 661 CAATCCATTTCAGTGGGAGGATTTGTAATTCGAACAGGTCTGCGTGTGTGTCAT 720  
Db 706 CAATCCATTTCAGTGGGAGGATTTGTAATTCGAACAGGTCTGCGTGTGTGTCAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 825  
QY 781 CTCCTGA 786  
Db 826 CTCCTGA 831

RESULT 15

US-08-477-733A-11  
; Sequence 11, Application US/08477733A  
; GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477.733A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELEPHONE: 2065870606  
TELEPHONE: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831

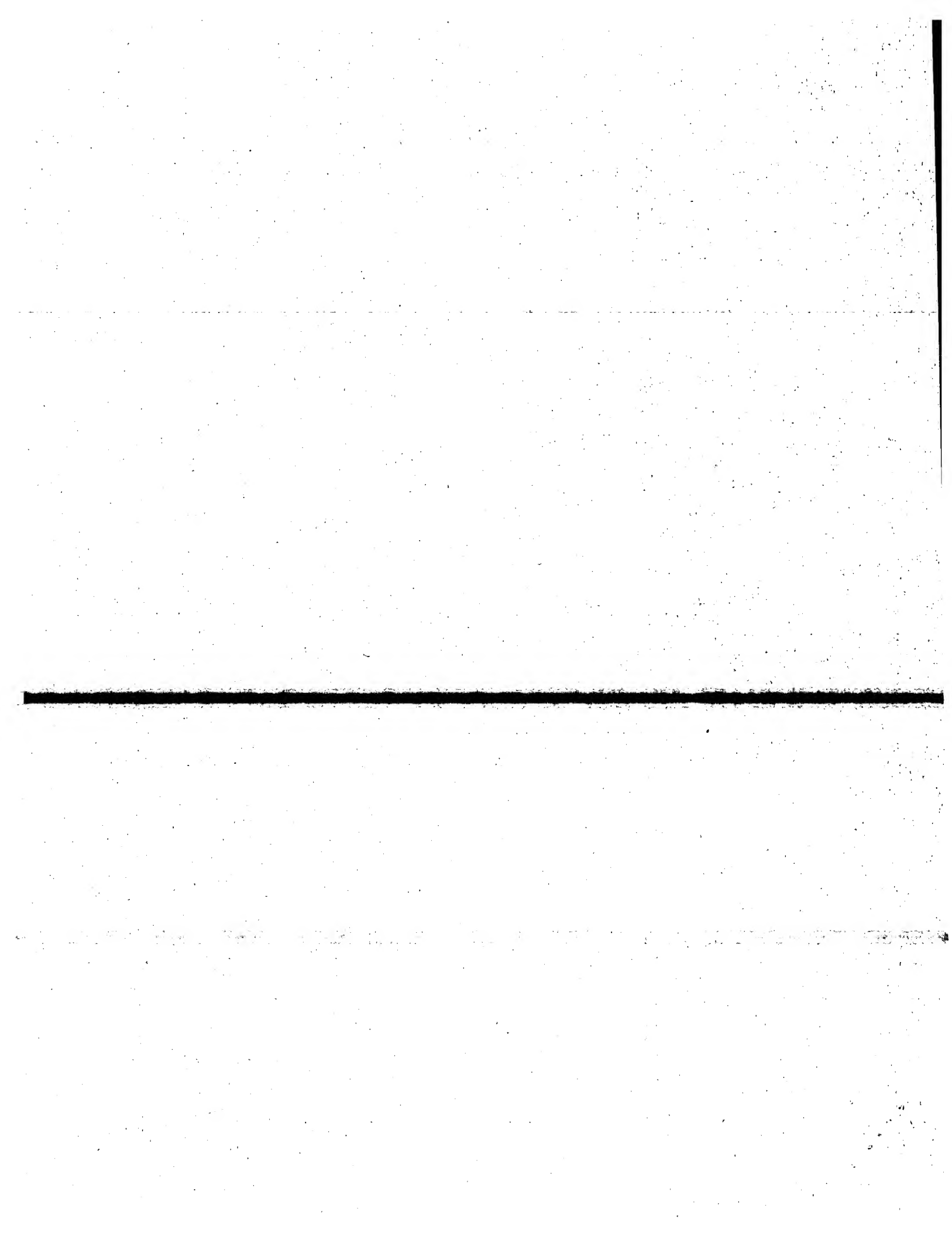
US-08-477-733A-11

Query Match 98.8%; Score 776.4; DB 8; Length 840;  
Best Local Similarity 99.2%; Pred. No. 7.5e-197;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAATCAACCAACTCTCCCGATCTGGGCGCACTGGACTGCCATCAGC 60  
Db 46 ATGATCGAATCAACCAACTCTCCCGATCTGGGCGCACTGGACTGCCATCAGC 105

Qy 61 ATGAAAATTTTATGTAATTTACTTGTCTTCTTATCAACCAATGATTGGATCTGTG 120  
Db 106 ATGAAAATTTTATGTAATTTACTTGTCTTCTTATCAACCAATGATTGGATCTGTG 165  
Qy 121 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT 180  
Db 166 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATCAAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240  
Db 226 GAAGATTTTGTATTCATCAAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 285  
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTA 345  
Qy 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 360  
Db 346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 405  
Qy 361 CAAATTCGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
Db 406 CAAATTCGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGGATACACACCATGAGCAACAACTTGTGTAACCTGGGAAAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACACACCATGAGCAACAACTTGTGTAACCTGGGAAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
Qy 601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAA 660  
Db 646 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGCGGCAA 705  
Qy 661 CAATCCATTCACTGGGAGGAGTATTGTAATTGCAACAGGTCCTCGGTGTTGTCTCAAT 720  
Db 706 CAATCCATTCACTGGGAGGAGTATTGTAATTGCAACAGGTCCTCGGTGTTGTCTCAAT 765  
Qy 721 GTGACTGATCCAAGCAAGTGGCCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAGCAAGTGGCCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAAA 825  
Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

Search completed: May 30, 2002, 05:22:53  
Job time: 18652 sec



Result No.	Score	Match	Query %	Length	DB	ID	Description
1	776.4	98.8	1816	5	US-09-053-375B-226	Sequence 226, Apr	
2	776.4	98.8	1816	5	US-09-442-384B-457	Sequence 457, Apr	
3	571.6	72.7	1250	5	US-09-053-375B-821	Sequence 821, Apr	
4	360.6	45.9	508	5	US-09-911-904-131	Sequence 131, Apr	
5	147.8	18.8	2395	5	US-09-875-453A-9	Sequence 9, Apr	
6	45.6	5.8	569	1	PCT-US02-10421-202	Sequence 202, Apr	
7	45.6	5.8	569	6	US-10-112-699-202	Sequence 202, Apr	
8	44	5.6	2127	5	US-09-919-002-664	Sequence 664, Apr	
9	39.4	5.0	234	5	US-09-940-210B-7000	Sequence 7000, Apr	
10	38.2	4.9	230	5	US-09-540-120B-14649	Sequence 14649, Apr	
11	38.2	4.9	775	6	US-10-123-155-120	Sequence 120, Apr	
12	38	4.8	663	6	US-10-027-632-206146	Sequence 206146, Apr	
13	38	4.8	663	6	US-10-027-632-206147	Sequence 206147, Apr	
14	36.8	4.7	438	5	US-09-539-331D-28090	Sequence 26090, Apr	
15	36.4	4.6	1751	6	US-10-105-299-1996	Sequence 1996, Apr	
16	36.4	4.6	1751	6	US-10-106-698-239	Sequence 239, Apr	
17	35.8	4.6	418	5	US-09-789-189-1323	Sequence 1323, Apr	
18	35.8	4.6	621	6	US-10-027-632-83794	Sequence 83794, Apr	
19	35.8	4.6	621	6	US-10-027-632-83795	Sequence 83795, Apr	
20	35.8	4.6	10351	5	US-09-442-384B-628	Sequence 628, Apr	
21	35.6	4.5	803	6	US-10-105-299-824	Sequence 824, Apr	
22	35.4	4.5	766	6	US-10-027-632-27253	Sequence 27253, Apr	
23	35.4	4.5	2259	5	US-09-053-375B-514	Sequence 514, Apr	
24	35.2	4.5	646	5	US-09-919-002-11896	Sequence 11896, Apr	
25	35.2	4.5	695	6	US-10-027-632-241769	Sequence 241769, Apr	
26	35	4.5	1635	6	US-10-027-632-251270	Sequence 251270, Apr	

Db 280 ttactgaactgagagagattaaagccagtttgaagcctttgtgaagataatgta 339  
QY 301 AACAAAGAGGACGACGAGAAAGAAACACCTTTGAATGCAAAAGGTTGATCAGAACTCT 360  
Db 340 acaaaagagagacgagaaagaaacagctttgaatgcaaaagggatcagaaatcct 399  
QY 361 CAAATTCGGCGACATGCTATAAGTGAGGCGACAGTAAACAAACATCTGTGTACAGTGG 420  
Db 400 caaatgcygagacatgctataagtgagggcagcagtaaaacaacatctgtgtacagtgg 459  
QY 421 GCTGAAAAGGATGACTACACCATGAGCAACAACTTGGTAAACCTGGAAATGGAAACAG 480  
Db 460 gctgaaaaagataactacacacttgtaacccctggtaacccctggaaatgggaaacag 519  
QY 481 CTGACGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 540  
Db 520 ctgacccgtttaaagacaagagactctattatctatgcccgaagtcacctctgttccaat 579  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCGCGTAGA 600  
Db 580 cgggaagcttcgagtaacgctcatttatagccagcctctgctaaagtcctctgttccaat 639  
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCCGCAACCTTCGGGCGCAA 660  
Db 640 ttcgagagaatcttactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699  
QY 661 CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTGGTGTGTTCAT 720  
Db 700 caatccattcacttgggagagattttgaattgcaacagtgcttgcgtgttgcctcaat 759  
QY 721 GTGACTGATCCAAAGCAAGTGCAGCTGCAAAATACCCACAGTTCCCGCAACCTTCGGGCGCAA 660  
Db 760 gtgactgatccaaagcagtgagccatggcactggcttcaagtccttggcttactcaaa 819  
QY 781 CTCTGA 786  
Db 820 ctctga 825

RESULT 3  
US-09-053-375B-821  
; Sequence 821, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 821  
; LENGTH: 1250  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-053-375B-821

Query Match 72.7%; Score 571.6; DB 5; Length 1250;  
Best Local Similarity 83.8%; Pred. No. 6, 6e-140;  
Matches 659; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACCAAACTTCCTCCGATCTCGCGCCACTGCGAGTGCCTCCATCAGC 60  
Db 13 atgatgaaacatacagcaaaccttccccagatcggtggcaactggacttccagcgagc 72  
QY 61 ATGAAAATTTTATGATTTACTTACTTGTTCCTTATCACCACCAATGATTTGATCTGTG 120  
Db 73 atgaagattttatgatttacttactgttttcttactcaccacaaatgattgactgtg 132  
QY 121 CTTTTCGTGTGTATCTTCTATAGAAAGTTGGCAACATGAGATGAAAGGATCTTCAT 180

Db 400 caaatgcygacatgctataagtgagccagcagtaaaacaacatctgtgtacagtgg 459  
QY 421 GCTGAAAAGGATGACTACACCATGAGCAAACTTTGTAACCTTGGAAATGGGAAACAG 480  
Db 460 gctgaaaaagataactacacactgagcaacacacttggtaacccctggaaatgggaaacag 519  
QY 481 CTGACGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCTCAAT 540  
Db 520 ctgacccgtttaaagacaagagactctattatctatgcccgaagtcacctctgttccaat 579  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAAGTCCCGCGTAGA 600  
Db 580 cgggaagcttcgagtaacgctcatttatagccagcctctgctaaagtcctctgttccaat 639  
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCCGCAACCTTCGGGCGCAA 660  
Db 640 ttcgagagaatcttactcagagctgcaaataccacagttccgcaaaccttgcgggcaa 699  
QY 661 CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTGGTGTGTTCAT 720  
Db 700 caatccattcacttgggagagattttgaattgcaacagtgcttgcgtgttgcctcaat 759  
QY 721 GTGACTGATCCAAAGCAAGTGCAGCTGCAAAATACCCACAGTTCCCGCAACCTTCGGGCGCAA 780  
Db 760 gtgactgatccaaagcagtgagccatggcactggcttcaagtccttggcttactcaaa 819  
QY 781 CTCTGA 786  
Db 820 ctctga 825

RESULT 2  
US-09-442-384B-457  
; Sequence 457, Application US/09442384B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashchev, Matvey  
; TITLE OF INVENTION: Hematology/Immunology Array  
; FILE REFERENCE: CLON-006CIP15  
; CURRENT APPLICATION NUMBER: US/09/442,384B  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 830  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-442-384B-457

Query Match 98.8%; Score 776.4; DB 5; Length 1816;  
Best Local Similarity 99.2%; Pred. No. 2.1e-193;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAAACTTCCTCCGATCTCGCGCCACTGCGAGTGCCTCCATCAGC 60  
Db 40 atgatgaaacatacagcaaaccttccccagatctgcccagctggactggcctcagc 99  
QY 61 ATGAAAATTTTATGATTTACTTACTTGTTCCTTATCACCACCAATGATTTGATCTGTG 120  
Db 100 atgaaaattttatgatttacttactgttttcttactcaccacaaagattgggtcagca 159  
QY 121 CTTTTCGTGTGTATCTTCTATAGAAAGTTGGCAACATGAGATGAAAGGATCTTCAT 180  
Db 160 ctttttgcgtgtactctcagaggttggacaagatagatgaaagaaatcttcat 219  
QY 181 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACACAGAGAGAAAGATCTTCCTCC 240  
Db 220 gaagattttgtattcattgaaacacatagagatgcaacacagagagaaagatcctatcc 279  
QY 241 TTACTGAAGTGTGAGGAGATTAAAGCCAGTTTGAAGCCTTGTGCAGGATATAATGTTA 300

Db 133 ctttttgcgtgtatcttctatagagattggatagaagtcgagaggagtaaaaccttcat 192  
 Qy 181 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAGAAAGATCTTATCC 240  
 Db 193 gaagattttgtatctataaaagactaaagagatgcaacaagagagagatctttatcc 252  
 Qy 241 TTACTGAACGTGTAGGAGATTAAGCCAGGTTTGAAGCTTTTGAAGGATATATAGTGA 300  
 Db 253 ttgctgaactgtgaggagatgagagcgcaatttgaagaccttgcgaagatataacgtta 312  
 Qy 301 AACAAAGAGAGACGAGAAAGAAAGAAAGCTTTGAATGCAAAAGGTTGATCAGAATCCT 360  
 Db 313 acaaaagaaga--gaaaaagaagaagccttgaaatgcaaaagagtgagagatccct 369  
 Qy 361 CAATTTGGCGCACATGTCATAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
 Db 370 caaattgcagcacactgttgtaagcgaagcgaacagtaagcagatcgcttctacagtgg 429  
 Qy 421 GCTGAAAGAGGATACACCATCAGCAACAACTTGGTAAACCTTGGAAATGGAAACAG 480  
 Db 430 gccaaagaagatattataccatgaaagcaacttggttaagtgtgaaatgggaacag 489  
 Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCCCAAGTCACTTGTGTCCAA 540  
 Db 490 ctgacggttaaaagagagactctattatgtctacactcaagtcacactctctctaat 549  
 Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCCCTAAAGTCCCGGTAGA 600  
 Db 550 cggagacctgcagtcacacgcccattcaatcgccctgctgagcagcagctgga 609  
 Qy 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 660  
 Db 610 tctgagagaactcttactcaagcggcgaataaccacacagttctcccgagcag 669  
 Qy 661 CAATCCATCTACTTGGGAGGAGTATTGAATTGAACAGAGTGTGCGGTGTTGTCAAT 720  
 Db 670 cagctgttcaactggcgagggtgttggaattacaagctggtctgtctgtttgtcaac 729  
 Qy 721 GTGACTGATCCAAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780  
 Db 730 gtgactgaagcaagcgaagtgatccacagagttggcttctcatcttttggcttactcaaa 789  
 Qy 781 CTCCTGA 786  
 Db 790 cctctga 795

RESULT 4

US-09-911-904-131  
 ; Sequence 131, Application US/09911904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fair, Spencer B.  
 ; APPLICANT: Pickett, Gavin G.  
 ; APPLICANT: Neft, Robin Eileen  
 ; APPLICANT: Dunn, II, Robert Thomas  
 ; TITLE OF INVENTION: CANINE TOXICITY GENES  
 ; FILE REFERENCE: 400742000200  
 ; CURRENT APPLICATION NUMBER: US/09/911,904  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/220,057  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 386  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 131  
 ; LENGTH: 508  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-911-904-131

Query Match 45.9%; Score 360.6; DB 5; Length 508;  
 Best Local Similarity 83.0%; Pred. No. 7.7e-85;  
 Matches 424; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

Qy 267 CCAGTTTCAAGCGTTTGTGAAGGATATATATGTTAAACAAAGAGAGACGAGAAAGAAA 326  
 Db 1 ccaatttgaagcctttctcaagggagataatgctctaaacaacgaataagaaagaagaaaa 60  
 Qy 327 CAGCTTTGAAATGCAAAAGAGTGTATGAGTCTCAATTCGGGACATGTCATTAAGTGA 386  
 Db 61 ca---tgcgaatgcaaaaagtgatcagagatcctcgaattgagcccatgtcataagtga 117  
 Qy 387 GCCCAGCAGTAAACCAACATCTGTGTACAGTGGGCTGAAAGAGGATATCTACACCATGAG 446  
 Db 118 ggcctagtagtaaccagcgtccgttctcgtggtggtggtggtggtggtggtggtggtggt 177  
 Qy 447 CAACAACTTGGTAAACCTTGGAAATGGAAACAGCTGACCGTTAAAGACAAAGGACTCTA 506  
 Db 178 cagcaacctgtgagcctcgagaaatggaaacagttggtggtggtggtggtggtggtggtggt 237  
 Qy 507 TTATATCTATGCCCAAGTCACTTCTGTTCCTCAATTCGGAAGCTTCGAGTCAAGTCCAT 566  
 Db 238 ttagtctatgcccaagtcacacttctgtcctcaatcggtcgtcgtcgtcgtcgtcgtcgtcgt 297  
 Qy 567 TATAGCCAGCTCTGCCCTAAAGTCCCGGTAGATTCAGAGAGATCTTACTCAGAGCTGC 626  
 Db 298 cgtgcagcagctatgctccctcattcccgagtggaacgagagagagagagagagagagagag 357  
 Qy 627 AAATACCCACAGTTCGCCCAACCTTGGCGCAACCAATCCATTCACCTTGGGAGGAGTATT 686  
 Db 358 gagctcccgctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 417  
 Qy 687 TGAATTCGAACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746  
 Db 418 tgaattgcatcaggtgttcggtgttcggtgttcggtgttcggtgttcggtgttcggtgttcggt 477  
 Qy 747 TGGCACTGGCTTCAGTCTCTTGGCTTACTC 777  
 Db 478 cgggaccggcttcacgtctcttttggcttactc 508

RESULT 5

US-09-875-453A-9  
 ; Sequence 9, Application US/09875453A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kim, Jungshuh P.  
 ; APPLICANT: Starr, Douglas B.  
 ; APPLICANT: Tam, Albert W.  
 ; APPLICANT: Laurence, Megan E.  
 ; APPLICANT: Michelotti, Emil F.  
 ; APPLICANT: Velligan, Mark D.  
 ; APPLICANT: Latour, Derek R.  
 ; APPLICANT: Thomas, Rita L.  
 ; APPLICANT: Kongpachith, Ana  
 ; APPLICANT: Sheppard, Liana T.  
 ; APPLICANT: Lim, Moon Young  
 ; APPLICANT: Bruice, Thomas W.  
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION  
 ; FILE REFERENCE: 54600-8135.US00  
 ; CURRENT APPLICATION NUMBER: US/09/875,453A  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: US 60/209,549  
 ; PRIOR FILING DATE: 2000-06-06  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 2395  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-875-453A-9

Query Match 18.8%; Score 147.8; DB 5; Length 2395;  
 Best Local Similarity 88.0%; Pred. No. 5.4e-29;  
 Matches 161; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

RESULT      6
PCT-US02-10421-202
; Sequence 202, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siging
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
; FILE REFERENCE: 210121.565PEC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10421-202

```

	Query Match	5.8%	Score 45.6	DB 1	Length 569	
	Best Local Similarity	49.6%	Pred: NO	0.019		
	Matches 117	Conservative	0	Mismatches 119	Indels	Gaps
QY	238	TCCTTACTGA	CTGTGAGGACAT	TAAAGCCAGCTTGAAGGCTTCTG	GAAGCATATAATG	297
Db	165	tccatcacattacag	tggtggaa	caaaaattgggata	ggaatgggtccggagagacagata	224
QY	298	TTAAACAAAGAGGAGCAG	AGAAAGAAAACAGCTTTGAAATGCA	AAAAAGGTGATCAGAAAT		357
Db	225	ctcaaatcgtggacaccaa	tttcagaaacacgaggaacttcaaaaagcccaatcagggag			284
QY	358	CCTCAAAATGCGGCACATGT	CATTAAGTGTAGGCCAGCAGTAAACACACATCTGTGTTACAG			417
Db	285	cagtatgcagaggggaagat	gagagggggtgtccccaggaagaagacacttggtgtgcaa			344
QY	418	TGGCGTGA	AAAAAGGATACTACACATGAGCAACAACTTGTAAACCCCTGGAAAAATGG			473
Db	245	caaaaatttttgaggttgaac	caaaaadagacacagaaaacacccctggaattgg			400

```

RESULT      7
US-10-112-699-202
; Sequence 202, Application US/10112699
; GENERAL INFORMATION:
; APPLICANT: Wang, tongtong
; APPLICANT: Wang, Siqing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
; FILE REFERENCE: 210121.565
; CURRENT APPLICATION NUMBER: US/10/112,699
; CURRENT FILING DATE: 2002-03-28

```

Query Match: 5.8%; Score 45.6; DB 6; Length 569;  
Best Local Similarity 49.6%; Pred. NO. 0.019;  
Matches 117; Conservative 0; Mismatches 119; Indels

	QY	238	TCCTTACTGAATGTGAGGAGATTAAAGCCAGTTTGAGCGCTTGTGAAGCATATAATG	299
	Db	165	ttcatacttacagtggttggtaaaaaattgggatgaatggtgccggagagcaggata	224
	QY	298	TTAACAAGAGGAGCAGGAAGAAAGAAAACGCTTTGAAATGCCAAAAGGGTGATCAGAAAT	357
	Db	225	ctcaaatacgtggaccaccaatttcagaaacacgcgagaaacttcaaaaagccaatcaggag	284
	QY	358	CCTCAAAATTCGCACATCTGCATAGTAGGCGCAGCTAAAAACAACATCTCTGTTACAG	417
	Db	285	cagtatgcagaggggaagtatgagaggcgctcccccagaagaagacatctggtctgcaa	344
	QY	418	TGGCGCTGAAAAAGGATACTACACCATGAGCACAACTTCGTTACCTGGAANAATGG	473
	b	245	cagaaacaattctgaattgaaacccaagaagaacaaacacagaacaacacctggaattg	400

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RESULT      8
US-09-919-002-664
; sequence 664, Application US/09919002.
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 664
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
; TS-09-919-002-664

```

Query Match	5.6%	Score	44	DB	5	Length	2127
Best Local Similarity	49.2%	Pred. NO.	0.072				
Conservative		0	Mismatches	120	Indels	0	Gaps
							0

QY	238	TCCTTACTGAAC	CTGTGAGCAGAT	TAAACGCCAG	TTTGAAGCGCTTT	TCTGAAGGATATA	TATG	297
Db	238	ttcatccattcag	tggttggaataaaa	attgggatgaat	gggttcctccg	agagagcagag	tta	297
QY	298	TTAAACAAAGAG	CAGACGAAAGAA	AAACACGCTTT	GAATTC	CAAAAAGG	TGATCAGAT	357
Db	298	ctcaaatacgt	ggacacccaatt	tgcagaacac	gagcagaactt	caaaaagcc	aatcaggag	357
QY	358	CCTCAAAATTC	GGGCACATG	TCATTAAGT	GAGGCCAGCAG	TAAACACACAT	CTCTGTTACAG	417
Db	358	cagtatgcagag	gggaagtgcag	gtgaggggtg	cccccagaag	agaagaact	ctctggtctgc	aa 417
QY	418	TGGGCTGAAAA	AGGATAC	TACCATC	TGAGCACAAC	ATTTGGT	TAAACCTG	GAATAATG 473
b	418	cagaacaaatt	ttgaattgaac	tcgaaacg	aaagaaac	aaacacac	aaacac	ctctggaaatg 473



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; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7000
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00141818
; NAME/KEY: unsure
; LOCATION: 24, 113
; OTHER INFORMATION: a, t, c, g, or other
; US-09-540-210B-7000

Query Match          5.0%; Score 39.4; DB 5; Length 234;
Best Local Similarity 48.8%; Pred.No. 0.61;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0

QY 263 AAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTAAACAAGAGGAGGACGAAGAAAG 322
Db 1 aaaaagggatgaatgggtcccnagagcagagtactcaaatcaglggacaccaattg 60

QY 323 AAAACACGCTTTGGAANTGCAAAAAAGGTGATCAGAACTCTCAAAATGCGGCACATGTCATAA 392
Db 61 agaaacagcgagcaacttcaaaagccaatcaggagcagtgatgcagagggggaanattgag 120

QY 383 GTGAGGCGCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATACTACACCA 442
Db 121 gggctgccccaggaagaagacatctggtctgcaacagaaaaatgttgagtgaaaaacga 180

QY 443 TGAGCAACAACACTTGGTAACCCCTGGAAAAATGG 473
Db 181 aagaacaaacagaaaaacacctggaaatgg 211

RESULT 10
US-09-540-210B-14649
; Sequence 14649, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.

```

APPLICANT: Stave, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE  
FILE REFERENCE: PD-1037 CIP  
CURRENT APPLICATION NUMBER: US/09/540,210B  
CURRENT FILING DATE: 2002-04-03  
PRIOR FILING DATE: 08/972,899  
PRIOR FILING DATE: November 18, 1997  
PRIOR APPLICATION NUMBER: 08/395,244  
PRIOR FILING DATE: February 27, 1995  
PRIOR APPLICATION NUMBER: 08/722,922  
PRIOR FILING DATE: September 27, 1996  
PRIOR APPLICATION NUMBER: 60/005,526  
PRIOR FILING DATE: September 29, 1995  
PRIOR APPLICATION NUMBER: 08/824,029  
PRIOR FILING DATE: March 25, 1997  
PRIOR APPLICATION NUMBER: 60/014,010  
PRIOR FILING DATE: March 25, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/903,555  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/862,178  
PRIOR FILING DATE: May 22, 1997  
PRIOR APPLICATION NUMBER: 60/018,217  
PRIOR FILING DATE: May 23, 1996  
PRIOR APPLICATION NUMBER: 08/881,589  
PRIOR FILING DATE: June 24, 1997  
PRIOR APPLICATION NUMBER: 60/021,275  
PRIOR FILING DATE: June 25, 1996  
PRIOR APPLICATION NUMBER: 08/903,802  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/905,881  
PRIOR FILING DATE: August 1, 1997  
PRIOR APPLICATION NUMBER: 60/025,204  
PRIOR FILING DATE: August 1, 1996  
PRIOR APPLICATION NUMBER: 08/903,471  
PRIOR FILING DATE: July 30, 1997  
PRIOR APPLICATION NUMBER: 60/025,478  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/903,556  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/025,217  
PRIOR FILING DATE: August 22, 1996  
PRIOR APPLICATION NUMBER: 08/937,142  
PRIOR FILING DATE: September 23, 1997  
PRIOR APPLICATION NUMBER: 60/026,598  
PRIOR FILING DATE: September 24, 1996  
PRIOR APPLICATION NUMBER: 08/960,746  
PRIOR FILING DATE: October 29, 1997  
PRIOR APPLICATION NUMBER: 60/030,144  
PRIOR FILING DATE: October 30, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/755,524  
PRIOR FILING DATE: November 22, 1996  
PRIOR APPLICATION NUMBER: 60/007,495  
PRIOR FILING DATE: November 22, 1995  
PRIOR APPLICATION NUMBER: 09/021,031  
PRIOR FILING DATE: February 10, 1998  
PRIOR APPLICATION NUMBER: 60/039,325  
PRIOR FILING DATE: February 13, 1997  
PRIOR APPLICATION NUMBER: 09/035,172  
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431  
PRIOR FILING DATE: March 5, 1997  
PRIOR APPLICATION NUMBER: 09/041,894  
PRIOR FILING DATE: March 12, 1998  
PRIOR APPLICATION NUMBER: 60/040,199  
PRIOR FILING DATE: March 14, 1997  
PRIOR APPLICATION NUMBER: 09/050,817  
PRIOR FILING DATE: March 30, 1998  
PRIOR APPLICATION NUMBER: 60/043,792  
PRIOR FILING DATE: April 11, 1997  
PRIOR APPLICATION NUMBER: 09/074,999  
PRIOR FILING DATE: May 8, 1998  
PRIOR APPLICATION NUMBER: 60/048,431  
PRIOR FILING DATE: May 29, 1997  
PRIOR APPLICATION NUMBER: 09/107,592  
PRIOR FILING DATE: June 30, 1998  
PRIOR APPLICATION NUMBER: 60/052,751  
PRIOR FILING DATE: July 1, 1997  
PRIOR APPLICATION NUMBER: 09/094,079  
PRIOR FILING DATE: June 9, 1998  
PRIOR APPLICATION NUMBER: 60/049,975  
PRIOR FILING DATE: June 13, 1997  
NUMBER OF SEQ ID NOS: 35654  
SOFTWARE: PERL Program  
SEQ ID NO 14649  
LENGTH: 230  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu00678829  
US-09-540-210B-14649

Query Match 4.9%; Score 38.2; DB 5; Length 230;  
Best Local Similarity 50.8%; Pred. NO. 1.2;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297  
DB 32 ttcatactattacagtggttggaataaaatttgatgaatgggtccgagagcagagta 91  
QY 298 TTAACAAAGAGGAGGACGAGAAAGAAACAGCTTTGAATGCCAAAAGGTGATCAGAT 357  
DB 92 ctcaaatcgtggacaccaaatttcagaaacagcgaaactcaaaagccatcaggag 151  
QY 358 CTTCAAAATTCGCGACATGTCATAGTGAGCGCAGTAAACAAACATCTGTTTACA 416  
DB 152 cagtatgcagagggggaagatgagaggggctgccccaggaaagagacatctggtctgca 210

RESULT 11  
US-10-123-155-120  
Sequence 120, Application US/10123155  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206146
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206146

Query Match          4.8%; Score 38; DB 6; Length 663;
Best Local Similarity 51.1%; Pred.No.1.9;
Matches 89; Conservative 0; Mismatches 85; Indels 0;

QY 176 TTCATCAACATTTTCATTATCATGAAACGATACAGAGATCCAACACAGGAGAAAGATCCT
Db 173 ttaagaaacacccagtgaaacaccagaaaaatgcgaatgaaacattccaacaaatgagaaa
QY 236 TATCCTTTACTGAACCTGTGAGGAGGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATA
Db 233 aacagtaagtgcacgaatgagaatttaacagagattgaaataatttttaagaatccaac
QY 296 TGTTAAACAAACAGAGACGACGAGAAAGAAACACACCTTTGAATTCGCAAAAAGGTG 349
Db 293 gagatcatcaggagctgaaaaatacaatgaaataatgcgaataatgcgaatagagag 346

RESULT 13
US-10-027-632-206147
; Sequence 206147, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206147
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206147

Query Match          4.8%; Score 38; DB 6; Length 663;

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Best Local Similarity 51.1%; Pred. No. 1.9;  
Matches 89; Conservative 0; Mismatches 85; Indels. 0; Gaps 0;  
QY 176 TTCATGACAGATTTTCATTCATGAAACGATACAGAGATGCAACACAGAGAGAAAGATCCT 235  
Db 173 ttaagaaacactcagtgacacccaagaataatgcaatgaaatcaacaaatgagaaa 232  
QY 236 TATCCTTACTGAACTGTGAGGAGATTAAAGCCATTTTGAAGGCTTTGTGAAGATATAA 295  
Db 233 aacagtaagtgcaggaatgagaaatttaacagagattgaaataatttttaagaatcaaa 292  
QY 296 TGTAAACAACAG 349  
Db 293 gagatatacaggagctgtaaaatacaataatgtaaaatgcaatagagag 346  
RESULT 14  
US-09-539-331D-26090  
Sequence 26090, Application US/09539331D  
GENERAL INFORMATION:  
APPLICANT: Seilhamer, Jeffrey J.  
APPLICANT: Deleageane, Angelo M.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE  
FILE REFERENCE: PD-1022 CIP  
CURRENT APPLICATION NUMBER: US/09/539,331D  
CURRENT FILING DATE: 2000-03-30  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 40961  
SOFTWARE: PERL Program  
SEQ ID NO 26090  
LENGTH: 438  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: hu00341082  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 262, 268, 288, 330, 338, 353, 371  
OTHER INFORMATION: a, t, c, g, or other  
US-09-539-331D-26090

Query Match 4.7%; Score 36.8; DB 5; Length 438;  
Best Local Similarity 49.7%; Pred. No. 3.5;  
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTCAAGGATATAATG 297  
Db 112 ttcatacatcagtggttggaataaaattggatgaattgggtcccgagagcagagta 171  
QY 298 TTAACAAGAGGAGACCAAGCAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAT 357  
Db 172 ctcaaatcagtggaacaacatttcagadaacagcagcagcagcagcagcagcagcag 231  
QY 358 COTCAAAATGGCGGCACATGTGATAGTGAGGCCAGCCAGAGTAAACAAACATCTGTGTACA 416  
Db 232 cagtagcagagggggaagatgagagggtctnccccangaaagagacatctcgtctnca 290  
RESULT 15  
US-10-105-299-1996/c  
Sequence 1996, Application US/10105299  
GENERAL INFORMATION:  
APPLICANT: Rosen, et. al  
TITLE OF INVENTION: Human Secreted Proteins  
FILE REFERENCE: PS950  
CURRENT APPLICATION NUMBER: US/10/105,299  
CURRENT FILING DATE: 2002-03-26

NUMBER OF SEQ ID NOS: 15197  
Prior Application removed - See File Wrapper or Palm  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1996  
LENGTH: 1751  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc.feature  
LOCATION: (1741)..(1742)  
OTHER INFORMATION: n equals a,t,g, or c  
US-10-105-299-1996  
Query Match 4.6%; Score 36.4; DB 6; Length 1751;  
Best Local Similarity 53.5%; Pred. No. 6.6;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATCTTA 300  
Db 1174 TAACTGAAGTGTGAAATTAACAAAGAAATGATATAGTCCGTTATTTAAATCCCTCTTA 1115  
QY 301 AACAAAGAGGAGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 360  
Db 1114 CACAGAAAAAAGAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1055  
QY 361 CAAATTGGCGGCACATGTCATAA 382  
Db 1054 GAAATTTGTTGAAATGTTTGA 1033  
Search completed: May 30, 2002, 05:39:00  
Job time: 16714 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:25 ; Search time 139.75 seconds  
(without alignments)  
1381.524 Million cell updates/sec

Title: US-08-982-272-4  
Perfect score: 786  
Sequence: 1 ATGATCGAACAATACAACCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	776.4	98.8	786	1	US-08-446-922-3
2	776.4	98.8	786	5	PCT-US93-10034-3
3	776.4	98.8	840	1	US-07-940-605A-1
4	776.4	98.8	840	1	US-08-184-422-7
5	776.4	98.8	840	1	US-08-360-923A-1
6	776.4	98.8	840	1	US-08-431-055-3
7	776.4	98.8	840	2	US-08-690-096-1
8	776.4	98.8	840	2	US-08-249-189-11
9	776.4	98.8	840	2	US-08-484-624A-11
10	776.4	98.8	840	2	US-08-477-733B-11
11	776.4	98.8	840	3	US-08-763-995-1
12	776.4	98.8	840	3	US-09-088-913A-11
13	776.4	98.8	840	3	US-08-589-771B-7
14	776.4	98.8	840	4	US-08-769-819-11
15	776.4	98.8	840	4	US-08-770-974-11
16	776.4	98.8	840	4	US-08-858-197-3
17	638.2	81.2	1425	2	US-08-249-189-15
18	638.2	81.2	1425	2	US-08-484-624A-15
19	638.2	81.2	1425	2	US-08-477-733B-15
20	638.2	81.2	1425	3	US-09-088-913A-15
21	638.2	81.2	1425	4	US-08-769-819-15
22	638.2	81.2	1425	4	US-08-770-974-15
23	637.2	81.1	929	1	US-08-446-922-10
24	637.2	81.1	929	2	US-08-249-189-20
25	637.2	81.1	929	2	US-08-484-624A-20
26	637.2	81.1	929	2	US-08-477-733B-20
27	637.2	81.1	929	3	US-09-088-913A-20

28	637.2	81.1	929	4	US-08-769-819-20
29	637.2	81.1	929	4	US-08-770-974-20
30	571.6	72.7	783	1	US-08-446-922-5
31	571.6	72.7	783	2	US-08-249-189-1
32	571.6	72.7	783	2	US-08-484-624A-1
33	571.6	72.7	783	2	US-08-477-733B-1
34	571.6	72.7	783	3	US-09-088-913A-1
35	571.6	72.7	783	4	US-08-769-819-1
36	571.6	72.7	783	4	US-08-770-974-1
37	571.6	72.7	783	5	PCT-US93-10034-5
38	570	72.5	818	1	US-08-431-055-1
39	570	72.5	818	4	US-08-858-197-1
40	445.6	56.7	878	2	US-08-249-189-22
41	445.6	56.7	878	2	US-08-484-624A-22
42	445.6	56.7	878	2	US-08-477-733B-22
43	445.6	56.7	878	3	US-09-088-913A-22
44	445.6	56.7	878	4	US-08-769-819-22
45	445.6	56.7	878	4	US-08-770-974-22

ALIGNMENTS

RESULT 1  
US-08-446-922-3  
; Sequence 3, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 786 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; STRAIN: CD40-L  
; FEATURE:

NAME/KEY: CDS  
LOCATION: 1..783  
US-08-446-922-3

Query Match 98.8%; Score 776.4; DB 1; Length 786;  
Best Local Similarity 99.2%; Pred. No. 2e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60  
Db 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60

QY 61 ATGAAATTTTATGTATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
Db 61 ATGAAATTTTATGTATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120

QY 121 CTTTCTGCTGTATCTTCTTATAGAGTTGGACAAGTTGGAAGATGAAAGGAATCTTCA 180  
Db 121 CTTTCTGCTGTATCTTCTTATAGAGTTGGACAAGTTGGAAGATGAAAGGAATCTTCA 180

QY 181 GAAGATTTTGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
Db 181 GAAGATTTTGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 240

QY 241 TTTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300  
Db 241 TTTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300

QY 301 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGATCCT 360  
Db 301 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGATCCT 360

QY 361 CAATTCGGGACATGTCATAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGA 420  
Db 361 CAATTCGGGACATGTCATAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGA 420

QY 421 GCTGAAAGAGGATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGAAACAG 480  
Db 421 GCTGAAAGAGGATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGAAACAG 480

QY 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCAAGTCACTTCTGTTCGAAT 540  
Db 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCAAGTCACTTCTGTTCGAAT 540

QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600  
Db 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600

QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTGGGGCAA 660  
Db 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTGGGGCAA 660

QY 661 CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACAGAGTCTCGGTGTTGTCAAT 720  
Db 661 CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACAGAGTCTCGGTGTTGTCAAT 720

QY 721 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGGCTTTCAGTCTTGGCTTACTCAA 780  
Db 721 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGGCTTTCAGTCTTGGCTTACTCAA 780

QY 781 CTCTGA 786  
Db 781 CTCTGA 786

RESULT 2  
PCT-US93-10034-3  
; Sequence 3, Application PC/TUS9310034  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10034  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PCT-US93-10034-3

Query Match 98.8%; Score 776.4; DB 5; Length 786;  
Best Local Similarity 99.2%; Pred. No. 2e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60  
Db 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 60

QY 61 ATGAAATTTTATGTATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
Db 61 ATGAAATTTTATGTATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120

QY 121 CTTTCTGCTGTATCTTCTTATAGAGTTGGACAAGTTGGAAGATGAAAGGAATCTTCA 180  
Db 121 CTTTCTGCTGTATCTTCTTATAGAGTTGGACAAGTTGGAAGATGAAAGGAATCTTCA 180

QY 181 GAAGATTTTGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
Db 181 GAAGATTTTGTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 240

QY 241 TTTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300  
Db 241 TTTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300

QY 301 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGATCCT 360  
Db 301 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATGCAAAAGTGATCAGATCCT 360

QY 361 CAATTCGGGACATGTCATAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGA 420  
Db 361 CAATTCGGGACATGTCATAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGA 420

QY 421 GCTGAAAGAGGATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGAAACAG 480  
Db 421 GCTGAAAGAGGATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGAAACAG 480

QY 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCAAGTCACTTCTGTTCGAAT 540  
Db 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCAAGTCACTTCTGTTCGAAT 540

QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600  
Db 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTAGA 600

QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTGGGGCAA 660  
Db 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACCTTGGGGCAA 660

QY 661 CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACAGAGTCTCGGTGTTGTCAAT 720  
Db 661 CAATCCATTCACCTTGGGAGGAGTATTTGAAATGCAACAGAGTCTCGGTGTTGTCAAT 720

QY 721 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGGCTTTCAGTCTTGGCTTACTCAA 780  
Db 721 GTGACTGTATCCAAAGCAAGTGAAGCATGGCACTGGCTTTCAGTCTTGGCTTACTCAA 780

QY 781 CTCTGA 786  
Db 781 CTCTGA 786



APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSCH, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,422  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-184-422-7

Query Match 98.88; Score 776.4; DB 1; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGATCGAACATACAAACCACTTCCTCCGCTGCTCGGCGCACTGCGATGCCCATCAGC 60  
DB 46 ATGATCGAACATACAAACCACTTCCTCCGCTGCTCGGCGCACTGCGATGCCCATCAGC 105  
QY 61. ATGAAATTTTATGTTTACTTCTTCTTCTTATACCCCAATGATGGATCTGTG 120  
DB 106 ATGAAATTTTATGTTTACTTCTTCTTCTTATACCCCAATGATGGATCTGTG 165  
QY 121 CTTTTCGTGTATCTATAGAAAGGTGGACAAGATAGAGATGAAGAAATCTTCAT 180  
DB 166 CTTTTCGTGTATCTATAGAAAGGTGGACAAGATAGAGATGAAGAAATCTTCAT 225  
QY 181 GAAGATTTTGTATCATGAACCATACAGAGATGCAACAGAGAGAAAGATCTTATCC 240  
DB 226 GAAGATTTTGTATCATGAACCATACAGAGATGCAACAGAGAGAAAGATCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300

DB 286 TTACTGAACCTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGAGACGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATFCAGAACTCT 360  
DB 346 AACAAAGAGAGACGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATFCAGAACTCT 405  
QY 361 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGG 420  
DB 406 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGG 465  
QY 421 GCTGAAAGAGATACACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAACAG 480  
DB 466 GCTGAAAGAGATACACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAACAG 525  
QY 481 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAT 540  
DB 526 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCCTTCCTAAAGTCCCGGCTAG 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCCTTCCTAAAGTCCCGGCTAG 645  
QY 601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGGCA 660  
DB 646 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGGCA 705  
QY 661 CAATCCATTCTGAGGAGGAGTATTTCAATTCGAACCAAGTTCGCTGCTGTTTCTCAAT 720  
DB 706 CAATCCATTCTGAGGAGGAGTATTTCAATTCGAACCAAGTTCGCTGCTGTTTCTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGAGCCATGCGCTTCAGCTTCCTTTGGCTTACTCAAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGAGCCATGCGCTTCAGCTTCCTTTGGCTTACTCAAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

RESULT 5  
US-08-360-923A-1  
; Sequence 1, Application US/08360923A  
; Patent No. 5674492  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,923A  
FILING DATE: December 21, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424





APPLICATION NUMBER: US/08/690,096  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/940,605  
FILING DATE: 04-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22..807  
US-08-690-096-1

Query Match 98.8%; Score 776.4; DB 2; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGGCCACTGGACTCCCATCAGC 60  
DB 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGGCCACTGGACTCCCATCAGC 81  
QY 61 ATGAAATTTTATCTATTACTTACTCTTTCTTATCACCACAAATGATTGATCTGTG 120  
DB 82 ATGAAATTTTATCTATTACTTACTCTTTCTTATCACCACAAATGATTGATCTGTG 141  
QY 121 CTTTGTGCTGTATCTTCTATGAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT 180  
DB 142 CTTTGTGCTGTATCTTCTATGAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT 201  
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240  
DB 202 GAAGATTTTGTATTCATGAAACAGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261  
QY 241 TTAGTGAATGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 300  
DB 262 TTAGTGAATGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 321  
QY 301 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 360  
DB 322 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 381  
QY 361 CAAATTCGGSCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 420  
DB 382 CAAATTCGGSCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 441  
QY 421 GCTGAAAGAGGATCTACACCATGACCAACTTGTAACTGCTGAAATGGGAAACAG 480  
DB 442 GCTGAAAGAGGATCTACACCATGACCAACTTGTAACTGCTGAAATGGGAAACAG 501  
QY 481 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCAT 540  
DB 502 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCAT 561  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCCCTAAAGTCCCGGTAGA 600  
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCCCTAAAGTCCCGGTAGA 621  
QY 601 TTCGAGAGATCTTACACAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAA 660

QY 121 CTTTGTGCTGTATCTTCTATGAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT 180  
DB 142 CTTTGTGCTGTATCTTCTATGAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT 201  
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240  
DB 202 GAAGATTTTGTATTCATGAAACAGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261  
QY 241 TTAGTGAATGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 300  
DB 262 TTAGTGAATGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 321  
QY 301 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 360  
DB 322 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCT 381  
QY 361 CAAATTCGGSCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 420  
DB 382 CAAATTCGGSCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 441  
QY 421 GCTGAAAGAGGATCTACACCATGACCAACTTGTAACTGCTGAAATGGGAAACAG 480  
DB 442 GCTGAAAGAGGATCTACACCATGACCAACTTGTAACTGCTGAAATGGGAAACAG 501  
QY 481 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCAT 540  
DB 502 CTGACCGTTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCAT 561  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCCCTAAAGTCCCGGTAGA 600  
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCCCTAAAGTCCCGGTAGA 621  
QY 601 TTCGAGAGATCTTACACAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAA 660  
DB 622 TTCGAGAGATCTTACACAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGGGCAA 681  
QY 661 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGCAAT 720  
DB 682 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTGCAAT 741  
QY 721 GTGACTGATCCAAAGCAGTGGCCATGGCACTGGCTTTCAGTCCCTTACCTACAAA 780  
DB 742 GTGACTGATCCAAAGCAGTGGCCATGGCACTGGCTTTCAGTCCCTTACCTACAAA 801  
QY 781 CTCTGA 786  
DB 802 CTCTGA 807

RESULT 7  
US-08-690-096-1  
Sequence 1, Application US/086900096  
Patent No. 5945513  
GENERAL INFORMATION:  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: HOLLENBAUGH, DIANE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
\* OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

Db 622 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAA 681  
Qy 661 CAATCCATTCTACTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCCGCTGTTTGTCAAT 720  
Db 682 CAATCCATTCTACTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCCGCTGTTTGTCAAT 741  
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTTCAGGCTTCTTGGCTTACTCAAA 780  
Db 742 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTTCAGGCTTCTTGGCTTACTCAAA 801  
Qy 781 CTCTGA 786  
Db 802 CTCTGA 807

RESULT 8  
US-08-249-189-11  
; Sequence 11, Application US/08249189  
; Patent No. 5961974  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,189  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
; US-08-249-189-11  
  
Query Match 98.8%; Score 776.4; DB 2; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 105  
Qy 61 ATGAAATTTTATGTATTTACTTACTCTTTCTTATACCCCAATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTTACTTACTCTTTCTTATACCCCAATGATGGATCTGTG 165  
Qy 121 CTTTTTGTGTATCTTCTATAGAAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180  
Db 166 CTTTTTGTGTATCTTCTATAGAAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 285  
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 345  
Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360  
Db 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405  
Qy 361 CAAATTCGGGCACATGTCTAAGTGAAGCCAGTGAAGCTTTTGAAGGATATAATGTTA 420  
Db 406 CAAATTCGGGCACATGTCTAAGTGAAGCCAGTGAAGCTTTTGAAGGATATAATGTTA 465  
Qy 421 CTTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGGAAACAG 480  
Db 466 CTTGAAAGAGGATCTACACCATGAGCAACAACCTTGGTAAACCTGGAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGAAAGCTTCGAGTCAAGTCCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 600  
Db 586 CGGAAAGCTTCGAGTCAAGTCCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 645  
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAA 660  
Db 646 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAAAACCTTGGCGGCAA 705  
Qy 661 CAATCCATTCTACTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCCGCTGTTTGTCAAT 720  
Db 706 CAATCCATTCTACTGGGAGGAGTATTTGAATTGCAACAGAGTCTTCCGCTGTTTGTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTTCAGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCACTGGCTTTCAGGCTTACTCAAA 825  
Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 9  
US-08-484-624A-11  
; Sequence 11, Application US/08484624A  
; Patent No. 5962406

GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,624A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-484-624A-11

Query Match 98.8%; Score 776.4; DB 2: Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAACTTCTCCCGGATCTGGCGGCACCTGGACTGCCCATCAGC 60

Db 46 ATGATCGAAACATACAACTTCTCCCGGATCTGGCGGCACCTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACAAATGATGATCTGTG 120  
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACAGATGATGGGTGCA 165  
QY 121 CTTTGTCTGTATCTTCTATAGAGGTGGACAAAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTGTCTGTATCTTCTATAGAGGTGGACAAAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAGATTTTCTATGATGAAACGATACAGAGATGCAACACAGAGAGAGATCTTATCC 240  
Db 226 GAGATTTTCTATGATGAAACGATACAGAGATGCAACACAGAGAGAGATCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCTCT 360  
Db 346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCTCT 405  
QY 361 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGG 420  
Db 406 CAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAAAGGATATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGGAAACAG 480  
Db 466 GCTGAAAAAGGATATACACCATGAGCAACAACTTGTGTAACCTTGGAAATGGGAAACAG 525  
QY 481 CTGACCTTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 540  
Db 526 CTGACCTTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGCGGCAA 660  
Db 646 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTGGCGGCAA 705  
QY 661 CAATCCATTCTCTGGGAGGATTTGAATTGCAACACAGTGTCTCGTGTTCCTCAAT 720  
Db 706 CAATCCATTCTCTGGGAGGATTTGAATTGCAACACAGTGTCTCGTGTTCCTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGGAGCCATGCGCTTCCACGCTCTTCCGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGCGCTTCCACGCTCTTCCGCTTACTCAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 10  
US-08-477-733B-11  
Sequence 11, Application US/08477733B  
Patent No. 5981724  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET

CITY:	SEATTLE
STATE:	WASHINGTON
COUNTRY:	USA
ZIP:	98101
MEDIUM TYPE:	Floppy disk
COMPUTER:	Apple Macintosh
OPERATING SYSTEM:	Apple Operating System 7.5.5
SOFTWARE:	MS Word for Apple Power Macintosh, version 6.0.1
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/477,733B
FILING DATE:	June 07, 1995
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/249,189
FILING DATE:	May 24, 1994
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/969,703
FILING DATE:	October 23, 1992
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/805,723
FILING DATE:	December 5, 1991
CLASSIFICATION:	435
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	07/783,707
FILING DATE:	October 25, 1991
CLASSIFICATION:	435
ATTORNEY/AGENT INFORMATION:	
NAME:	Perkins, Patricia A.
REGISTRATION NUMBER:	34,693
REFERENCE/DOCKET NUMBER:	2802-D
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	2065870430
TELEFAX:	2065870606
INFORMATION FOR SEQ ID NO:	11:
SEQUENCE CHARACTERISTICS:	
LENGTH:	840 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	CDNA
HYPOTHETICAL:	NO
ANTI-SENSE:	NO
ORIGINAL SOURCE:	
ORGANISM:	Homo sapiens
IMMEDIATE SOURCE:	
CLONE:	CD40-L
FEATURE:	
NAME/KEY:	CDS
LOCATION:	46..831
US-08-477-733B-11	
Query Match	98.8%; Score 776.4; DB 2; Length 840;
Best Local Similarity	99.2%; pred. No. 2.le-220;
Matches	780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	1 ATGATCGAAACATACACCAGCACTTCCCGCATCTGGGGGCACCTGGACTGCCCATCAGC 60 
Db	46 ATGATCGAAACATACACCAGCACTTCCCGCATCTGGGGGCACCTGGACTGCCCATCAGC 105 
QY	61 ATGAAAATTTTGATGTATTACTTACTTCTTCCTTATCACCCCAAAATCATGGATCTGTG 120 
Db	106 ATGAAAATTTTGATGTATTACTTACTTCTTCCTTATCACCCCAAAATCATGGATCTGTG 165 
QY	121 CTTTTTCTGTGTATCTTCATAGAGGTTGGCAAGATAGAAGATGAAGAAATCTTCAT 180 
Db	166 CTTTTTCTGTGTATCTTCATAGAGGTTGGCAAGATAGAAGATGAAGAAATCTTCAT 225 
QY	181 GAAGATTTTGTATTTCATGAAACAGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240 

REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELEPHONE: (206)597-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-763-995-1

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220; Indels 0; Gaps 0;  
Matches 780; Conservative 0; Mismatches 6;

QY	1	ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGCGCCACTGAGTGCCTTCATCAGC	60
DB	46	ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGCGCCACTGAGTGCCTTCATCAGC	105
QY	61	ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATCTGTG	120
DB	106	ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCACCAATGATGATGATGATGATG	165
QY	121	CTTTTCTGCTGATCTTCTAGAGGTTGGACAAGATAGAGATGAAGGATGATCTTCAT	180
DB	166	CTTTTCTGCTGATCTTCTAGAGGTTGGACAAGATAGAGATGAAGGATGATCTTCAT	225
QY	181	GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGATGATCTTCATCC	240
DB	226	GAAGATTTTGTATTCATGAAGATACAGAGATGCAACAGAGAGAGATGATCTTCATCC	285
QY	241	TTACTGAACGTGAGGAGATTAAGGACCTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
DB	286	TTACTGAACGTGAGGAGATTAAGGACCTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAGGTATCAGATTCCT	360
DB	346	AACAAAGAGGAGACGAAGAAGAAACAGCTTTGAAATGCAAAAGGTATCAGATTCCT	405
QY	361	CAAAATCGGCACATGTCATAAGTGAGCGCAGTAAACACATCTGTGTTACAGTGG	420
DB	406	CAAAATCGGCACATGTCATAAGTGAGCGCAGTAAACACATCTGTGTTACAGTGG	465
QY	421	GCTGAAAGAGGATACACCATCAGCAACACTTGTGTAACCTTGGAAATGGAAACAG	480
DB	466	GCTGAAAGAGGATACACCATCAGCAACACTTGTGTAACCTTGGAAATGGAAACAG	525
QY	481	CTGACCGTTAAACACAGGACTTATATATCTATCCCAAGTCACCTCTGTTCAT	540
DB	526	CTGACCGTTAAACACAGGACTTATATATCTATCCCAAGTCACCTCTGTTCAT	585
QY	541	CGGAAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTTAGA	600
DB	586	CGGAAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGGTTAGA	645
QY	601	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA	660
DB	646	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGGGCAA	705
QY	661	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACAGGTCCTTCGCTTTGTCAAT	720

DB	706	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACAGGTCCTTCGGTGTTCAT	765
QY	721	GTGACTGATCCAAAGCCAAAGTGAGCCATGGCCTTTCAGTCTTGGCTTACTCAAA	780
DB	766	GTGACTGATCCAAAGCCAAAGTGAGCCATGGCCTTTCAGTCTTGGCTTACTCAAA	825
QY	781	CTCTGA 786	
DB	826	CTCTGA 831	

RESULT 12  
US-09-088-913A-11  
; Sequence 11, Application US/09088913A  
; Patent No. 6087329  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLON, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088.913A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:

ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-088-913A-11

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACAAACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105

Qy 61 ATGAAATTTTATGTATTTACTTACTTACTTCTTATCATCCCAATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTTACTTACTTCTTATCATCCCAATGATGGATCTGTG 165

Qy 121 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGAAATCTTCAT 180  
Db 166 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGAAATCTTCAT 225

Qy 181 GAAGATTTTGTATTCATGAACGATACAGAGATGCAACAGAGAGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAACGATACAGAGATGCAACAGAGAGAGATCTTATCC 285

Qy 241 TTACTGAAGCTGAGGAGATTAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300  
Db 286 TTACTGAAGCTGAGGAGATTAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 345

Qy 301 AACAAAG 360  
Db 346 AACAAAG 405

Qy 361 CAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTG 420  
Db 406 CAATTCGGGCACATGTATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTG 465

Qy 421 GCTCAAAAGAGATACACACATGAGCAACACTTGTAAACCTTGGAAATGGAAACAG 480  
Db 466 GCTCAAAAGAGATACACACATGAGCAACACTTGTAAACCTTGGAAATGGAAACAG 525

Qy 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCCCCAAGTCACCTCTGTTCAT 540  
Db 526 CTGACCGTTAAAGACAGAGGACTTATATATCTATGCCCCAAGTCACCTCTGTTCAT 585

Qy 541 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGTAGA 600  
Db 586 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGTAGA 645

Qy 601 TTCAGAGATCTTACTCAGAGCTGCAATACCCACAGCTTCGCGCAACCTTGGGGGCA 660  
Db 646 TTCAGAGATCTTACTCAGAGCTGCAATACCCACAGCTTCGCGCAACCTTGGGGGCA 705

Qy 661 CAATCCATTTACTTGGGAGGAGTATTTGAATTCGAACAGGCTCTCGGTCTTCTCAAT 720  
Db 706 CAATCCATTTACTTGGGAGGAGTATTTGAATTCGAACAGGCTCTCGGTCTTCTCAAT 765

Qy 721 GTGACTGATCCAAAGCCAGTGGAGCCATGGCACTGGCTTCCCTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCCAGTGGAGCCATGGCACTGGCTTCCCTTGGCTTACTCAAA 825

Qy 781 CTCGA 786  
Db 826 CTCGA 831

RESULT 13  
US-08-589-771B-7  
; Sequence 7, Application US/08589771B

Patent No. 6106832  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSCH, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING  
DEFECTIVE CD40L (as amended)  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589,771B  
FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JANIS C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-589-771B-7

Query Match 98.8%; Score 776.4; DB 3; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACAAACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105

Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTATCATCCCAATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTTACTTACTTCTTATCATCCCAATGATGGATCTGTG 165

Qy 121 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGAAATCTTCAT 180  
Db 166 CTTTTTGTGTATCTTCATAGAGGTTGGACAAGATAGAAAGATGAAAGAAATCTTCAT 225



181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240  
|||||  
226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 285  
|||||  
241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
|||||  
301 AACAAAGAGAGACGAGAGAAAGAAACACAGCTTTGAATGCAAAAAGGTGATCAGATCCT 360  
346 AACAAAGAGAGACGAGAGAAAGAAACACAGCTTTGAATGCAAAAAGGTGATCAGATCCT 405  
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361 CAATTTGCGGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
406 CAATTTGCGGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465  
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421 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAATGGAATGGAAACAG 480  
466 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAATGGAATGGAAACAG 525  
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481 CTGACCGTTAAAGACAGGAGCTTATATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 540  
526 CTGACCGTTAAAGACAGGAGCTTATATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 585  
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586 CGGGAACCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTAAAGTCCCGCGGTAGA 645  
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601 TTCGAGAGATCTTACTCAGAGTGCMAATACCCACAGTTCCGCCAAACCTTCGCGGCA 660  
646 TTCGAGAGATCTTACTCAGAGTGCMAATACCCACAGTTCCGCCAAACCTTCGCGGCA 705  
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661 CAATCCATTCATCTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTGCAAT 720  
706 CAATCCATTCATCTGGGAGGAGTATTGAAATGCAACAGGCTCTCGGTGTTGTGCAAT 765  
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721 GTGACTGATCCAAAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
766 GTGACTGATCCAAAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825  
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781 CTCGA 786  
826 CTCGA 831

RESULT 14  
US-08-769-819-11  
; Sequence 11, Application US/08769819.  
; Patent No. 6264951  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769, 819  
; FILING DATE: 19-DEC-1996  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-769-819-11

Query Match 98.8%; Score 776.4; DB 4; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGGGCCACTGGACTGCCATCAGC 60  
DB 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGGGGCCACTGGACTGCCATCAGC 105  
QY 61 ATGAAATTTTATGTATTTACTTACTGTCTTATCACCACCAATGATTTGGATCTGTG 120  
DB 106 ATGAAATTTTATGTATTTACTTACTGTCTTATCACCACCAATGATTTGGATCTGTG 165  
QY 121 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAAGATGAGAAGATGAAAGGATCTTCAT 180  
DB 166 CTTTGTGCTGTATCTTTCATAGAGGTTGGACAAGATGAGAAGATGAAAGGATCTTCAT 225  
QY 181 GAAGATTTTGTATTTATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTTATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
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QY 301 AACAAAGAGAGACGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360  
DB 346 AACAAAGAGAGACGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405  
QY 361 CAATTTGCGGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 406 CAATTTGCGGCACATGTCATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465  
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAATGGAATGGAAACAG 480



Db 466 GCTGAAAGGATACACCATGAGCAACACTTGGTAACCTCGAAATGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCAAGTCACTTCTGTCCCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCAAGTCACTTCTGTCCCAAT 585  
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 600  
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Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGGCTTCACTGCTTTCGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGGCTTCACTGCTTTCGCTTACTCAA 825  
Qy 781 CTCCTGA 786  
Db 826 CTCCTGA 831

RESULT 15

US-08-770-974-11  
; Sequence 11, Application US/08770974  
; Patent No. 6290972  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/770,974  
; FILING DATE: 20-DEC-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: 02-AUG-1995  
; APPLICATION NUMBER: 08/249,189  
; FILING DATE: May 24, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
; US-08-770-974-11

Query Match 98.8%; Score 776.4; DB 4; Length 840;  
Best Local Similarity 99.2%; Pred. No. 2.1e-220;  
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 60  
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGCGGCCACTGGACTGCCATCAGC 105  
Qy 61 ATGAAATTTTATGTATTACTTACTTCTTATCACCACCAATGATTGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTACTTACTTCTTATCACCACCAATGATTGGATCTGTG 165  
Qy 121 CTTTTGCTGTCTATCTTCTATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCA 180  
Db 166 CTTTTGCTGTCTATCTTCTATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCA 225  
Qy 181 GAAGATTTTGTATTATGAAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTATGAAACGATACAGATGCAACACAGGAGAAAGATCTTATCC 285  
Qy 241 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300  
Db 286 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345  
Qy 301 AACAAAGGAGACGAGAAAGAAACACCTTTGAATGCAAAAGGATGATCAGATCTCT 360  
Db 346 AACAAAGGAGACGAGAAAGAAAGAAACACCTTTGAATGCAAAAGGATGATCAGATCTCT 405  
Qy 361 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACACATCTCTGTTACAGTGG 420  
Db 406 CAAATTCGCGCACATCTCATAGTGGCCAGCAGTAAACACATCTCTGTTACAGTGG 465  
Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAG 480  
Db 466 GCTGAAAAGGATACCTACACCATGAGCACAACCTTGGTAACCTGGAAATGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCAAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 600  
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA 645  
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA 660  
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGCGGCAA 705  
Qy 661 CAATCCATTCCTCTGGGAGGAGTATTGAAATGCAACAGGCTTTCGGTGTTCGTCAT 720

Thu May 30 05:46:07 2002

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Qy	781	CTCTGA	786
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Search completed: May 30, 2002, 02:51:32  
Job time: 11596 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:52 ; Search time 6499.83 Seconds  
(without alignments)  
2520.909 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783  
Sequence: 1 ATGATGGAACATACACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_da: \*  
2: gb\_htg: \*  
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4: gb\_ov: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
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24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	760.6	97.1	818	6	AR044778	AR044778 Sequence
2	760.6	97.1	818	6	AR171646	AR171646 Sequence
3	760.6	97.1	1250	6	AX208160	AX208160 Sequence
4	759	96.9	783	6	AR076918	AR076918 Sequence
5	759	96.9	783	6	AR078308	AR078308 Sequence
6	759	96.9	783	6	AR085411	AR085411 Sequence
7	759	96.9	783	6	AR103367	AR103367 Sequence
8	759	96.9	783	6	AR169224	AR169224 Sequence
9	759	96.9	783	6	187865	187865 Sequence
10	759	96.9	1250	10	MDC40	X65433 M.musculus
11	687	87.7	783	10	AF013985	AF013985 Rattus no
12	683.8	87.3	783	10	AF116582	AF116582 Rattus no
13	631.4	80.6	878	6	AR076933	AR076933 Sequence
14	631.4	80.6	878	6	AR078323	AR078323 Sequence
15	631.4	80.6	878	6	AR085426	AR085426 Sequence
16	631.4	80.6	878	6	AR103382	AR103382 Sequence
17	631.4	80.6	878	6	AR169239	AR169239 Sequence
18	582.8	74.4	840	6	187864	187864 Sequence
19	582.8	74.4	840	6	AR044779	AR044779 Sequence
20	582.8	74.4	840	6	AR076926	AR076926 Sequence
21	582.8	74.4	840	6	AR078316	AR078316 Sequence
22	582.8	74.4	840	6	AR085419	AR085419 Sequence
23	582.8	74.4	840	6	AR103375	AR103375 Sequence
24	582.8	74.4	840	6	AR106246	AR106246 Sequence
25	582.8	74.4	840	6	AR169232	AR169232 Sequence
26	582.8	74.4	840	6	AR171647	AR171647 Sequence
27	582.8	74.4	840	6	123893	123893 Sequence
28	582.8	74.4	840	6	127345	127345 Sequence
29	582.8	74.4	840	6	167828	167828 Sequence
30	582.8	74.4	879	6	AX090039	AX090039 Sequence
31	582.8	74.4	879	9	HSCP39MR	215017 H.sapiens m
32	582.8	74.4	1803	9	HSCD40	X67878 H.sapiens m
33	582.8	74.4	1816	9	HUMCD40L	L07414 Human CD40-
34	581.2	74.2	1822	9	HSTRAPA	X68550 H.sapiens t
35	573.2	73.2	1058	9	AF344841	AF344841 Cercopitu
36	573.2	73.2	1058	9	AF344859	AF344859 Macaca mu
37	567.6	72.5	839	9	HACD40L	X66710 H.sapiens m
38	566.8	72.4	974	9	AF344860	AF344860 Actinus tri
39	563.6	72.0	975	9	AF344844	AF344844 Callithrix
40	534.8	68.3	864	4	BTCD40LIG	Z48469 B.taurus mr
41	527	67.3	788	4	AF079105	AF079105 Felis cat
42	523.8	66.9	788	4	AF086711	AF086711 Canis fam
43	458	58.5	904	6	AF344853	AF344853 Macaca ne
44	446.2	57.0	1425	6	AR076929	AR076929 Sequence
45	446.2	57.0	1425	6	AR078319	AR078319 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS AR044778 818 bp DNA Linear PAT 29-SEP-1999  
DEFINITION Sequence 1 from patent US 5817516.  
ACCESSION AR044778  
VERSION AR044778.1 GI:5966243  
KEYWORDS  
SOURCE Unknown:  
ORGANISM Unknown:  
REFERENCE 1 (bases 1 to 818)  
AUTHORS Kehry M. and Castle, B.  
TITLE Methods for proliferating and differentiating B cells with high  
JOURNAL density membrane CD40 ligand  
FEATURES Patent: US 5817516-A 1 06-OCY-1998;  
source Location/Qualifiers  
1..818  
/organism="unknown"

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Query Match 97.1%; Score 760.6; DB 6; Length 818;

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Patent: US 6297052-A 1 02-OCT-2001;  
JOURNAL

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132

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099

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732

780 ·

792

- AUG - 2001

DEFINITION Sequence 1 from Patent WO0156602.  
 AX208160  
 VERSION GI:15422583  
 KEYWORDS  
 SOURCE  
 ORGANISM Mus sp.  
 Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1250)  
 AUTHORS Tripp, R.A., Anderson, L.J. and Brown, M.P.  
 TITLE Ccd40 ligand adjuvant for respiratory syncytial virus  
 JOURNAL Patent: WO 0156602-A 1 09-AUG-2001;  
 The Secretary, Department of Health and Human Services (US)  
 FEATURES  
 source 1..1250  
 /organism="Mus sp."  
 /db\_xref="taxon:10095"  
 BASE COUNT 379 a 273 c 285 g 313 t  
 ORIGIN

Query Match 97.1%; Score 760.6; DB 6; Length 1250;  
 Best Local Similarity 98.2%; Pred. No. 7.2e-187;  
 Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1 ATGATCGAAGACATACACCAAACTCTCCGATCGCGCCACTGAGCTGCCATCAGC 60  
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 61 ATGAAATTTTATGATATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 120  
 73 ATGAAGATTTTATGATATTTACTTACTGTTTCTTATACCCCAATGATGATCTGTG 132  
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 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240  
 193 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCC 252  
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 253 TTGCTGAAGCTGTGAGAGATGAGAGCAATTTGAAGCTTGTCAAGATATTAACGTTA 312  
 301 AACAAAG 360  
 313 AACAAAG 372  
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 421 AAGAAAGATATTTATACATGAAAAAGCACTGTAATGCTTGAATGGAAGAACAGCTG 480  
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 673 TCTGTTCACTTGGGCGGAGGCTTTGAATTAACAGCTGCTGCTGCTTTGCTCAAGCTG 732

721 ACTGAGACAGCCAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
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 781 TGA 783  
 793 TGA 795

## RESULT 4

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 DEFINITION Sequence 1 from patent US 5961974.  
 AR076918  
 AR076918  
 VERSION AR076918.1 GI:10003664  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 783)  
 AUTHORS Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.  
 TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition  
 JOURNAL comprising the same and hybridomas producing the same  
 Patent: US 5961974-A 1 05-OCT-1999;  
 FEATURES  
 source 1..783  
 /organism="unknown"

BASE COUNT 243 a 159 c 178 g 203 t  
 ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;  
 Best Local Similarity 98.1%; Pred. No. 1.9e-186;  
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 361 ATTGAGACACAGCTGTGAAGCAAGCCAAAGTATGAGAGATCGCTCTACAGTGGGCC 420  
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 481 ACGGTTAAAG 540  
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 541 GAGCCTTGAGTCAACGCCCATTCATGCTGGGCTCTGGGAGAGAGAGAGAGAGAGAG 600

Db 541 GAGCCTTCGATGACAGCCCATTCATCTGCGCTCTGCTGAGGCCAGAGTGTACT 600  
QY 601 GAGAGATCTTACTCAAGCGCGCAATACCACAGTTCCTCCAGCTTTGCGAGCAG 660  
Db 601 GAGAGATCTTACTCAAGCGCGCAATACCACAGTTCCTCCAGCTTTGCGAGCAG 660  
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCGCTCTGCTGAGGCCAGT 720  
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCGCTCTGCTGAGGCCAGT 720  
QY 721 ACTGAGCAGCCAGTGTATCCACAGAGTGTGCTTCACTTTGCTTACTCAAACTC 780  
Db 721 ACTGAGCAGCCAGTGTATCCACAGAGTGTGCTTCACTTTGCTTACTCAAACTC 780  
QY 781 TGA 783  
Db 781 TGA 783

RESULT 5  
AR078308 783 bp DNA linear PAT 31-AUG-2000  
LOCUS AR078308  
DEFINITION Sequence 1 from patent US 5962406.  
ACCESSION AR078308  
VERSION AR078308.1 GI:10005054  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,  
Gibson, M.G., Morris, A.E. and McGrew, J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical  
composition containing the same  
JOURNAL Patent: US 5962406-A 1 05-OCT-1999;  
FEATURES  
source 1. 783  
location/Qualifiers  
BASE COUNT 243 a 159 c 178 g 203 t  
ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;  
Best Local Similarity 98.1%; Pred. No. 1; 9e-186;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATACCAACCACTTCCCGATCTGCGGCACTGAGCTCCCATCAGC 60  
Db 1 ATGATAGAAACATACAGCCACCTTCCCGATCTGCGGCACTGAGCTCCCATCAGC 60  
QY 61 ATGAATAATTTATATTTACTTACTTCTTCTTCTTATCACCACCAATGATGATCTGTG 120  
Db 61 ATGAAGATTTTATATTTACTTACTTCTTCTTCTTATCACCACCAATGATGATCTGTG 120  
QY 121 CTTTGTGCTGTATCTTATGAAAGATTGATAAGTTCGAAGAGAGAGTAAACCTTCAT 180  
Db 121 CTTTGTGCTGTATCTTATGAAAGATTGATAAGTTCGAAGAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATCTTAAATAAAGCTAAAGAGATGACAAAGAGAGAGATCTTTATCC 240  
Db 181 GAAGATTTTGTATCTTAAATAAAGCTAAAGAGATGACAAAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAAGCTGTAGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300  
Db 241 TTGCTGAAGCTGTAGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300  
QY 301 AACAAAG 360  
Db 301 AACAAAG 360  
QY 361 ATTGAGCAGACAGCTTGAAGCAGAGCAAGATTAATGAGCATCGCTTCTACAGTGGCC 420  
Db 361 ATTGAGCAGACAGCTTGAAGCAGAGCAAGATTAATGAGCATCGCTTCTACAGTGGCC 420

QY 421 AAGAAGATATTTATACATGAAAGCAACTTGGTAATGCTTGAATAATGGAAGACAGT 480  
Db 421 AAGAAGATATTTATACATGAAAGCAACTTGGTAATGCTTGAATAATGGAAGACAGT 480  
QY 481 ACGGTTAAAG 540  
Db 481 ACGGTTAAAG 540  
QY 541 GAGCCTTCGATGACAGCCCATTCATCTGCGCTCTGCTGAGGCCAGCAGTGTACT 600  
Db 541 GAGCCTTCGATGACAGCCCATTCATCTGCGCTCTGCTGAGGCCAGCAGTGTACT 600  
QY 601 GAGAGATCTTACTCAAGCGCGCAATACCACAGTTCCTCCAGCTTTGCGAGCAGCAG 660  
Db 601 GAGAGATCTTACTCAAGCGCGCAATACCACAGTTCCTCCAGCTTTGCGAGCAGCAG 660  
QY 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCGCTCTGCTGAGGCCAGT 720  
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGCGCTCTGCTGAGGCCAGT 720  
QY 721 ACTGAGCAGCCAGTGTATCCACAGAGTGTGCTTCACTTTGCTTACTCAAACTC 780  
Db 721 ACTGAGCAGCCAGTGTATCCACAGAGTGTGCTTCACTTTGCTTACTCAAACTC 780  
QY 781 TGA 783  
Db 781 TGA 783

RESULT 6  
AR085411 783 bp DNA linear PAT 01-SEP-2000  
LOCUS AR085411  
DEFINITION Sequence 1 from patent US 5981724.  
ACCESSION AR085411  
VERSION AR085411.1 GI:10012180  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S.,  
Gibson, M.G., Morris, A.E. and McGrew, J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40  
JOURNAL Patent: US 5981724-A 1 09-NOV-1999;  
FEATURES  
source 1. 783  
location/Qualifiers  
BASE COUNT 243 a 159 c 178 g 203 t  
ORIGIN

Query Match 96.9%; Score 759; DB 6; Length 783;  
Best Local Similarity 98.1%; Pred. No. 1; 9e-186;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAACAATACCAACCACTTCCCGATCTGCGGCACTGAGCTCCCATCAGC 60  
Db 1 ATGATAGAAACATACAGCCACCTTCCCGATCTGCGGCACTGAGCTCCCATCAGC 60  
QY 61 ATGAATAATTTATATTTACTTACTTCTTCTTCTTATCACCACCAATGATGATCTGTG 120  
Db 61 ATGAAGATTTTATATTTACTTACTTCTTCTTCTTATCACCACCAATGATGATCTGTG 120  
QY 121 CTTTGTGCTGTATCTTATGAAAGATTGATAAGTTCGAAGAGAGAGTAAACCTTCAT 180  
Db 121 CTTTGTGCTGTATCTTATGAAAGATTGATAAGTTCGAAGAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATCTTAAATAAAGCTAAAGAGATGACAAAGAGAGAGATCTTTATCC 240  
Db 181 GAAGATTTTGTATCTTAAATAAAGCTAAAGAGATGACAAAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAAGCTGTAGAGAGATGAGAGCAATTTGAAGACCTTGTCAAGATTAACGTTA 300

Db	241	TTGCGAAGCTGTGAGGAGATGAGAAAGCAATTGTGAAGACCTTGTCACAGATATATAACGTTA	300
QY	301	AACAAAGAAAGAAAAAAGAAAAACAGCTTTGAATTCGAAAAGGTGATGAGATCTCTAA	360
Db	301	AACAAAGAAAGAAAAAAGAAAAACAGCTTTGAATTCGAAAAGGTGATGAGATCTCTAA	360
QY	361	ATTTCAGACACACGTTTGTAAAGCGAAGCCAAACAGTAATGCAGATGCGCTTCACAGTGGGCC	420
Db	361	ATTTCAGACACACGTTTGTAAAGCGAAGCCAAACAGTAATGCAGATGCGCTTCACAGTGGGCC	420
QY	421	AAGAAAGATATTTATPACCATGAAAAAGCAACTTGGTATGCTGAAAAATGGGAAACAGCTG	480
Db	421	AAGAAAGATATTTATPACCATGAAAAAGCAACTTGGTATGCTGAAAAATGGGAAACAGCTG	480
QY	481	ACGGTAAAGAAAGAAAGCACTATTATGTCTACACTGACAGTACCTTGCTCTAATCGG	540
Db	481	ACGGTAAAGAAAGAAAGCACTATTATGTCTACACTGACAGTACCTTGCTCTAATCGG	540
QY	541	GAGCGCTTCGAGTCAACGCCCATTCATCGTTCGGCCTCTGGCTGGAAGCCGACAGATGATCT	600
Db	541	GAGCGCTTCGAGTCAACGCCCATTCATCGTTCGGCCTCTGGCTGGAAGCCGACAGATGATCT	600
QY	601	GAGAGAAATCTTACTACAGAGCGGCGCAAAATACCCACAGTTCCTCCACGTTTGGAGCAGCAG	660
Db	601	GAGAGAAATCTTACTACAGAGCGGCGCAAAATACCCACAGTTCCTCCACGTTTGGAGCAGCAG	660
QY	661	TCTGTTCACTTGGGCGGAGGTGTTGAATTAACAGTGGTGGCTGCTGTTGTCAAGCTG	720
Db	661	TCTGTTCACTTGGGCGGAGGTGTTGAATTAACAGTGGTGGCTGCTGTTGTGTCAAGCTG	720
QY	721	ACTGAGCAACCCAAAGTATATCCACAGAGTTGGCTTCTATCTTTTGGCTTACTCAACTC	780
Db	721	ACTGAGCAACCCAAAGTATATCCACAGAGTTGGCTTCTATCTTTTGGCTTACTCAACTC	780
QY	781	TGA 783	
Db	781	TGA 783	
RESULT	7	ARI03367	783 bp DNA linear PAT 14-FEB-2001
LOCUS		ARI03367	
DEFINITION		Sequence 1 from patent US 6087329.	
ACCESSION		ARI03367	
VERSION		ARI03367.1	
KEYWORDS		GI:12814955	
SOURCE		Unknown.	
ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 783)	
TITLE		Armitage, R.J., Fanslow, W.C. and Spriggs, M.K.	
JOURNAL		CD40 ligand polypeptide	
FEATURES		Patent: US 6087329-A 1 11-JUL-2000;	
		Location/Qualifiers	
		1..783	
		/organism="unknown"	
BASE COUNT		243 a 159 c 178 g 203 t	
ORIGIN			

Query Match	96.9%	Score 759	DB 6	Length 783
Best Local Similarity	98.1%	Pred. 0	1.9e-166	
Matches 768	Conservative	0	Mismatches 15	Indels 0
			Gaps	0

Oy	1	ATGATCGAAACATCATCAACCAACTCTCCCGCATGTCGGGCACATCGAGCTGCCCATCAGC	60
Db	1	ATGATGGAACAATACAGCCACCTTCCCCCAATCCGAGCACTGGAGCTTCCACGCGAGC	60
Oy	61	ATGAAATTTTATCTATTACTACTGTTTTCTTATACCCAAATGATGGATCTGTG	120
Db	61	ATGAAGATTTTATCTATTACTACTCTCTTTCTTATACCCAAATGATGGATCTGTG	120

OY	121	CTTTTGGTGTACTTTCATCTAGAGATTTGGTAATGCTCGAAGAGAGTAACCTTAT	180
DB	121	CTTTTGGTGTATCTTCATCATGAAATTTGGATTAAAGTTCGAAGAGAACTTAACCTTAT	180
OY	181	GAGATATTTTGTATTCATAAAAAGCTTAAGAGATGCAACAAAGAGAAAGATCTTATCC	240
DB	181	GAGATATTTTGTATTCATAAAAAGCTTAAGAGATGCAACAAAGAGAAAGATCTTATCC	240
OY	241	TTGCTGAACCTGTGAGAGATGAGAAAGCAATTTGAAACCTTTGTCAAGATATTAACGTTA	300
DB	241	TTGCTGAACCTGTGAGAGATGAGAAAGCAATTTGAAACCTTTGTCAAGATATTAACGTTA	300
OY	301	AACAAAGAGAGAAAAAAGAAAACGCTTTGAAATGCAAAAGGTGATGAGATCTTCAA	360
DB	301	AACAAAGAGAGAAAAAAGAAAACGCTTTGAAATGCAAAAGGTGATGAGATCTTCAA	360
OY	361	ATTGCAGACACAGTTGTAAAGCGAACCCAAACAGTAATGAGCATTCCGTTCTACAGTGGCC	420
DB	361	ATTGCAGACACAGTTGTAAAGCGAACCCAAACAGTAATGAGCATTCCGTTCTACAGTGGCC	420
OY	421	AAGAAAGGATATTTATACCATGAAAGCAACTTGTATGCTTGAATGCGAAGACAGCTG	480
DB	421	AAGAAAGGATATTTATACCATGAAAGCAACTTGTATGCTTGAATGCGAAGACAGCTG	480
OY	481	ACGGTAAAAAGGAGAGGACTCTATATGTCTACACTCAAGTACCTTTCGCTCTAATGGG	540
DB	481	ACGGTAAAAAGGAGAGGACTCTATATGTCTACACTCAAGTACCTTTCGCTCTAATGGG	540
OY	541	GAGCCTTGAGTCAACAGCCATTCAATCGTCGCGCTCTGGCTGAAGCCCAAGCATTTGGATCT	600
DB	541	GAGCCTTGAGTCAACAGCCATTCAATCGTCGCGCTCTGGCTGAAGCCCAAGCATTTGGATCT	600
OY	601	GAGAGATCTTACTCAAGCGGCGCAAAATACCCACAGTTCCTCCACGCTTTGGCAGCAGAG	660
DB	601	GAGAGATCTTACTCAAGCGGCGCAAAATACCCACAGTTCCTCCACGCTTTGGCAGCAGAG	660
OY	661	TCTGTCTACTTGGGGGGGAGTGTTTTAATTAACAAGTGGTGTCTCTGTCTTGTCTCAAGCTG	720
DB	661	TCTGTCTACTTGGGGGGGAGTGTTTTAATTAACAAGTGGTGTCTCTGTCTTGTCTCAAGCTG	720
OY	721	ACTGAGCAAGCAAGTGAATCCACAGAGTGGCTTCATCTTTTGGGTACTCAAACTC	780
DB	721	ACTGAGCAAGCAAGTGAATCCACAGAGTGGCTTCATCTTTTGGGTACTCAAACTC	780
OY	781	TGA 783	
DB	781	TGA 783	

LOCUS	ARI69224	783 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6290972.				
ACCESSION	ARI69224				
VERSION	ARI69224.1	GI:17907035			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 783) Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S. and Gibson, M.G.				
TITLE	Method of augmenting a vaccine response by administering CD40 ligand				
JOURNAL	Patent: US 6290972-A 1 18-SEP-2001;				
FEATURES	Location/Qualifiers				
Source	1..783 /organism="unknown"				
BASE COUNT	243 a	159 c	178 g	203 t	
ORIGIN					
Query Match	96.9%	Score	759	DB 6	Length 783

Best Local Similarity 98.1%; Pred. No. 1.9e-186;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0.

OY	1	ATTGTGAACATATACAAACCAAACTTCTCCCGCATCTGCGGCCACTGAGACTGGCCATCTCAGC	60
Db	1	ATGATATGAACATATACACCACTTCCCGCATCTGCGGCCACTGAGACTGGCCATCTCAGC	60
OY	61	ATGAAAAATTTTATATATATTTACTGTTTCTTCTATATACCAAAATGATGGATCTGTG	120
Db	61	ATGAAAGATTTTATATATATTTACTGTTTCTTCTATATACCAAAATGATGGATCTGTG	120
OY	121	CTTTTTCGTGTATCTCTCATATAGAAATGGATAGAGTGGAGAGAGAACTTAACCTCAT	180
Db	121	CTTTTTCGTGTATCTCTCATATAGAAATGGATAGAGTGGAGAGAGAACTTAACCTCAT	180
OY	181	GAGATTTTGTATTCATATAAAAAGCTTAAGAGATGACACAAAGAGAGAGATCTTTATCC	240
Db	181	GAGATTTTGTATTCATATAAAAAGCTTAAGAGATGACACAAAGAGAGAGATCTTTATCC	240
OY	241	TTTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAAGCTTGTCAAGATATTAAGCTTA	300
Db	241	TTTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAAGCTTGTCAAGATATTAAGCTTA	300
OY	301	AACAAAGAGAGAAAAAAGAAAAAGCTTTGAAATGCAAAAGAGTGTAGAGATCTCTCAA	360
Db	301	AACAAAGAGAGAAAAAAGAAAAAGCTTTGAAATGCAAAAGAGTGTAGAGATCTCTCAA	360
OY	361	ATTGCAGACACGTTGTATAGCGAAGCCAAACAGTAAATGCACATCCGTTCTTACAGTGGGCC	420
Db	361	ATTGCAGACACAGTTGTATAGCGAAGCCAAAGTAAATGCACATCCGTTCTTACAGTGGGCC	420
OY	421	AAGAAAGATATTTATACCATGAAAAAGCACTTGGTAAATGCTTGAAATGGGAACAAGCTG	480
Db	421	AAGAAAGATATTTATATCCATGAAAAAGCACTTGGTAAATGCTTGAAATGGGAACAAGCTG	480
OY	481	ACGGTAAAGAGAGAGACTATTTATGTCTACACTGAAGTACAGCTTCTCTCTTAATCGG	540
Db	481	ACGGTAAAGAGAGAGACTATTTATGTCTACACTGAAGTACAGCTTCTCTCTTAATCGG	540
OY	541	GAGCCTTGAGTCAACGCCCATTTATCGTGGGCTCTGGTGAAGCCGACATATGATCT	600
Db	541	GAGCCTTGAGTCAACGCCCATTTATCGTGGGCTCTGGTGAAGCCGACATATGATCT	600
OY	601	GAGAGATTTTACTCAAGGCGGCAAAATCCCAAGTTCTTCCAGCTTGGCGAGACAG	660
Db	601	GAGAGATTTTACTCAAGGCGGCAAAATCCCAAGTTCTTCCAGCTTGGCGAGACAG	660
OY	661	TCGTGTACACTTGGGCGGAGTGTGTAATTTACAAGCTGTGTCTGTGTGTGTCAAAGTG	720
Db	661	TCGTGTACACTTGGGCGGAGTGTGTAATTTACAAGCTGTGTCTGTGTGTGTCAAAGTG	720
OY	721	ACTGAAGCAGCCAAAGTATTCACAGAGTGGCTCTCATCTTTGGCTTACTCAACTC	780
Db	721	ACTGAAGCAGCCAAAGTATTCACAGAGTGGCTCTCATCTTTGGCTTACTCAACTC	780
OY	781	TGA 783.	
Db	781	TGA 783	

RESULT	9			
LOCUS	187865	783 bp	DNA	linear
DEFINITION	Sequence 5 from patent US 5716805.			
ACCESSION	187865			
VERSION	187865.1	GI:3407805		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1. (bases 1 to 783)			
TITLE	Srinivasan, S. and Springs, M.K.			
	Methods of preparing soluble, oligomeric proteins			

JOURNL	Patent: US 5716805-A 5 10-FEB-1998
FEATURES	Location/Qualifiers
SOURCE	1..783
	/Organization="unknown"
BASE COUNT	243 a 159 g 203
ORIGIN	

Query Match	96.9%	Score 759;	DB 6;	Length 783;
Best Local Similarity	98.1%	Pred. No. 1.9e-186;		
Matches 768; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0

[illegible]

RESULT	10
MIMCD40	
LOCUS	1250 bp
DEFINITION	m.musculus mRNA for CD40. llsdng.
	mRNA linear ROD 26-APR-2001



ACCESSION X65453  
 VERSION X65453.2 GI:13872516  
 KEYWORDS CD4 antigen.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 1250)  
 Ambridge, R., Fanslow, W., Sato, T. A., Clifford, K. N., Strockbine, L., Macduff, B. M., Anderson, D. M., Gimpel, S. D., Davis-Smith, T., Maliszewski, C. R., Clark, E. A., Smith, C. A., Grabstein, K. H., Cosman, D. and Spriggs, M. K.  
 Molecular and biological characterization of a murine ligand for CD40  
 Nature 357 (6373), 80-82 (1992)  
 JOURNAL MEDLINE 92244364  
 REFERENCE 2 (bases 1 to 1250)  
 AUTHORS Spriggs, M. K.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-APR-1992) M. K. Spriggs, Immunex Research & Development, Molecular Biology, 51 University Street, Seattle, Washington, 98101, USA  
 REMARK revised by [3]  
 3 (bases 1 to 1250)  
 REFERENCE Spriggs, M. K.  
 AUTHORS Direct Submission  
 TITLE Submitted (24-APR-2001) Strockbine, L. Immunex Research & Development, Molecular Biology, 51 University Street, Seattle, Washington, 98101, USA  
 JOURNAL On Apr 27, 2001 this sequence version replaced g1:50351.  
 COMMENT Location/Qualifiers  
 source 1..1250  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 13..795  
 /gene="CD40L"  
 13..795  
 /gene="CD40L"  
 /codon\_start=1  
 /product="CD40 surface protein"  
 /protein\_id="CAA46448.2"  
 /db\_xref="GI:13872517"  
 /translation="MIETYSQSPRSVATGIPASMKIFMYLTVFLITOMIGSLFVAY YLRRRLDKVEEYVNLHEDFVFIKLRKCNKGESLSLNCENMRPREDLVKDTLTK EEKENSFEORDEDEPOIAHYVSEANSMAVSLQAKGTYTMRKNLWYEMGKRL TVRREGIYTYTQVTRCSNRPSSORPFTIGLMKRPSSGBRIILKANTHSSQDCE QQSVHLGGVEELDAGASVFNVTESQVHHRVFSFGLKL"  
 BASE COUNT 379 a 273 c 286 g 312 t  
 ORIGIN  
 Query Match 96.9%; Score 759; DB 10; Length 1250;  
 Best Local Similarity 98.1%; Pred. No. 1.9e-186;  
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 253 TTGCTGAAGTGTGAGAGATGATGAAGGCAATTGTAAGCACTTGTCACAGATATTAACGTTA 312  
 Qy 301 AACAAAGAAGAAAAAAGAAAAAGCAAGCTTTGAAATGCAAAAGAGTATGAGATCTCTCA 360  
 Db 313 AACAAAGAAGAAAAAAGAAAAAGCAAGCTTTGAAATGCAAAAGAGTATGAGATCTCTCA 372  
 Qy 361 ATTGAGACACAGCTTGTAGAGCAAGCAACAGTATGAGATGAGATGAGTGGGCC 420  
 Db 373 ATTGAGACACAGCTTGTAGAGCAAGCAACAGTATGAGATGAGATGAGTGGGCC 432  
 Qy 421 AAGAAGGATATTATACCATGAAAAAGCAACTTGTATGCTTGAATAATGGAAAGAGCTG 480  
 Db 433 AAGAAGGATATTATACCATGAAAAAGCAACTTGTATGCTTGAATAATGGAAAGAGCTG 492  
 Qy 481 ACGGTTAAAGAAGAGAGCTATATGCTTACACTCAAGTACCTTGTGCTTAATGG 540  
 Db 493 ACGGTTAAAGAAGAGAGCTATATGCTTACACTCAAGTACCTTGTGCTTAATGG 552  
 Qy 541 GAGCCTTGAGTCAACGCCCATTCATCGTGGCCTGTGAGTGAAGCCAGCATGATGATCT 600  
 Db 553 GAGCCTTGAGTCAACGCCCATTCATCGTGGCCTGTGAGTGAAGCCAGCATGATGATCT 612  
 Qy 601 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTGGCAGCAGCAG 660  
 Db 613 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTGGCAGCAGCAG 672  
 Qy 661 TCTGTTCACTTGGGGGGAGTGTGAATTAACAAGTGGGCTTGCTGTGTTCAACGCG 720  
 Db 673 TCTGTTCACTTGGGGGGAGTGTGAATTAACAAGTGGGCTTGCTGTGTTCAACGCG 732  
 Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 780  
 Db 723 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTGGCTTACTCAACTC 792  
 Qy 781 TGA 783  
 Db 793 TGA 795  
 RESULT 11  
 AF013985  
 LOCUS AF013985 783 bp mRNA linear ROD 26-JAN-1999  
 DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.  
 ACCESSION AF013985  
 VERSION AF013985.1 GI:4102613  
 KEYWORDS  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 783)  
 Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M., Farzaneh, F. and Gaken, J. A.  
 Cloning and sequencing of rat CD40 ligand unpublished  
 2 (bases 1 to 783)  
 Daniel, K. C., Foss, Y., Mousavi, A., Macary, P., Kemeny, D. M., Farzaneh, F. and Gaken, J. A.  
 Direct Submission  
 Submitted (14-JUL-1997) Immunology, King's College School of Medicine and Dentistry, 123 Coldharbour Lane, London SE5 9NU, United Kingdom  
 FEATURES  
 source location/Qualifiers  
 1..783  
 /organism="Rattus norvegicus"  
 /strain="PVG"  
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 /tissue-type="spleen"  
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 /product="CD40 ligand"

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 EEKKEKSEMRORFEDLVKRNKESGLSLINCEMRORFEDLVKDISLTK  
 TVKREGLYTVTOVTFCSNRPLISORPITVSLMKPSSGSRILLRANHTSSSKLCE  
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BASE COUNT 236 a 152 c 189 g 206 t  
 ORIGIN

Query Match 87.7% Score 687; DB 10; Length 783;  
 Best Local Similarity 92.3%; Pred. No. 9, 3e-168;  
 Matches 723; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

1 ATGATGAAACATACACCAACTTCTCCCGATCGGCGGCACTGGATGCCATCACC 60  
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 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 301 AACAAAG 360  
 301 AACAAAG 360  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 421 AAGAAAGATATTTATACCATGAAAGCACTTGTGTAATGCTTGAAGTGAAGAGAGAG 480  
 421 AAGAAAGATATTTATACCATGAAAGCACTTGTGTAATGCTTGAAGTGAAGAGAGAG 480  
 481 ACGGTTAAAG 540  
 481 ACGGTTAAAG 540  
 541 GAGCCTTGCAGTACAGCCCATTCATCGTGGCTTGGCTGAGAGAGAGAGAGAGAGAG 600  
 541 GAGCCTTGCAGTACAGCCCATTCATCGTGGCTTGGCTGAGAGAGAGAGAGAGAGAG 600  
 601 GAGAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 660  
 601 GAGAGATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATGATTTAT 660  
 661 TCGTTCACCTTGGCGGAGATGTTGAATTAACAAGCTGTGCTTGTGTTTCAACGTTG 720  
 661 TCGTTCACCTTGGCGGAGATGTTGAATTAACAAGCTGTGCTTGTGTTTCAACGTTG 720  
 721 ACTGAAGCAAGCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 721 ACTGAAGCAAGCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 781 TGA 783  
 781 TGA 783

RESULT 12

AF116582  
 LOCUS AF116582 783 bp. mRNA linear ROD 12-JUL-2000  
 DEFINITION Rattus norvegicus CD40 ligand mRNA, complete cds.  
 ACCESSION AF116582  
 VERSION AF116582.1 GI:4545249  
 KEYWORDS  
 SOURCE  
 ORGANISM

## REFERENCE

1 (bases 1 to 783)  
 Hallett, K.M. and Oaks, M.K.  
 Nucleotide sequence of the rat CD40 ligand  
 DNA Seq. 10 (6), 405-406 (2000)  
 20284949  
 PUBMED 10826698  
 REFERENCE  
 Hallett, K.M. and Oaks, M.K.  
 Direct Submission  
 Submitted (24-DEC-1998) Transplant Research, St. Luke's Medical  
 Center, 2900 W. Oklahoma Ave., Milwaukee, WI 53215, USA  
 Location/Qualifiers

## FEATURES

1..783  
 /organism="Rattus norvegicus"  
 /strain="Sprague Dawley"  
 /db\_xref="taxon:10116"  
 /cell\_type="splenocyte"  
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 /codon\_start=1  
 /product="CD40 ligand"  
 /protein\_id="AAD22460.1"  
 /db\_xref="GI:4545250"

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1 ATGATGAAACATACACCAACTTCTCCCGATCGGCGGCACTGGATGCCATCACC 60  
 1 ATGATGAAACATACACCAACTTCTCCCGATCGGCGGCACTGGATGCCATCACC 60  
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 301 AACAAAG 360  
 301 AACAAAG 360  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

## BASE COUNT

237 a 153 c 189 g 204 t

## ORIGIN

Query Match 87.3% Score 683.8; DB 10; Length 783;  
 Best Local Similarity 92.1%; Pred. No. 6, 3e-167;  
 Matches 721; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

1 ATGATGAAACATACACCAACTTCTCCCGATCGGCGGCACTGGATGCCATCACC 60  
 1 ATGATGAAACATACACCAACTTCTCCCGATCGGCGGCACTGGATGCCATCACC 60  
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCCCAATGATGGATCTGTG 120  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 121 CTTTTCCTGCTATCTTATAGATTTGATTAAGTGAAGTGAAGAGCAACCTTATC 180  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 181 GAAATTTTATGATTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 241 TTGCTGACCTGTGAGAGATGAGAGAGCAATTTGAGAGCTTGTCAAGATATACGTTA 300  
 301 AACAAAG 360  
 301 AACAAAG 360  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 361 ATTGACAGACAGTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

421 AGAAGATATATATACATGAAGACACTGTGTAATGCTTGAATAATGGAAACAGCTG 480  
421 AAGAAAGATATATATACATGAAGACACTGTGTAATGCTTGAATAATGGAAACAGCTG 480  
481 ACGGTTAAAGAGAGAGACTCTATTAATGCTACACTCAAGTCACTTCTGCTTAATCG 540  
481 ACGGTTAAAGAGAGAGACTCTATTAATGCTACACTCAAGTCACTTCTGCTTAATCG 540  
541 GAGCCTTCAGTCAAGCCCATTCATGCTGGCTCTGGCTGAAGCCGACGATTGATCT 600  
541 GAACCTTTGAGTCAAGCTTCATTCATGCTGGCTGAAGCCGACGATTGATCT 600  
601 GAGAGATCTTACTCAAGGGGCAATATCCACAGTCTCTCCAGCTTTGGGACAGAG 660  
601 GAGAGATCTTACTCAAGGGGCAATATCCACAGTCTCTCCAGCTTTGGGACAGAG 660  
661 TCTGTTCACTTGGGGGAGTGTGTAATTAACAAGCTGTGCTTCTGTTTGTCAAGCTG 720  
661 TCCATTCATCTGGGGGAGTGTGTAATTAACAAGCTGTGCTTCTGTTTGTCAAGCTG 720  
721 ACTGAAGCAAGCCCAAGTATCCACAGTGTGCTTCTCACTTCTTGGCTTAACACTC 780  
721 ACTGAAGCAAGCCCAAGTATCCACAGTGTGCTTCTCACTTCTTGGCTTAACACTC 780  
781 TGA 783  
781 TGA 783

RESULT 13  
AR076933 LOCUS AR076933 878 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 22 from patent US 5961974.  
ACCESSION AR076933  
VERSION AR076933.1 GI:10003679  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 878)  
AUTHORS Amilage,R.J., Fanslow,W.C. and Spriggs,M.K.  
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition  
JOURNAL Patent: US 5961974-A 22 05-OCT-1999;  
FEATURES  
Source 1. 878  
Location/Qualifiers  
BASE COUNT 277 a 178 c 203 g 220 t  
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;  
Best Local Similarity 99.8%; Pred. No. 2.6e-153;  
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
151 GATAAGGTGCAAGAGAGTAACCTTCATGAAGATTTGTATCATTAATAAGCTAAG 210  
225 GATAAGGTGCAAGAGAGTAACCTTCATGAAGATTTGTATCATTAATAAGCTAAG 284  
211 AGATGCAACAAGAGAGAGATCTTATCTCTGTAAGTGTGAGAGATGAGAGCAA 270  
285 AGATGCAACAAGAGAGAGATCTTATCTCTGTAAGTGTGAGAGATGAGAGCAA 344  
271 TTGGAAGACCTTGTCAAGATATTAAGCTTAACAAGAGAGAGAGAGAGAGCTTT 330  
345 TTGGAAGACCTTGTCAAGATATTAAGCTTAACAAGAGAGAGAGAGAGAGCTTT 404  
331 GAAATGCAAGAGAGATGAGAGATCTTAATTTGAGAGAGAGAGAGAGAGCTTT 390  
405 GAAATGCAAGAGAGATGAGAGATCTTAATTTGAGAGAGAGAGAGAGAGCTTT 464  
391 AGTAATGAGAGATCGCTTCTACAGTGGGCAAGAGAGATTTATACATGAAGAGAAC 450

465 AGTAATGAGAGATCGCTTCTACAGTGGGCAAGAGAGATTTATACATGAAGAGAAC 524  
451 TTGTAATGCTTGAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510  
525 TTGTAATGCTTGAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 584  
511 TACACTCAAGTCAAGTCTTGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAG 570  
585 TACACTCAAGTCAAGTCTTGTCTTAATGAGAGAGAGAGAGAGAGAGAGAGAG 644  
571 GGCTCTGGCTGAAG 630  
645 GGCTCTGGCTGAAG 704  
631 CACAGTCTCTCCAG 690  
705 CACAGTCTCTCCAG 764  
691 CACAGTCTCTCCAG 750  
765 CACAGTCTCTCCAG 824  
825 GGCCTTCATCTTTTGGCTTACTCAACTCTGA 857

RESULT 14  
AR078323 LOCUS AR078323 878 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 22 from patent US 5962406.  
ACCESSION AR078323  
VERSION AR078323.1 GI:10005069  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 878)  
AUTHORS Amilage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical  
JOURNAL Patent: US 5962406-A 22 05-OCT-1999;  
FEATURES  
Source 1. 878  
Location/Qualifiers  
BASE COUNT 277 a 178 c 203 g 220 t  
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;  
Best Local Similarity 99.8%; Pred. No. 2.6e-153;  
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
151 GATAAGGTGCAAGAGAGTAACCTTCATGAAGATTTGTATCATTAATAAGCTAAG 210  
225 GATAAGGTGCAAGAGAGTAACCTTCATGAAGATTTGTATCATTAATAAGCTAAG 284  
211 AGATGCAACAAGAGAGAGATCTTATCTCTGTAAGTGTGAGAGATGAGAGCAA 270  
285 AGATGCAACAAGAGAGAGATCTTATCTCTGTAAGTGTGAGAGATGAGAGCAA 344  
271 TTGGAAGACCTTGTCAAGATATTAAGCTTAACAAGAGAGAGAGAGAGAGCTTT 330  
345 TTGGAAGACCTTGTCAAGATATTAAGCTTAACAAGAGAGAGAGAGAGAGCTTT 404  
331 GAAATGCAAGAGAGATGAGAGATCTTAATTTGAGAGAGAGAGAGAGAGCTTT 390  
405 GAAATGCAAGAGAGATGAGAGATCTTAATTTGAGAGAGAGAGAGAGAGCTTT 464  
391 AGTAATGAGAGATCGCTTCTACAGTGGGCAAGAGAGATTTATACATGAAGAGAAC 450

Db 465 AGTAATGACGATCCGTTCTACAGTGGCCCAAGAAAGATATATACATGAAAAGCAAC 524  
OY 451 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGAGACTATATATGTC 510  
Db 525 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGAGACTATATATGTC 584  
OY 511 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCCATTCATGTC 570  
Db 585 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCCATTCATGTC 644  
OY 571 GGCCTGCTGCTGAAGCCCAAGTATGAGAGATCTTACTCAAGCGGCAAAATACC 630  
Db 645 GGCCTGCTGCTGAAGCCCAAGTATGAGAGATCTTACTCAAGCGGCAAAATACC 704  
OY 631 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 690  
Db 705 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 764  
OY 691 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 750  
Db 765 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 824  
OY 751 GGCCTCTCATCTTTGGCTTACTCAAACTCTGA 783  
Db 825 GGCCTCTCATCTTTGGCTTACTCAAACTCTGA 857

RESULT 15  
AR085426 AR085426 878 bp DNA linear PAT 01-SEP-2000

LOCUS AR085426  
DEFINITION Sequence 22 from patent US 5981724.  
ACCESSION AR085426  
VERSION AR085426.1 GI:10012195

KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 878)  
Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,

AUTHORS Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40

JOURNAL Patent: US 5981724-A 22 09-NOV-1999;  
FEATURES Location/Qualifiers

source 1..878

BASE COUNT 277 a 178 c 203 g 220 t  
ORIGIN

Query Match 80.6%; Score 631.4; DB 6; Length 878;  
Best Local Similarity 99.8%; Pred. No. 2,6e-153;

Matches 632: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 151 GATAAGGTCGAGAGAGAACTTAACCTTCATGAGATTTTGTATGTAATAAAAGCTAAG 210  
Db 225 GATAAGGTCGAGAGAGAACTTAACCTTCATGAGATTTTGTATGTAATAAAAGCTAAG 284  
OY 211 AGATGCAAAAGAGAGAAAGATCTTATCTGCTGAGACTGAGAGATGAGAGGCA 270  
Db 285 AGATGCAAAAGAGAGAGAAAGATCTTATCTGCTGAGACTGAGAGATGAGAGGCA 344  
OY 271 TTGAGACCTTGTCAAGGATATTAACGTTAAACAAAGAGAGAGAGAGAGAGCTTT 330  
Db 345 TTGAGACCTTGTCAAGGATATTAACGTTAAACAAAGAGAGAGAGAGAGAGCTTT 404  
OY 331 GAAATGCAAGAGAGATGATGATCTCTCAAAATTTGCGACAGCAGCTTGAAGCAAGCAAC 390  
Db 405 GAAATGCAAGAGAGATGATGATCTCTCAAAATTTGCGACAGCAGCTTGAAGCAAGCAAC 464  
OY 391 AGTAATGACGATCCGTTCTACAGTGGGCCAAGAAAGATATTAATCAATGAAAAGCAAC 450  
Db 465 AGTAATGACGATCCGTTCTACAGTGGGCCAAGAAAGATATTAATCAATGAAAAGCAAC 524

OY 451 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGAGACTATATATGTC 510  
Db 525 TTGGTAATGCTTGAATAATGGGAAACAGCTGACGGTTAAAGAGAGAGACTATATATGTC 584  
OY 511 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCCATTCATGTC 570  
Db 585 TACACTCAAGTACCTTCTGCTCTAATGCGGAGCCTTGAGAGCAAGCCCATTCATGTC 644  
OY 571 GGCCTGCTGCTGAAGCCCAAGTATGAGAGATCTTACTCAAGCGGCAAAATACC 630  
Db 645 GGCCTGCTGCTGAAGCCCAAGTATGAGAGATCTTACTCAAGCGGCAAAATACC 704  
OY 631 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 690  
Db 705 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 764  
OY 691 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 750  
Db 765 CACAGTCTCTCCAGCTTTGCGAGACAGCTGCTTCCTTGGGGGAGTGTGAATTA 824  
OY 751 GGCCTCTCATCTTTGGCTTACTCAAACTCTGA 783  
Db 825 GGCCTCTCATCTTTGGCTTACTCAAACTCTGA 857

Search completed: May 30, 2002, 02:48:59  
Job time: 22018 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:07 ; Search time 5112.58 Seconds  
(without alignments)  
2067,081 Million cell updates/sec

Title: US-08-982-272-5  
Perfect score: 783  
Sequence: 1 ATGATCGAACAACATACACCA.....TTGGCTTACTCAACTCTGA .783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estbda:\*  
2: em\_estbhum:\*  
3: em\_estlin:\*  
4: em\_estlm:\*  
5: em\_estloy:\*  
6: em\_estlpl:\*  
7: em\_estlo:\*  
8: em\_estli:\*  
9: gb\_estl2:\*  
10: gb\_estl:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	305.8	39.1	492	10	BF599437 263218 MA
2	248.4	31.7	398	9	AM486605
3	72.8	9.3	638	9	AI982044 pat.pk007
4	55.8	7.1	997	12	CNS0057E
5	52.8	6.7	797	9	AL534423
6	51.2	6.5	1043	12	CNS0145P
7	51	6.5	1038	12	CNS0108N
8	49.8	6.4	878	12	CNS0187R
9	49.2	6.3	1101	12	CNS0039G
10	47.6	6.1	920	12	AZ691914
11	46.8	6.0	423	12	AZ438784
12	46.8	6.0	458	9	AL514085
13	45.6	5.8	802	12	CNS0383B
14	45.6	5.8	828	12	CNS011TX
15	45.2	5.8	458	9	AL514085
16	45.2	5.8	559	12	A0373239
17	44.8	5.7	1101	12	CNS0181N

18	44.6	5.7	329	9	AL513719
19	44.6	5.7	529	9	AL514657
20	44.6	5.7	611	10	B1389827
21	44.4	5.7	597	9	AL514721
22	44.4	5.7	814	12	AZ203738
23	44.2	5.6	633	9	AL513979
24	44.2	5.6	938	12	CNS0067Y
25	43.8	5.6	330	9	AL513817
26	43.8	5.6	799	12	CNS011SA
27	43.8	5.6	1101	12	CNS000D1
28	43.8	5.6	1101	12	CNS0182P
29	43.6	5.6	588	12	A0451757
30	43.6	5.6	828	12	CNS018FA
31	43.4	5.5	625	12	CNS036A2
32	43.2	5.5	870	12	CNS060UZ
33	43	5.5	468	9	AL514541
34	43	5.5	548	9	BE022382
35	43	5.5	642	10	BJ096268
36	42.8	5.5	807	12	CNS0119V
37	42.6	5.4	415	10	R41111
38	42.6	5.4	595	12	A0521025
39	42.6	5.4	744	12	AG044338
40	42.6	5.4	805	9	AL537564
41	42.6	5.4	959	12	CNS00655
42	42.6	5.4	1007	12	CNS06X9S
43	42.4	5.4	634	9	AL514497
44	42.4	5.4	918	12	CNS006MW
45	42.2	5.4	431	12	CNS04J60

## ALIGNMENTS

RESULT 1  
BF599437 492 bp mRNA linear EST 25-APR-2001  
LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION BF599437  
ACCESSION BF599437  
VERSION BF599437.1 GI:11695919  
KEYWORDS EST.

## SOURCE

ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

## REFERENCE

1 (bases 1 to 492)  
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McCown,C.G.,  
Pettea,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and  
Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

## COMMENT

CONTACT: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smitht@mail.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

PCR PRIMERS  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 33 row: N column: 5  
Seq primer: ATTGATGACACTATAG.

## FEATURES

source location/Qualifiers  
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/organism="Bos taurus"  
/db\_xref="taxon:9913"

/clone.lib="MARC.3BOV"  
/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: PCMV SPOT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

BASE COUNT 163 a 103 c 104 g 122 t  
ORIGIN

Query Match 39.1%; Score 305.8; DB 10; Length 492;  
Best Local Similarity 82.0%; Pred. No. 2.7e-54;

Matches 305; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

OY 1 ATGATGAAACATACACCAAACTTCTCCGATGCGGCGCACTGACCTGCCATCAGC 60  
|||||  
DB 46 ATGATGAAACATACACCACTTCTCCGATGCGGCGCACTGACCTGCCATCAGT 105  
OY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGATGCTGTG 120  
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DB 106 ATGAAATTTTATGATTTACTTACTGATTTCTTATACCCAGATGATGGCTAGCG 165  
OY 121 CTTTTCGCTGATCTTCTATAGATGATGATGATGATGATGATGATGATGAT 180  
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DB 166 CTTTTCGCTGATCTTCTATAGATGATGATGATGATGATGATGATGATGAT 225  
OY 181 GAAGATTTTCTATTCATTAATAAGCTTAAGATGCAACAAAGGAGATCTTTATCC 240  
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DB 226 GAAGATTTTCTGTCATGAAAGCATACAGAGATGCAATTAAGAGGAGGCTCTATCC 285  
OY 241 TTGCTGACGTCGAGGATGATGATGATGATGATGATGATGATGATGATGAT 300  
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DB 286 TTACTGACCTGTGATGAAATTAAGACCGGTTTGAACTTGTCAAGATTAATAGCA 345  
OY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAATGCAAGAGGTATGAGATCCT 357  
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DB 346 AACAAAGAGTAAAGAAAGAAAGAAAGAAAGCTTTGAAATGCAAGAGGTATGAGAGCCT 405  
OY 358 CAATTCGACACGACGTCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417  
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DB 406 CAGATGACGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465  
OY 418 GCCAAGAAAGATATTTATACATGA 442  
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DB 466 GCCCCCAAGATATCTACACCTTA 490

## RESULT 2

AM486605 398 bp mRNA linear EST 25-APR-2001  
LOCUS 75217.MARC IBOV Bos taurus cDNA 5', mRNA sequence.

AM486605  
VERSION AM486605.1 GI:7056711  
KEYWORDS EST.

## SOURCE

ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

## REFERENCE

1 (bases 1 to 398)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahnenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Perle,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and  
Keefe,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

## TITLE

JOURNAL MEDLINE  
Contact: Smith TPL  
USDA, ARS US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemali.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mismscore 20  
and -mismatch 12 options.

PCR primers  
FORWARD: AGGAACAGCATGACCAT  
BACKWARD: GTTTCCTGCTGACGAG  
Plate: 34 row: F column: 23  
Seq primer: ATTGAGGACATATAG.

## FEATURES

Location/Qualifiers  
1..398  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone.lib="MARC.1BOV"  
/tissue\_type="pooled"

BASE COUNT 134 a 77 c 82 g 105 t  
ORIGIN

Query Match 31.7%; Score 248.4; DB 9; Length 398;  
Best Local Similarity 84.4%; Pred. No. 3.1e-42;

Matches 292; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

OY 1 ATGATGAAACATACACCAAACTTCTCCGATGCGGCGCACTGACCTGCCATCAGC 60  
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DB 53 ATGATGAAACATACACCACTTCTCCGATGCGGCGCACTGACCTGCCATCAGT 112  
OY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAAATGATGATGCTGTG 120  
|||||  
DB 113 ATGAAATTTTATGATTTACTTACTGATTTCTTATACCCAGATGATGGCTAGCG 172  
OY 121 CTTTTCGCTGATCTTCTATAGATGATGATGATGATGATGATGATGATGAT 180  
|||||  
DB 173 CTTTTCGCTGATCTTCTATAGATGATGATGATGATGATGATGATGATGAT 232  
OY 181 GAAGATTTTCTATTCATTAATAAGCTTAAGATGCAACAAAGGAGAGATCTTTATCC 240  
|||||  
DB 233 GAAGATTTTCTGTCATGAAAGCATACAGATGCAATTAAGAGGAGGCTCTATCC 292  
OY 241 TTGCTGACCTGTGAGGATGAGATGAGAGCAATTTGAAGCTTGTCAAGATTAATGCA 300  
|||||  
DB 293 TTACTGACCTGTGAGGAAATTAAGACCGGTTTGAACTTGTCAAGATTAATGCA 352  
OY 301 AACAAAGAG--AGAAAAAGAAACAGCTTTGAAATGCAAGAG 343  
|||||  
DB 353 AACAAAGAGTAAAGAAAGAAAGAAAGCTTTGAAATGCAAGAG 398

## RESULT 3

AI982044 638 bp mRNA linear EST 07-MAY-2001  
LOCUS pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cDNA

AI982044  
DEFINITION clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.

## ACCESSION

## KEYWORDS

## SOURCE

## ORGANISM

chicken.  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianidae; Gallus.  
Mitsunaga,Y.G., Sofer,L., Cui,J. and Burnside,J.  
An expressed sequence tag database of T-cell-enriched activated  
chicken splenocytes: sequence analysis of 5251 clones  
Genomics 66 (2), 144-151 (2000)

## COMMENT

Contact: Joan Burnside  
Molecular Endocrinology  
University of Delaware  
40 Townsend Hall Newark, DE 19717, USA  
Tel: 302 831-1345  
Fax: 302-831-3411  
Email: joan@udel.edu, www.chickest.udel.edu  
Seq primer: T7.

## FEATURES

## source

Location/Qualifiers  
1..638

/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="pat.PK0072.c9.f"  
/clone.lib="chicken activated T cell cDNA"  
/sex="male"  
/cell\_type="Con A-activated splenic T cell"  
/lab\_host="E.coli TOP10 F"  
/note="Vector: pCDNA3"

BASE COUNT 132 a 171 c 151 g 180 t 4 others  
ORIGIN

Query Match 9.38: Score 72.8; DB 9; Length 638;  
Best Local Similarity 58.38; Pred. No. 2.2e-05;  
Matches 169; Conservative 0; Mismatches 112; Indels 9; Gaps 2;

OY 495 AGGACTATATATGCTCACTCAAGTACCTTGTCTATCGGAGCCTTCAGTCA 554  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 2 AGGCTCTACATCATCTACACAGTACGCTTCGCCACCAAGGGGGGCTTCG- 56  
OY 555 AGGCCATTCATCGTGGGCTTGGCTGAAGCCAGCATTTGATCTGAGAACTTACT 614  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 57 -GGCGATTAACCCCTATATTTATTTGTACCTCCCATGAGAGACCGGCTCTCAT 115  
OY 615 CAAGGCGCAATACCCCACTTCTCCAG---CTTGCAGACGCGCTGTTCACTT 671  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 116 GAAGGAGCTTACACAGCAGCACCCTCCAGCTCTGTGAGCTCCATCCATCCGGGA 175  
OY 672 GGGGAGATGTTTGAATATACAGCTGCTGCTTGTGTCACAGGAGTGAAGCAAG 731  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 176 GGGGAGTCTTCGAGCTGCGGCGAGGCGACATGCTTTGTTCATGTGACGACTCAAC 235  
OY 732 CCAAGTATCCACAGAGTGTGCTTCTCATCTTTGGCTTACTCAAACTCT 781  
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 236 AGCAGTGAACGTCAAACCTGGCAACACTTGTGATGTTCAAGCTGT 285

## RESULT 4

## CNS005TE/c

## LOCUS

## DEFINITION

CNS005TE 997 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR12K22 of RPI1-98 library from Drosophila melanogaster (fruit  
fly) genomic survey sequence.

## ACCESSION

AL060767  
AL060767.1 GI:4943573

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

fruit fly  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscophora; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and

## FEATURES

## source

Location/Qualifiers  
1..997

Aaron Mammosser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPI1-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

BASE COUNT 89 a 99 c 13 g 258 t 538 others  
ORIGIN

Query Match 7.18: Score 55.8; DB 12; Length 997;  
Best Local Similarity 19.58; Pred. No. 0.076; Indels 0; Gaps 0;  
Matches 69; Conservative 131; Mismatches 153;

OY 140 ATAGAGATTGGATAGGTCGAAGAGAGTAACCTTCATGAGATTGTTGATTCATTA 199  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 881 AARARARRARAKAARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 822  
OY 200 AAAGCTTAAGATGACCAACAAAGAGATCTTTATCTCTGCTGAAGTGTGAGACA 259  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 821 RGAARARARRRRARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 762  
OY 260 TGAGAGCAATTTGAGACCTTTCAGGATATTAAGTTAAAGAAAGAAAGAAAAAG 319  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 761 AARA 702  
OY 320 AAACAGCTTGAATGCAAGAGGTGATGAGATCTCAATTCAGCAGCATTTGTAA 379  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 701 GAGARRAGA 642  
OY 380 GCGAAGCCACAGTATGACATCCGTTCTACAGTGGGCCAAGAAAGATTTTATACCA 439  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 641 RRRARRA 582  
OY 440 TGAAGCAACTTGTATGCTTGAATGGAACAGCTGACGGTTAAAGA 492  
||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 581 GAGARRRRRRRRARARARARARARARARARARARARARARARARARARAR 529

## RESULT 5

## AL534423

## LOCUS

## DEFINITION

AL534423 797 bp mRNA linear EST 13-FEB-2001  
AL534423 LTI\_FL013\_Fbrn1 Homo sapiens cDNA clone CSDFP004YD24 5  
prime, mRNA sequence.

## ACCESSION

AL534423  
AL534423.1 GI:12797916

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

human  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1..797  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"



Query Match	6.7%	Score 52.8	DB 9	length 797
Best Local Similarity	38.9%	Pred No. 0.33		
Matches 1/1; Conservative	36	Mismatches 233		
				Incls 0; Gaps 0

RESULT	6				
CNS0145P/c.					
LOCUS		1043 bp	DNA	linear	GSS 26-JUL-1999
DEFINITION	CNS0145P				
	Drosophila melanogaster genome survey sequence T7 end of BAC				
	BACN11G1 of DrosBAC library from Drosophila melanogaster (fruit				
	fly), genomic survey sequence.				

ACCESSION	AL103735	GI:5615346
VERSION	AL103735.1	
KEYWORDS	GSS.	
SOURCE	fruit fly:	
ORGANISM	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1043)	
AUTHORS	Genoscope.	
TITLE	Direct, Submission	

<http://www.edgp.ebi.ac.uk>. This *Drosophila melanogaster* BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES	Location/Qualifiers
source	1. .1043
	Location="Thrysochilia melanogaster"
	Location="Thrysochilia melanogaster"

```
BASE COUNT      277 a      96 c      121 g      382 t      167 others
ORIGIN:
//plasmid="pBelobAC11"
//db_xref="taxon:7227"
//clone.lib="DrosBAC"
//clone="BAC11g11"
//note="end : 177"
```

Query Match	6.5%	Score 51.2;	DB 12;	Length 1043;
Best Local Similarity	36.28;	Pred. No. 0.7;		
Matches 102;	Conservative 48;	Mismatches 132;	Indels 0;	Gaps 0

[illegible]

LOCUS	DEFINITION	RESULT 7
CNS0108N		
CNS0108N	1038 bp DNA linear GSS 26-JUL-1995	
	Drosophila melanogaster genome survey sequence S6 end of BAC	
	BAC03L01 of Drosophila library from Drosophila melanogaster (fruit	
	fly), genomic survey sequence.	

ACCESSION	AL098657
VERSION	AL098657.1
KEYWORDS	GI:5610268
SOURCE	GSS.
ORGANISM	fruit fly, <i>Drosophila melanogaster</i>
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1038)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of
	determination of the human <i>Drosophila</i> genome project (EDGP)

http://www.edg.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC



and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
1. 1101  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone.lib="RPCI-98"  
/clone="BACR08K10"  
/note="end : TTT3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others  
ORIGIN

Query Match 6.3%; Score 49.2; DB 12; Length 1101;  
Best Local Similarity 13.7%; Pred. No. 1.8; Indels 2; Gaps 1;  
Matches 60; Conservative 221; Mismatches 155; Indels 2; Gaps 1;

62 TGAATTTTATGATTTACTTACTTCTTATCACCACCAATGATGATCTGTGC 121  
1084 DDMWMTWMTWMTKDRADRRWAGDADRWMDAGTWTATWMTWMTWMTWMDKMW 1025  
122 TTTTGTCTGTATCTCATAGAAAGATTGATGATGATGATGATGATGATGAT 181  
1024 WMTATATATATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTW 965  
182 AAGATTTTGTATCATATAAAGCTAAAGATGCAACAAGAGAGATCTTATCCT 241  
964 DGGDDKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGK 905  
242 TGTGTAAGTGTGAGAGATGAGAGAGCA--ATTGAGACCTGTCAAGATTAACGT 299  
904 DADDTDTKDDDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDDKDD 845  
300 AAACAAG 359  
844 WADDWMDAMWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTW 785  
360 AATTCAGACACAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419  
784 AATWTTWTTTTRTDDDMWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 725  
420 CAGAAGAGATTTATACATGAAAGCACTTGTATGCTTGAATGGAAAGAGCT 479  
724 KRDRIRWDADADDTARDDRRRGGADAGGKRTGRRRRRRRATWDRDAMWADAW 665  
480 GACGGTTAAAGAGAGAG 497  
664 WTTTDTDTDDMDKDRRR 647

RESULT 10  
LOCUS AZ691914 920 bp DNA linear GSS 14-DEC-2000  
DEFINITION ENTW026TR Entamoeba histolytica Sheared DNA Entamoeba histolytica  
ACCESSION AZ691914  
VERSION AZ691914.1 GI:11829180  
KEYWORDS GSS.  
SOURCE Entamoeba histolytica.  
ORGANISM Entamoeba histolytica.  
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 920)  
AUTHORS Loftus, B., Van Aken, S., and Fraser, C.  
TITLE Determination of clone end sequences from Entamoeba histolytica  
HMI:IMSS sheared DNA library.  
JOURNAL Unpublished (2000).  
COMMENT Contact: Brendan J. Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library  
Seq primer: M13-Reverse  
Class: shotgun  
High quality sequence start: 15  
High quality sequence stop: 330.  
Location/Qualifiers  
1. 920  
/organism="Entamoeba histolytica"  
/strain="HMI:IMSS"  
/db\_xref="taxon:5759"  
/clone.lib="Entamoeba histolytica Sheared DNA"  
/note="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a light size distribution (~2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O., and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Bartell, Oxford University Press, 1999)."

BASE COUNT 354 a 54 c 131 g 381 t  
ORIGIN

Query Match 6.1%; Score 47.6; DB 12; Length 920;  
Best Local Similarity 47.9%; Pred. No. 4;  
Matches 137; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

68 TTTTATGATTTACTTACTTCTTATCACCACCAATGATGATGATGATGATGAT 127  
569 TTTTATGATTTACTTACTTCTTATCACCACCAATGATGATGATGATGATGAT 628  
128 CTGTATCTCATATAAAGCTAAAGATGCAACAAGAGAGATCTTATCCT 187  
629 TTTTATGATTTACTTACTTCTTATCACCACCAATGATGATGATGATGATGAT 688  
188 TTTTATGATTTACTTACTTCTTATCACCACCAATGATGATGATGATGATGAT 247  
689 TTTTATGATTTACTTACTTCTTATCACCACCAATGATGATGATGATGATGAT 748  
248 ACTGTAGAGATGAGAGAGCAATTGAGACCTGTCAAGATTAACGTTAAACAAG 307  
749 ATGGGGGGGAGGGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808  
308 AACAG 353  
609 AAAAGATGAG 854

RESULT 11  
LOCUS AZ438784/c 423 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0229106F Mouse 10kb plasmid U06C1M library Mus musculus genomic  
ACCESSION AZ438784  
VERSION AZ438784.1 GI:10562797  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 423)  
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingy, A., von Niederhausen, A., and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

SOURCE ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 458)
AUTHORS	Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 131 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Location/Qualifiers  
1. .458

[illegible]

## TCATAGAGATTCGATAAGC

[illegible]

QY	248	ACTGTGAGGACATGAAGAGCAATTGTGAAGCCTTGTCAAGATATACGTTAAACAAG	307
Db	124	AA	65
QY	308	AAGGAAAAAAAAAGAAACACGCTTTGAATGCAAGA	342
Db	64	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	30

RESULT	13
LOCUS	CNS0383B
DEFINITION	802 bp DNA linear GSS 15-MAY-2004 Tetradon nigroviridis genome survey sequence pUC-ori end of clone 004012 of library G from Tetradon nigroviridis, genomic survey

.1 GI:7891247

KEYWORDS genome survey sequence.  
SOURCE Tetradodon nigroviridis.  
ORGANISM Tetradodon nigroviridis.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetradon.  
1 (bases 1 to 802)  
Roest-Crolius, H., Jallón, O., Dasilva, C., Frazmes, C., Fisher, C.,  
Ribeiro, T., Williams, A., Chastel, Saurin, W., Bernot, A. and  
Bouček, P. 2019. A new species of *Tetradodon* from the

characterization and repeat analysis of the compact genome of the freshwater pufterfish *Tetraodon nigroviridis*

<sup>2</sup> (bases 1 to 802)  
Roest-Crollius, H., Jallon, O., Dasilva, C., Bouneau, L., Fisher, C.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

Unpublished  
3 . (bases 1 to 802)

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
This sequence is a single read and was generated as part of a large  
project to determine the sequence of the Marburg virus genome.

genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

Location/Qualifiers  
1. .802

```

/db_xref="taxon:99883"
/clone="004012"
/clone_lib="G"

```

299 a	144 c	63 g	236 t	60 others
-------	-------	------	-------	-----------

Query Match	5.83;	Score 45.6;	DB 12;	Length 802;
Best Local Similarity	40.98;	Pred. No. 11;		
Matches 108; Conservative	26;	Mismatches 130;	Indels 0;	Gaps 0

68 TTTTATGATTACTACTGTTCCTATCACCCAATGATGGAGCGTGCTTTTTTG 124  
||| :: : |||| :: | : || | | : : | | | | | | : |||  
Db 363 TTAAKMATWTTTATAWTTTTCCKTTTGTGTTWTTTTTTTTTTAAWKTPTTATTTTWTTT 304

DQ 128 CTGCTATCTTCATAGAGATTGGATTAAGCTCGAAGAGGAAGTAAACCTTCATGAAGAATT 18  
| || | : : || : | || | || |  
DB 303 AACTTTATGTGKWKGAAKTWATAAAAAATAWAGATTTTATTAAAGCTKAKTTTTTTTT 244

[illegible]

248 ACTGTGAGGACATGAGAAGCCAAATTGAAGACCTTGCAAGGATATACGTTAACAAG 30

0Y 308 AAGAGAAAAAGAAACACCTTG 331  
| | | | | | | | | | | | | | | |

RESULT 14

CONSULTANT/LOCUS	CONSULTANT/DEFINITION	828 bp	DNA	linear	GSS 26-JUL-1999
CNS011TX	Drosophila melanogaster genome survey sequence T7 end of BAC				
RAC06A02	of DrosBAC library from Drosophila melanogaster (fruit				

ACCESSION	AL100719	genomic survey
VERSION	AL100719.1	GI:56123300
REVISION	1	1

ORGANISM  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta

pterygota; Neoptera; Endopterygota; Diptera; Brachycera  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 828)

Direct Submission  
Genoscope - Centre National de Sequencage :  
Submitted ( 23-JUL-1999 )  
PR 101 01006 EVRY cedex - FRANCE (E-mail : [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr))

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila genome project (EDGP)

Collaboration with the EMBL database. This *Drosophila melanogaster* BAC <http://www.ebgl.ebl.ac.uk> was made by Alain Billard at CEPH (Centre library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

Location/Qualifiers  
1. .828

```
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1lb="DrosBAC"
```

143 a .	127 c .	20 g	449 t	89 others
---------	---------	------	-------	-----------

Query Match	5.8%;	Score 45.6;	DB 12;	Length 828;
Best Local Similarity	39.7%;	Pred. No. 11;		
Matches 120;	Conservative . 29;	Mismatches 153;	Indels 0;	Gaps 0

QY 194 TCATATAAAGCTAAAGAGATGCAACAAAGAAGGAGGAAGGATTTTATTCCTTGCTGACACTGTG 253  
| | | | | : | | | | | : | | | | |  
Db 600 TAAAAAAGGAATAGAGATTAAGAAWAAAGCTTMAAMTWATATGATATAAAANWAAAAGAGC 541

QY 254 AGGAGATGAGAAGCGCAATTGTGAAGACCTTTGTCAAGCATATTAACGTTAAACAAGAAGACAGA 313  
+ + + + +  
Db 540 AAAAAGAGAGAAAAGAAAGGGGATGAAGATGTWAAAAAATWWGTTTTAAWAAAAAGAAAAAGA 481

QY 314 AAAAGAAACAGCTTTCGAATGCCAAGAGGTGATGAGGATCTCAAAATTGCAGCACACG 373

480 AAAAAATTAAGCAAAATTGAAANAAATGAWAAAGGMMWGAAGTWTATAAAAA 421

Db

OY 374 TTGTAAGCGAAGCCACACTAATGCAGCATTCCCTTCTACACTGTGGGCCAAGAAGATAT 433  
 :| | | :| | | :| | | :| | | :|  
Db. 420 AAAWAGAAAAAGCAAWWAGAAAAMWWMAAAAAGAATAATGAAGAGGAAWAAAGWMAAWTTAA 361

ATACCATGAAGCAACTTGGTAATGCTTGAAATCGGAACAGCTCAGGTTAAAAAG 49  
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
 ATGTAAAAGAATTGAGAGAGAMTTTTAAAAAATAAAGAAAAARAATWAAAWAAARAAAA 30

QY: 494 AA 495  
||  
200 20 200

DD 300 AA 299

RESULT 15

AL514085	458 bp	mRNA	linear	EST: 13-FEB-2001
LOCUS	AL514085			
DEFINITION	AL514085 LTI_NFI006_PL2 Homo sapiens CDNA clone GLOB0042E10.3			
	prime, mRNA sequence.			

ACCESSION	AL514085
VERSION	AL514085.1
KEYWORDS	GI:12777579
SOURCE	EST.
	human.

ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
REFERENCE	1 (bases 1 to 458)	

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)

## COMMENT

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

## FEATURES

Location/Qualifiers  
1. 458

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CLOBA004ZE10"  
/clone\_lib="TRI\_NFL006\_PL2"  
/tissue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

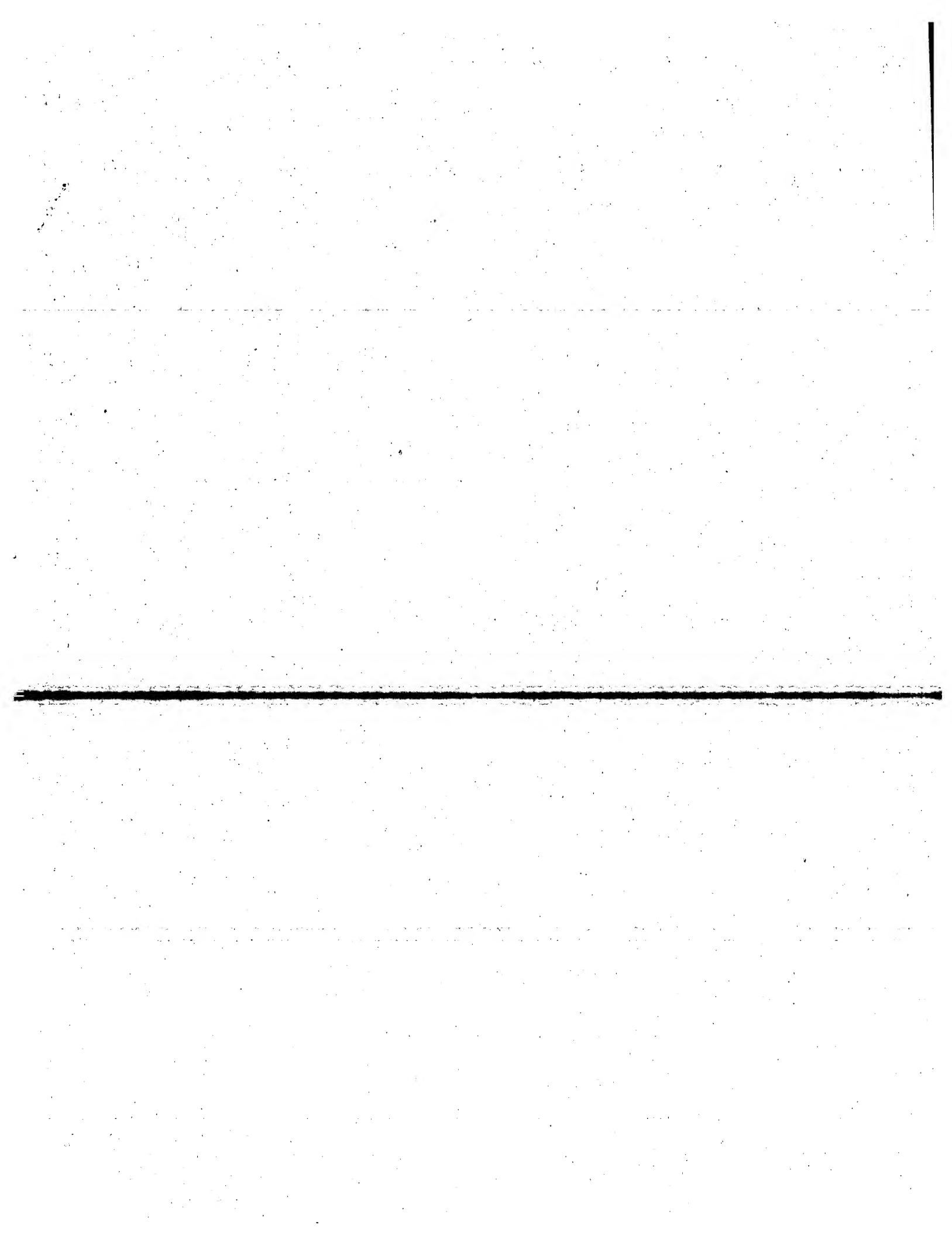
BASE COUNT 186 a 13 c 3 g 207 t 49 others  
ORIGIN

Query Match 5.88; Score 45.2; DB 9; Length 458;

Best Local Similarity 41.1%; Pred. No. 14;  
Matches 113; Conservative 18; Mismatches 144; Indels 0; Gaps 0;

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OY 68 TTTTATGTAATTTACTTCTGTTCCCTTATCACCCTTAATGATGTGATCTGCTTTTG 127
    ||||| |::| ||::| ||||| ||||| | | | | |
DB 162 TTTTATTTTATTTATTTTATTTTATTTTANNNNNNTTNNNTTTTNNTTTTCCTC 221
    ||||| |::| ||::| ||||| ||||| | | | | |
OY 128 CTGTGATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 187
    | | | | | | | | | | | | | | | | | | | | |
DB 222 CACCCTGCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 281
    | | | | | | | | | | | | | | | | | | | | |
OY 188 TTGTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 247
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DB 282 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 341
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OY 248 ACTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
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DB 342 AATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 401
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Search completed: May 30, 2002, 01:00:10  
Job time: 22220 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:15 ; Search time 680.87 Seconds  
(without alignments)  
1974.450 Million cell updates/sec

Title: US-08-982-272-5  
Perfect score: 783  
Sequence: 1 ATGATCGAACAATACCA.....TTGCTTACTCAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19	Exemplary CD40 lig
2	773.4	98.8	783	19	Exemplary CD40 lig
3	760.6	97.1	818	19	Murine CD40 ligand
4	759	96.9	783	15	Mouse CD40-L type
5	759	96.9	783	19	CD40 ligand coding
6	759	96.9	783	20	Mouse CD40-L codin
7	754.8	96.4	782	14	Murine CD40-L DNA
8	645.2	82.4	1477	22	Nucleotide sequenc
9					

10	642.2	82.0	818	16	AAT05762	Murine CD40 ligand
11	639	81.6	783	19	AAV42184	Exemplary nucleoti
12	631.4	80.6	878	20	AAZ27538	Mouse trimeric CD4
13	592.4	75.7	786	15	AAV39000	Exemplary CD40 lig
14	582.8	74.4	786	15	AAQ63959	Human CD40-L type
15	582.8	74.4	786	19	AAV38997	CD40 ligand gene u
16	582.8	74.4	786	19	AAV12852	CD40 ligand coding
17	582.8	74.4	840	14	AAQ41506	CD40-L DNA. Homo
18	582.8	74.4	840	15	AAQ67123	CD40 ligand gene.
19	582.8	74.4	840	16	AAQ05763	Human CD40 ligand
20	582.8	74.4	840	18	AAQ93782	cDNA of CD40L, a n
21	582.8	74.4	840	19	AAV61063	Human CD40 ligand
22	582.8	74.4	840	20	AAZ27525	Human CD40-L codin
23	582.8	74.4	879	22	AAV55539	Nucleotide sequenc
24	582.8	74.4	1816	21	AAV51745	Human CD40 ligand
25	582.8	74.4	1816	23	AAV86571	DNA encoding novel
26	581.4	74.3	840	18	AAV58122	Human CD40L mutain
27	579.6	74.0	840	15	AAQ57984	Genomic sequence o
28	578	73.8	840	16	AAQ94091	Human CD40-L cDNA.
29	570	72.8	786	19	AAV39003	Exemplary CD40 lig
30	560.4	71.6	786	19	AAV39002	Exemplary CD40 lig
31	534.8	68.3	864	19	AAV39004	CD40 ligand gene u
32	525.4	67.1	885	21	AAZ55540	Feline CD154 cDNA.
33	525.4	67.1	885	21	AAZ55541	Feline CD154 cDNA.
34	522.4	66.7	780	21	AAZ55542	Feline CD154 cDNA
35	522.4	66.7	780	21	AAZ55543	Feline CD154 cDNA
36	522.2	66.7	1878	21	AAZ55534	Canine CD154 cDNA.
37	522.2	66.7	1878	21	AAZ55535	Canine CD154 cDNA
38	519.2	66.3	780	21	AAZ55536	Canine CD154 cDNA
39	519.2	66.3	780	21	AAZ55537	Canine CD154 cDNA
40	454.6	58.1	1552	22	AAH25525	Nucleotide sequenc
41	449.2	57.4	865	22	AAH29333	HIV-1 gp120 V3 loo
42	449.2	57.4	906	22	AAH29332	HIV-1 gp120 V3 loo
43	449.2	57.4	2209	22	AAH29329	HIV-1 gp120-human
44	449.2	57.4	2252	22	AAH29328	HIV-1 gp120-human
45	446.2	57.0	1425	14	AAQ41516	Human CD40-L/Fc fu

ALIGNMENTS

RESULT 1  
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ID AAV39001 standard; DNA; 783 BP.  
XX  
AC AAV39001;  
XX  
DT 23-SEP-1998 (first entry)  
XX  
XX Exemplary CD40 ligand gene used in the course of the invention.  
DE  
DE  
XX  
KW CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Homo sapiens.  
PN WO9826061-A2.  
XX  
PD 18-JUN-1998.  
XX  
XX 08-DEC-1997; 97WO-US22740.  
XX  
PR 01-DEC-1997; 97US-0982272.  
PR 09-DEC-1996; 96US-0032145.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Cantwell M, Kipps TJ, Sharma S;  
XX  
DR WPI; 1998-348521/30.  
XX









DT 12-JAN-1995 (first entry)  
 DE Mouse CD40-L type II transmembrane protein coding sequence.  
 XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;  
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;  
 KW soluble CD40-L; tumour necrosis factor family; ss.  
 XX Mus musculus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 1..783  
 FT /\*tag= a  
 FT /product= mouse\_CD40-L  
 FT /note= "nucleotides 148-780 code for the  
 extracellular region (amino acids 50-260)"  
 XX  
 PN W09410308-A.  
 XX  
 PD 11-MAY-1994.  
 XX  
 XX 20-OCT-1993; 93WO-US10034.  
 XX  
 PR 23-OCT-1992; 92US-0969703.  
 PR 13-AUG-1993; 93US-0107353.  
 XX  
 XX (IMMUNEX CORP.  
 XX  
 XX Spriggs MK, Srinivasan S;  
 DR WPI; 1994-167465/20.  
 XX  
 DR P-PSDB; AAR53970.  
 XX  
 XX Prepn. of soluble oligomeric mammalian proteins - using host  
 PT cells to express a fusion protein comprising a leucine zipper  
 PT domain and a heterologous mammalian protein  
 XX  
 PS Example 1; Page 25-26; 35pp; English.  
 XX  
 CC A DNA fragment encoding the extracellular (soluble) region of mouse  
 CC CD40-L was ligated to a synthetic oligonucleotide sequence coding  
 CC for a leader peptide, a 33 amino acid leucine zipper sequence  
 CC (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the  
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L  
 CC in the supernatant. The leucine zipper sequence spontaneously  
 CC trimerises in solution and fusion proteins comprising  
 CC the sequence fused to a heterologous mammalian protein also form  
 CC oligomers.  
 CC  
 SQ Sequence 783 BP; 243 A; 159 C; 178 G; 203 T; 0 other;

Query Match 96.9%; Score 759; DB 15; Length 783;  
 Best Local Similarity 98.1%; Pred. No. 1.5e-201;  
 Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCAAAACATACAAACAACTTCCTCCGCTGCTGGCCACTGGACATCCCATCAGC 60  
 DB 1 atgataagaacatacagccaaacttccccagatccctggaactggacttccagcagc 60  
 QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATATATATATATATATATATATAT 120  
 DB 61 atgaagatttttattgtatttacttacttcttcttcttcttcttcttcttcttctg 120  
 QY 121 CTTTCTGCTGTATCTATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 DB 121 ctttctgctgtatcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 180  
 QY 181 GAAGATTTTGTATTTAT 240  
 DB 181 gaagattttgtatttatttatttatttatttatttatttatttatttatttatttatt 240  
 QY 241 TTGCTGAACGTGTGAGGAGATGAGAGCAATTTTGAAGACCTTGTCAAGGATATACGTTA 300

DB 241 ttgctgaactgtgaggagatgagagcaatttgaagaccttgaaggataatacgtta 300  
 QY 301 AACAAAGAAGAGAAAAAGAAACAGCTTTCAAATGCAAGAGGTGATGAGGATCCTCAA 360  
 DB 301 acaaaagaagaaaaaagaaacagctttaaatagaagaggtgagagagatcctcaa 360  
 QY 361 ATTCAGCACACAGTTGTAAGCAAGCAACAGTAAATGAGAGATCGTTTCTACAGTGGCC 420  
 DB 361 attgcagcacagttgtaagcgaagcgaacagtaatgcagcatccgttctacagtggcc 420  
 QY 421 AAGAAAGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480  
 DB 421 aagaagataattataccatgaaagcaacttggtaattgcttgaaatgggaacacagctg 480  
 QY 481 ACGGTTAAACAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTCTCTCTCTCTCT 540  
 DB 481 acggttaaagagagagactctattatgtctacactcaagtcacactctctctctaatcgg 540  
 QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTCGCCCTCTCGCTGAAGCCAGCATTTGATCT 600  
 DB 541 gagccttcgagtcacagcccaattcctgctgctgctgctgctgctgctgctgctgctg 600  
 QY 601 GAGAGAAATCTTACTCAAGCGCGCAAAATACCCACAGTTCCTCCAGCTTTTGGCAGCAG 660  
 DB 601 gagagaatcttactcaagcgcgcaaaataccacacagttctccacagcttgcgagcag 660  
 QY 661 TCTGTTCACTTGGCGGAGTGTGTAATACAGCTGCTGCTCTGCTCTGCTCTGCTCAACGTG 720  
 DB 661 tctgttcaacttggcgagtggttgaattacaagctgctgctgctgctgctgctgctgctg 720  
 QY 721 ACTGAAGCAAGCAAGTATCCAGAGTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 DB 721 actgaagcaagcgaagtatccacagagttggttctctctctctctctctctctctctc 780  
 QY 781 TGA 783  
 DB 781 tga 783

RESULT 6  
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 ID AAV12853 standard; cDNA to mRNA; 783 BP.  
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 AC AAV12853;  
 XX  
 DT 13-MAY-1998 (first entry)  
 XX  
 DE CD40 ligand coding sequence.  
 XX  
 KW Leucine zipper; fusion protein production; soluble oligomeric protein;  
 KW heterologous mammalian type II transmembrane protein; activated T cell;  
 KW heterologous mammalian type I transmembrane protein; antibody production;  
 KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..783  
 FT /\*tag= a  
 XX  
 PN US5716805-A.  
 PD 10-FEB-1998.  
 XX  
 PF 18-MAY-1995; 95US-0446922.  
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 PR 18-MAY-1995; 95US-0446922.  
 PR 25-OCT-1991; 91US-0783707.  
 PR 05-DEC-1991; 91US-0805723.  
 PR 23-OCT-1992; 92US-0969703.  
 PR 13-AUG-1993; 93US-0107353.  
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Query Match	96.9%	Score 759,	DB 19,	Length 783;
Best Local Similarity	98.1%	Prod. NO. 1.5e-201;		
Matches 768;	Conservative	0;	Mismatches 15;	Indels 0;
Gaps				
QY	1	ATGATCGAAACATACAACCAACTTCTCCCGCATCTCGCGCCACTGAGATGCCCATCAGC	60	
DB				
QY	1	atgataagaacatacagccacacctcccccagatccgtggaactggaacttcagcgagc	60	
DB				
QY	61	ATGAAATATTTTATGTATTTTACTTACTCTCTTTTCTCTTATCACCACAAATGATGTGATCTGTG	120	
DB				
QY	61	atgaagatttttatgtattacttactcgtttttcttattatccccaatgattggtatctgtg	120	
DB				
QY	121	CTTTTTCGTGTGTATCTTCTATAGAGATTTGGATTAAGTCTGAGAGGAAGTAAACCTTCAT	180	
DB				
QY	121	ctttttcgtgtatcttctatagaagattggaatggtctgaagagggaagtaaaccttcctat	180	
DB				
QY	181	GAAGATTTTGTATTCTATANAAGAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC	240	
DB				
QY	181	gaagattttgtattctataaagaagctaaagagatgcaacaagaagagagattttatcc	240	
DB				
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACCTTGTCAAGGATATACCGTTA	300	
DB				
QY	241	ttgctgaactgtgagagatgagaggcaaatttgaagaccttgtcaaggataataacgtta	300	
DB				
QY	301	AACAAGAAGAGAAAAAGAAACACGCTTTGAAATGCAAAAGAGGTGATGAGGATCCCTCAA	360	
DB				
QY	301	aacaaagaagagaaaaaagaaacagcttttgaaatgcaaaagagtgatgagagatccitcaa	360	
DB				
QY	361	ATTTCAGCACAGCTTGTGAAGCGAAGCAACAGTAATGTACAGATTCGGTTCTTACAGTGGGCC	420	
DB				
QY	361	atttcagcacacgcttgttaagcgaagccaacagtaatgcagcatccctgtctcagtgggcc	420	
DB				
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DB				
QY	421	aagaaagatattataccatgaaagaacacttggttaatgcttgyaaaaatgggaaacagctg	480	
DB				



The present sequence encodes a fusion protein comprising the mature murine surfactant protein D (including hub region, collagenous portion, and neck) fused to the murine CD40 ligand extracellular region (including stalk). The specification describes a method for constructing stable bioactive fusion proteins of the difficult to express tumor necrosis factor superfamily (TNFSF) proteins (especially CD40 ligand) as multimeric ligands fused onto branched protein backbones such as collectin molecules e.g. pulmonary surfactant protein D (SPD). The fusion proteins of the invention are useful for stimulating immune response in potentially immunocompetent cells (e.g., resting B cells). They are also useful for increasing antigenicity of cells such as tumor cells or human immunodeficiency virus (HIV) positive cells. They are also useful as a vaccine adjuvant since they stimulate B cells, macrophages and dendritic cells. Since the large size of the soluble fusion protein makes them less likely to diffuse into the circulation, they can be advantageously used as a vaccine adjuvant or tumor immunotherapy agent, injected locally to prevent them from diffusing away. Also, the TNFSF-collectin fusion proteins present new possibilities for the expression of highly active, multimeric, soluble TNFSF members. CD40L was a powerful stimulant for macrophages and dendritic cells.

Sequence 1477 BP; 418 A; 339 C; 421 G; 299 T; 0 other;

Query Match 82.4%; Score 645.2; DB 22; Length 1477;  
Best Local Similarity 99.5%; Pred. No. 1e-169;  
Matches 647; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 194 TCATAAAAGCTAAAGAGATGCAACAAAGAGAGATCTTTATCTCTGCTGAATGTG 253  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 254 AGGAGATGAGAGCAATTTCAAGACCTTGTCAAGGATATACCTTAAACAAGAGAGA 313  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 915 agggatgagaagcaatttgaagaccttgcaaggatatacaagcttaacaaagaga 974  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 314 AAAAGAAACAGCTTTTGAATGCAAGAGGTGATGAGATCTCAATTCAGACACAG 373  
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QY 975 aaaaagaaacagctttgaaatgcaagagtgatgagatccctcaaatgagcagcag 1034  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 374 TTGTAAGCGAAGCCCAACAGTAAATGAGATCGCTTCACAGTGGCCCAAGAGATATT 433  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1035 ttgtaagcgagcccaacagtaagtcagcatcgtctacagtgaggccaaagagatt 1094  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 434 ATACCATGAAAGCAACCTGGTAAATGCTTGAATGGGAAACAGCTGACGGTTAAAGAG 493  
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QY 1095 ataccatgaaagcaacttggcaatgcttgaaatgggaaacagctgacggttaaaag 1154  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 494 AAGGACTCTATTATGTCTACACTCAAGTCACTTCTGCTCTAATCGGAGCTTCAGTGC 553  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1155 aaggactctattatgtctacactcaagtcaccttctgcttaatcgagcctcgagtc 1214  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 554 AACGCCCATTCATCTGCTGCGCTCTGCTGAAGCCAGCATTTGCTGAGAGATCTTAC 613  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1215 aacgcccattcatcgctcgccctctgctgaagcccaagcatttgatctgaagaatctac 1274  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 614 TCAGGCGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTCTACTTGG 673  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 674 GCGGAGTGTGTTGAAATTACAGCTGGTCTGCTTCTGCTTGTGCTGAGAGATCTTAC 733  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1335 gcggagtggttgattacaagctggtgctgtgttctgcttcaacgtgactgaagcagcc 1394  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 734 AAGTGATCCACAGATTGGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 793  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1395 aagtgatccacagagtggtgcttctcatcttctgttggcttactcaactctga 1444  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 421 aagaaggatattataccatgaaagcaacttgtaatgcttgaaatgggaaacagctg 480  
QY 481 ACGGTTAAAGAGAGACTCTATTATGTCTACACTCAAGTCACTTCTGCTCTAATCGG 540  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 540 acggttaaagagagagactctattatgtctacactcaagtcacacttctgcttaacgg 540  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCTCTGGCTGAAGCCACGATGGATCT 600  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 541 gagccttcagtcacagcccaattcatcgctgctgctgagccagcagtgagctc 600  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 601 GAGAGATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTGCGAGCAGCAG 660  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 601 gagagaattctactcaagcgcaataaccacagttctctccagcttggcgagcagcag 660  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTCTGTTGTTGTCACAGTG 720  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 661 tctgttctacttggcgaggtttgaaattacaagctggtgcttctgttggtaacagtg 720  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 721 ACTGAAGCAAGCAAGTATGATCAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 721 actgaagcaagcaagtgatccacagagttggtctctcatcttttggcttactcaactc 780  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 781 TG 782  
Db ||  
QY 781 tg 782  
Db ||  
RESULT 9  
ID AAH25527  
XX AAH25527 standard; DNA; 1477 BP.  
AC AAH25527;  
XX AAH25527;  
XX 22-AUG-2001 (first entry)  
XX Nucleotide sequence of surfactant protein D fused to CD40 ligand.  
DE Fusion protein; CD40 ligand; tumour necrosis factor; TNF; collectin;  
XX pulmonary surfactant protein D; SPD; immunocompetent cell;  
KW cell antigenicity; vaccine adjuvant; chimera; ss.  
KW  
OS Chimeric - Mus sp.  
OS Chimeric - Mus sp.  
XX Location/Qualifiers  
XX Key 32..1444  
XX CDS /\*tag= a  
XX sig\_peptide 32..88 b  
XX /\*tag= b  
XX /\*note= "signal peptide from murine surfactant protein D"  
XX  
PN WO200142298-A1.  
XX PD 14-JUN-2001.  
XX 20-MAR-2000; 2000WO-US07380.  
XX 09-DEC-1999; 99US-0454223.  
XX (KORN/) KORNBLUTH R S.  
XX Kornbluth RS;  
XX WPI; 2001-381642/40.  
XX P-PSDB; AAB84421.  
XX Producing tumor necrosis factor superfamily proteins as multimeric  
PT ligands fused onto collectin molecules e.g. pulmonary surfactant  
PT protein D, useful as vaccine adjuvants against infectious agents and  
PT tumours -  
XX  
XX Claim 1; Page 65-68; 74pp; English.  
PS  
XX





QY	1	ATATCGAACAATACAAACCAACTTCTCCCGACTCGCGCCACTGGACTGCCCATCCAGC	60
Db	1	atgtcgaaacatacaccaaaactctcccgatctcgggccactcggaactgccatcagc	60
QY	61	ATGAAATATTTTATGTATTACTTACTGTGTTTCTTATCACCAAATGATGGGATCTGTG	120
Db	61	atgaaaaattttatgtatttacttactgtttcttattaccaccagatgattgggtcagca	120
QY	121	CTTTTCTGCTGTATCTTCATCAAAATTTGGATAGTGCGAAGAGGAAGTAAACCTTCAT	180
Db	121	ctttttctgtgtatctctc tagaagttaggaatcggaaggtcggaaggaagaaaccttcac	180
QY	181	GAAGATTTTGTATTATATAAAAAAGCTAAAGAGATGCAACAAGAGGAGAAGATCTTTTATCC	240
Db	181	gaagattttgtattcataaaaaagctaaagagatgcaacaagaagagaagatctttattcc	240
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGCCATTTTGAAGCTTGTCTCAAGGATATAACGTTA	300
Db	241	ttgtgaactgtgaggagatgagaagcaatttgagagccttgccaagagataatacgtta	300
QY	301	AACAAAGAAGAGAAAAAGAAACAGCTTTTGAATCTCAAGAGGCGATGAGGATCTCTAA	360
Db	301	aacaaagaagagaaaaaagaaaaaacagctttgaaatgcataaagagtgatcagaatcctcaa	360
QY	361	ATTGCGACACACCTGTGTAAGCGAAGCCAAACAGTAATGCAGCATCCGTTCTACAGTGGGCC	420
Db	361	attgcgcacatgtctataagtgaggccagcagtaaaacaacatctgtgtacagtgaggct	420
QY	421	AAGAAGGATATTATPACCATGAAAAGCAACTTGTGTAATGTTGAANAATGGGAACAGCTG	480
Db	421	gaaaagaagatactacaccatgagcaacaacttgtaaccctggataaactgggaacacagctg	480
QY	481	ACGGTTTAAAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTGCTCTAATCGG	540
Db	481	acggttaaaagacaaggactctattatctatctgccaaagtcaacctctgttccaatcgg	540
QY	541	GAGCCTTTCAGTCAACGCCCATTCATCGCTGGCCCTTGGGTGAAGCCACCATTTGATCT	600
Db	541	gaagcttcgagtcgaagctccattatagccagcctctgctaaagtcccccggtagattc	600
QY	601	GAGAGAACTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTCGGAGCAGCAG	660
Db	601	gagagaattctactcagagctgcaaataccacacagttccgcaaaccttcggggcaacaa	660
QY	661	TCTGTTCACCTTGGCGGAGTGTTTGAATTAACAAGTGTGCTTCTGTGTTTGTCAACGTG	720
Db	661	tccattccactctgggaggagatttgaaattgcaaccagtgcttcgggtgtttgtccaagt	720
QY	721	ACTGAAGCAAGCCAGTAGTCACAGAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC	780



Db 405 -gaaatgcaagagggtgatgagatcctcaaatgagcacacgctgttgtaagcgaagcccaac 464  
 Qy 331 AGTAATGAGCATCGCTTCTACAGTGGCCCAAGAGGATATATACCATGAAAAGCAAC 450  
 Db 465 agtaatgagcatcgcgttctacagtgggccaaagaagagattatcattacatgaaagcaac 524  
 Qy 451 TTGTAATGCTTGAATGGAAACAGCTGACGGTTAAAGAGAGAGGAGGACTCTATTATGTC 510  
 Db 525 ttggttaatgcttgaatggaaacagctgacgggttaaaagagaagagactctattatgc 584  
 Qy 511 TACACTCAAGTCACCTCTGCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570  
 Db 585 tacactcaagtcacctctgctctaatcgggagccttcgagtcacgccccattcatgc 644  
 Qy 571 GGCCTCTGGCTGAAGCCAGCATTTGATCTGAGAGAACTTACTCAAGCGGCAATACC 630  
 Db 645 ggcctctggctgaagccagcagtgatctgagaaattcttactcaagcggaataacc 704  
 Qy 631 CACAGTTCTCCAGCTTTGGAGCAGCAGCTGTGTTCACTTGGGGGAGTGTGTTGAATTA 690  
 Db 705 cacagttctccagccttgcgagcagcagctgtcttcacttggcgaggttttgaatta 764  
 Qy 691 CAAGCTGTGCTTCTGCTTTGTCACAGTGTGACTGAGCAAGCCCAAGTCAACAGAGTT 750  
 Db 765 caagctgtgcttctgtgttgcacagtgactgaagcaagccaagtgatccacagagtt 824  
 Qy 751 GCCTTCTCATCTTTGGCTTACTCAAACTCTGA 783  
 Db 825 ggcctctcatcttttggcttactcaaaactctga 857

RESULT 13  
 AAV39000  
 ID AAV39000 standard; DNA; 786 BP.  
 XX AC AAV39000;  
 XX DT 23-SEP-1998 (first entry)  
 XX EX Exemplary CD40 ligand gene used in the course of the invention.  
 KW CD40 ligand; alteration; immunoreactivity; human cell;  
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
 KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.  
 XX OS Chimeric - Mus sp.  
 XX OS Chimeric - Homo sapiens.  
 XX PN W09826061-A2.  
 XX PD 18-JUN-1998.  
 XX PF 08-DEC-1997; 97WO-US22740.  
 XX PR 01-DEC-1997; 97US-0982272.  
 XX PR 09-DEC-1996; 96US-0032145.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Cantwell M, Kipps TJ, Sharma S;  
 XX WI 1998-348521/30.  
 XX Vectors containing accessory molecule ligand genes - used for  
 PT altering immunoreactivity of cells, particularly for treatment of  
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
 XX PS Disclosure; Page 105; 167pp; English.  
 XX CC The present sequence represents an exemplary CD40 ligand gene,  
 CC comprising nucleotides encoding the extracellular domains (Domains III  
 CC and IV) of human CD40 ligand gene (AAV38998) are operatively linked to  
 CC nucleotides encoding the murine CD40 ligand transmembrane domain (Domain

CC I) (AAV38997) which is operatively linked to the human CD40 ligand gene  
 CC cytoplasmic domain (Domain I). The sequence is used to exemplify the  
 CC method of the invention. The specification describes a method for  
 CC altering the immunoreactivity of human cells which comprises introducing  
 CC a gene encoding an accessory molecule ligand (AML) into the cells so that  
 CC the AML is expressed on the surface of the cells. Vectors containing the  
 CC AML genes can be used in gene therapy for treating neoplasia or  
 CC autoimmune disorders such as rheumatoid arthritis. They can also be used  
 CC for vaccination to produce immunity against a virus cell, bacteria,  
 CC protein, fungus or neoplasia.  
 XX Sequence 786 BP; 250 A; 168 C; 167 G; 201 T; 0 other;  
 SQ  
 Query Match 75.7%; Score 592.4; DB 19; Length 786;  
 Best Local Similarity 85.5%; Pred. No. 4; 2e-155;  
 Matches 672; Conservative 0; Mismatches 111; Indels 3; Gaps 1;  
 Qy 1 ATGATCGAATCATACCAACAACTTCTCCCGATCTGCGGCACCTGGAGTGCCTTATCC 60  
 Db 1 atgatcgaaacatacaacaaacttctcccgatctgcgcaactggactgccatcagc 60  
 Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATATACCCAAATGATGGATCTGTG 120  
 Db 61 atgaaattttatgtatttacttactgttttcttataccccaatgattggatctgtg 120  
 Qy 121 CTTTTTGTGCTGATTCATAGAGATTGGATAGGTGCGAGAGAGAGTAAACCTTCAT 180  
 Db 121 ctttttgcgtgtatctctcatagaaggttggaacagatagaagatgaaagaatcttcat 180  
 Qy 181 GAAGATTTTGTATTTATCAATAAAGCTAAAGAGATCAACAAAGAGAGATCTTTATCC 240  
 Db 181 gaagattttgtattcatgaaacagatacagagatgcaacacagagaaatcttacc 240  
 Qy 241 TTGCTGAATCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAGAGATATACGTTA 300  
 Db 241 ttactgaactgtgaggattaaagccagtttgaagccttctgtgaagataataatgta 300  
 Qy 301 AACAAAGAGA--GAAAGAGAGAGAGAGTGTGAAATGCAAGAGGTGATGAGATCT 357  
 Db 301 acaaaagaggagacgaagaagaacagcttgaatgcaaaagggatcagaaatcct 360  
 Qy 358 CAAATTTGACGACACGCTTTGTAAGCGAAGCCAAACACATTAATGACAGATCTTACAGTGG 417  
 Db 361 caaattgcgacacatgtcataagtgaggccagcagtaaaacacatctgtttacagtgg 420  
 Qy 418 GCCAAGAAAGATATATTACCATGAAAGACACTTTGGTAAATGCTTGAAGTGGGAAACAG 477  
 Db 421 gctgaaaagagatactacacatgagcaacaacttggtaacccctggaaatgggaaacag 480  
 Qy 478 CTGACGGTTAAAGAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTGCTTAAT 537  
 Db 481 ctgaccgttaaaagacaagagactctattatctatctatgcccgaagtcaccttctgttccaat 540  
 Qy 538 CGGAGCCTTCAGTCAACGCCCATTCATCGTGGCCCTCTGCTGAGAGCCCAAGCATTTGGA 597  
 Db 541 cggaagcttcagtcagtcacagctccattatagccagcctctgcctaaagtcctcccggtaga 600  
 Qy 598 TCTGAGAAATCTTACTCAAGCGGCAATATCCACAGTTCCTCCAGCTTTGCGAGCAG 657  
 Db 601 ttcgagagaatcttactcagagctgcaaatccccacagttccgcgaacacccctgggcaaa 660  
 Qy 658 CAGTCTGTCTACTTGGCGGAGTGTTCATATACAGCTGGTGTCTCTGCTTTCTCAAC 717  
 Db 661 caatccatctcctgtggagagatttgaattgcaaccaggtgcttcggtgttgcatt 720  
 Qy 718 GTGACTGAAGCAAGCAAGTGTATCCACAGATTTGCTTCTCATCTTTTGGCTTACTCAA 777  
 Db 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtctcttggcttactcaaa 780  
 Qy 778 CTCTGA 783  
 Db 781 ctctga 786

Thu May 30 05:46:11 2002

```

RESULT 14
AAO63959
ID AAO63959 standard; cDNA to mRNA; 786 BP.
XX
XX AAO63959;
AC
XX
XX
XX
XX 11-JAN-1995 (first entry)
XX Human CD40-L type II transmembrane protein coding sequence.
XX
XX
XX Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;
XX hetero-oligomer; homo-oligomer; type II transmembrane protein;
XX soluble CD40-L; tumour necrosis factor family; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..786
XX /*tag= a
XX /product= human CD40-L
XX /note= "nucleotides 148-783 code for the
XX extracellular region (amino acids 50-261)."
```

Example 1; Page 22-23; 35pp; English.

A DNA fragment encoding the extracellular (soluble) region of human CD40-L was ligated to a synthetic oligonucleotide sequence coding for a leader peptide, a 33 amino acid leucine zipper sequence (AAR53968) and the Flag (RTM) linker sequence. Cells expressing the fusion construct are grown to accumulate oligomeric, soluble CD40-L in the supernatant. The leucine zipper sequence spontaneously trimerises in solution and fusion proteins comprising the sequence fused to a heterologous mammalian protein also form oligomers.

Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 74.4%; Score 582.8; DB 15; Length 786;  
Best Local Similarity 84.7%; Pred. No. 2e-152;  
Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

```

QY 1 ATGTCGAAACATCAACAACTTCCTCCGATCTCGGCCACTGACGTGCCCATCAGC 60
DB 1 atgacgaaacatacaacaaacttcccgatctcgccactggactgcccacagc 60
QY 61 ATGAAATTTTATGTTACTTACTTCTTATCACCACAAATGATTGGATCTGTG 120
DB 61 atgaaattttatgtattacttactgtttttcttatcccccagatgaggtcagca 120
QY 121 CTTTGTCTGTATCTTCATAGAGATTGGATGAAGGTCGAGGAAGTAACCTTCAT 180
```

```

121 cttttgtgtgtatcttcataaggttggaagatagaagatagaagaaatcttcat 180
181 GAAGATTTCATTATTAATAAGCTTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
181 gaagattttgtattatgaacacgatacagagatgcaacacagagagaaatcctatcc 240
241 TTCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTCTCAGGATATACGTTA 300
241 ttactgaactgtgagagatgaagattaaaagccagtttgaaggcttgaagataatgtta 300
301 AACAAAGAGA---GAAAAGAAACACAGCTTTGAAATGAAAGAGGTGATGAGATCCT 357
301 aacaaagagagacgaagaagaaacacagctttgaaatgcaaaaggtgtatcagaatcct 360
358 CAATTCAGACACAGCTTGTAAAGCAAGCCACAGTAAGTACGATCCCTTCTACAGTGG 417
361 caaattcggcacatgtcataagtgaagccagcagtaaaacacacatctgtgtacagtgg 420
418 GCCAAGAAAGATATTATACCATGAAGCAACTTGTGTAATGCTTGAATAATGGAAACAG 477
421 gctgaaaagagatactacacacatgagcaacacttggttaacctggaaaatgggaacag 480
478 CTGACGGTTAAAGAGAGAGACTCTATTATGTCTACACTCAAGTCACCTTCTCTCTAAT 537
481 ctgaccgttaaaagacaaagactctattatctatgcccaagtcaccttctgttccaat 540
538 CGGAGCCTTCGAGTCAACGCCCAATTCACTCGTGGGCTCTGGCTGAAGCCACGATGGA 597
541 cgggaagcttcgagtcgaagctccattatagccagcctctgctaaagtcccccgtaga 600
598 TCTGAGAGAACTTACTCAAGCGGCAAAATACCCACAGTTCTCTCCAGCTTTGGGACAG 657
601 ttcgagagaaatcttactcagagctgcaaaatcccaacagttccgcaaaccttgggcaa 660
658 CAGTCTGTCTACTTGGGCGGAGTGTTCGAATTACAAGCTGTGCTCTGTGTTTGTCAAC 717
661 caatccattcacttgggagagatttgaattgcaaccaggtgcttcggtgtttgtcaat 720
718 CTCAGTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAA 777
721 gtgactgataccaaagccaaagtggccatggcactggcttcacgtcccttgggtactcaa 780
778 CTCTGA 783
781 ctctga 786
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RESULT 15  
AAV38997  
ID AAV38997 standard; DNA; 786 BP.

AC AAV38997;

DT 23-SEP-1998 (first entry)

CD40 ligand gene used in the course of the invention.

CD40 ligand; alteration; immunoreactivity; human cell;  
accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
autoimmune disorder; rheumatoid arthritis; vaccine; ss.

Mus sp.

WO9826061-A2.

PN 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

XX 09-DEC-1996; 96US-0032145.

PA (REGC ) UNIV CALIFORNIA.

PI Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX  
PS Disclosure; Page 104; 167pp; English.

XX The present sequence represents the CD40 ligand gene. The sequence is

used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells  
CC which comprises introducing a gene encoding an accessory molecule  
CC ligand (AML) into the cells so that the AML is expressed on the surface  
CC of the cells. Vectors containing the AML genes can be used in gene  
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
CC arthritis. They can also be used for vaccination to produce immunity  
XX against a virus cell, bacteria, protein, fungus or neoplasia.

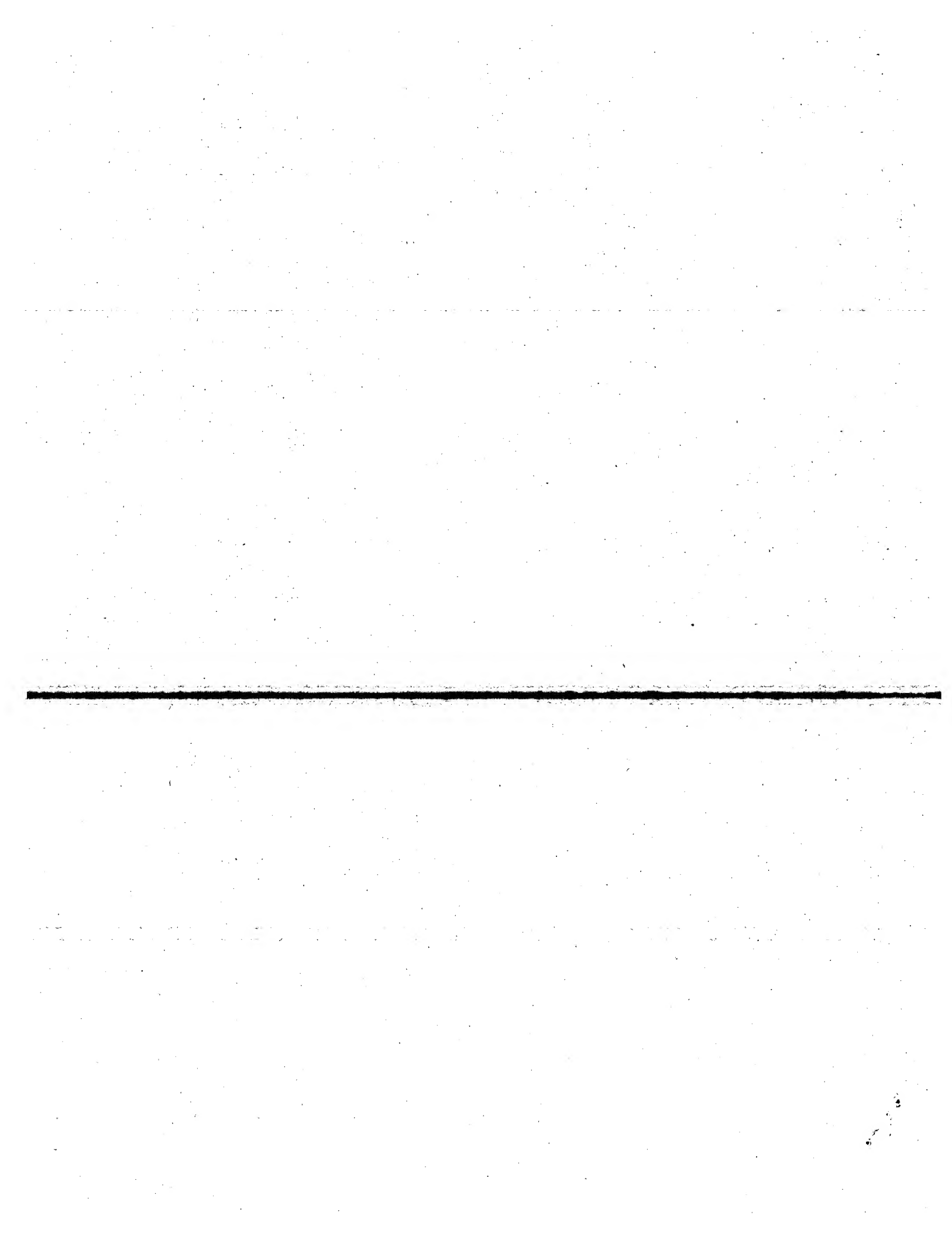
SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 74.4%; Score 582.8; DB 19; Length 786;  
Best Local Similarity 84.7%; Pred. No. 2e-152;  
Matches 566; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

OY 1 ATGATCGAACAATCAACAACTTCTCCCGATCTGGGCGACTGGCTTCTGCTGTTCTGCTCAAC 717  
DB 1 atgatcgaaacatacaacaaactctcccgatctggccactggactgcccacagc 60  
OY 61 ATGAAATTTTATCTATTACTTACTTCTTCTTATCACCCTTATGATGATCTGTG 120  
DB 61 atgaaaattttatctattacttcttcttcttccacccagatggtggcgca 120  
OY 121 CTTTGTGCTGTATCTATAGAGATTGATAGGTCGAAGAGGAGTAACCTTCAT 180  
DB 121 ctttgtgtgtatcttctatagaaggttggaagatagaagatgaaaggaatttcat 180  
OY 181 GAAGATTTTGTATCATATAAAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240  
DB 181 gaagattttgtattcatgaaacgatacagagatgcaacacagagagaaatccctatcc 240  
OY 241 TTGCTCAACTGTGAGGAGTGAAGGCAATTTGAGACCTTGTCAAGGATATAACGTTA 300  
DB 241 ttactgaactgtgaggagattaaagccagtttgaggctttgtgaggatataatgta 300  
OY 301 AACAAAGAAGA---GAAAAAGAAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCT 357  
DB 301 aacaaagaggagacgaagaagaacagctttgaaatgcaaaaggtgacgaatcct 360  
OY 358 CAAATTCAGACACAGTTGTAGCGAAGCCACAGTATGACGATCCGTTTCTACAGTGG 417  
DB 361 caaattgcgcacatgtcataagtgaggccagcagtaaaacacatctgtgtacagtgg 420  
OY 418 GCCAAGAAGGATATTATACCAATGAAAGCAACTTTGGTAAATGCGAAATGGGAAACAG 477  
DB 421 gctgaaaaggatatacaccatgagcaacaacttggtaaccctggaaaatgggaaacag 480  
OY 478 CTGACGGTTAAAGAGAAGGACTCTATTATGCTACACTCAAGTCAACCTTCTGCTCTAAT 537  
DB 481 ctgaccgttaaagaacagagactctattatctatgcccaagtcacaccttctgttccaat 540  
OY 538 CGGGAGCCTTCAGTCACGCCCATTCATGCTGGCCTCTGGCTGAAGCCACAGCATTTGA 597  
DB 541 cgggaagcttcgagtcagctcatttatagccagcctctgcctaaagtcctcccggtaga 600  
OY 598 TCTGAGAGATCTTACTCAAGGGGGCAATACCCACAGTTCTCCAGCTTTGCGAGCAG 657  
DB 601 ttcgagagaattactagagctgcaaataccacagttccgcgcaaaccttgcgggcaa 660

OY 658 CAGTCTGTTCACTTGGGCGAGTGTGTTGAATTACAAGCTGGTCTTCTGCTGTTCTCAAC 717  
DB 661 caatccattccacttggaggagcatttgaattgcaaccaggctccgctgttgcacat 720  
OY 718 GTGACTGAAGCAAGCCAAAGTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAA 777  
DB 721 gtgactgatccaagccaagtgagccatggcactggcttcaagctcttggcttactcaaa 780  
OY 778 CTCTGA 783  
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OM nucleic - nucleic search, using sw model

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Title: US-08-982-272-5

Perfect score: 783

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq:\*
- 26: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq:\*
- 27: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq:\*
- 28: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq:\*
- 29: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq:\*
- 30: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq:\*
- 31: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq:\*
- 32: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*
- 33: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*
- 34: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*
- 35: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq:\*
- 36: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*
- 37: /cgn2\_6/ptodata/2/pna/US100\_COMB.seq:\*
- 38: /cgn2\_6/ptodata/2/pna/US101\_COMB.seq:\*
- 39: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq:\*
- 40: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*
- 41: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*
- 42: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*
- 43: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

44: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*

45: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*

46: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*

47: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*

48: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*

49: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*

50: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*

51: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*

52: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*

53: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*

54: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*

55: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*

56: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*

57: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*

58: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*

59: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*

60: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*

61: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*

62: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq:\*

63: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*

64: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*

65: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*

66: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*

67: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*

68: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*

69: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*

70: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*

71: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*

72: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*

73: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq:\*

74: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*

75: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	783	100.0	783	13	US-08-982-272-5	Sequence 5, Appli
2	773.4	98.8	783	13	US-08-982-272-3	Sequence 3, Appli
3	760.6	97.1	783	3	US-07-969-703B-1	Sequence 1, Appli
4	760.6	97.1	783	13	US-08-982-272-2	Sequence 2, Appli
5	760.6	97.1	818	6	US-08-234-580-1	Sequence 1, Appli
6	759	96.9	783	3	US-07-969-703A-1	Sequence 1, Appli
7	759	96.9	783	5	US-08-107-353-5	Sequence 5, Appli
8	759	96.9	783	8	US-08-477-733A-1	Sequence 1, Appli
9	759	96.9	783	8	US-08-484-624-1	Sequence 1, Appli
10	759	96.9	783	11	US-08-770-981-1	Sequence 1, Appli
11	759	96.9	783	14	US-09-088-913-1	Sequence 1, Appli
12	759	96.9	783	17	US-09-322-021-1	Sequence 1, Appli
13	759	96.9	783	17	US-09-322-021A-1	Sequence 1, Appli
14	759	96.9	783	17	US-09-365-940-1	Sequence 1, Appli
15	759	96.9	783	17	US-09-365-940A-1	Sequence 1, Appli
16	759	96.9	783	17	US-09-392-618-1	Sequence 1, Appli
17	759	96.9	783	17	US-09-399-106-1	Sequence 1, Appli
18	759	96.9	1209	75	US-60-360-207-9611	Sequence 9611, Ap
19	759	96.9	1250	37	US-10-090-238-3	Sequence 3, Appli
20	757.6	96.8	780	3	US-07-783-707A-1	Sequence 1, Appli
21	757.6	96.8	780	3	US-07-805-723-1	Sequence 1, Appli
22	645.2	82.4	1477	18	US-09-454-223-5	Sequence 5, Appli
23	639	81.6	783	13	US-08-982-272-20	Sequence 20, Appli
24	631.4	80.6	878	8	US-08-477-733A-22	Sequence 22, Appli
25	631.4	80.6	878	8	US-08-484-624-22	Sequence 22, Appli
26	631.4	80.6	878	11	US-08-770-981-22	Sequence 22, Appli
27	631.4	80.6	878	14	US-09-088-913-22	Sequence 22, Appli
28	631.4	80.6	878	17	US-09-322-021-22	Sequence 22, Appli
29	631.4	80.6	878	17	US-09-322-021A-22	Sequence 22, Appli
30	631.4	80.6	878	17	US-09-365-940-22	Sequence 22, Appli
31	631.4	80.6	878	17	US-09-365-940A-22	Sequence 22, Appli



;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette,  
;; MEDIUM TYPE: 1.44 Mb Storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/982,272  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/132145  
;; FILING DATE: 12/9/96  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Guise, Jeffrey W.  
;; REGISTRATION NUMBER: 34,613  
;; REFERENCE/DOCKET NUMBER: 231/003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 783 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-982-272-3

Query Match 98.8%; Score 773.4; DB 13; Length 783;  
Best Local Similarity 99.2%; Pred. No. 7.2e-183;  
Matches 777; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACCAAACTTCTCCCGGATCTGGCCACTGGACTGCCATCAGC 60  
Db 1 ATGATCGAAACATCAACCAAACTTCTCCCGGATCTGGCCACTGGACTGCCATCAGC 60  
Qy 61 ATGAAATTTTATGTTATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120  
Db 61 ATGAAATTTTATGTTATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120  
Qy 121 CTTTTTGTGTATCTTCTATAGAGATTGGATAGGTCGAGAGAGAGTAACCTTTCAT 180  
Db 121 CTTTTTGTGTATCTTCTATAGAGATTGGATAGGTCGAGAGAGAGTAACCTTTCAT 180  
Qy 181 GAAGATTTTGTATCAAAAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
Db 181 GAAGATTTTGTATCAAAAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
Qy 241 TTGCTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300  
Db 241 TTGCTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300  
Qy 301 AACAAAG 360  
Db 301 AACAAAG 360  
Qy 361 ATTGACGACAGCTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420  
Db 361 ATTGACGACAGCTTGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 420  
Qy 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGGGAAAGCAAGCTG 480  
Db 421 AAGAAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATGGGAAAGCAAGCTG 480

Qy 481 ACGGTTAAAG 540  
Db 481 ACGGTTAAAG 540  
Qy 541 GAGCCTTTCGAGTCAACGCGGATTCATCGTCGCGCTCTGGCTGAAGCCAGCATTTGATCT 600  
Db 541 GAGCCTTTCGAGTCAACGCGGATTCATCGTCGCGCTCTGGCTGAAGCCAGCATTTGATCT 600  
Qy 601 GAGAGAATCTTACTCAAGGCGGCAATACCCACAGTTCTCTCCAGCTTTGGGAGAGAGAG 660  
Db 601 GAGAGAATCTTACTCAAGGCGGCAATACCCACAGTTCTCTCCAGCTTTGGGAGAGAGAG 660  
Qy 661 TCTGTTCACTTTGGGCGGAGTGTGTAATTAACAAGTGTGCTTCTGCTTTGTTGTCACAGTG 720  
Db 661 TCTGTTCACTTTGGGCGGAGTGTGTAATTAACAAGTGTGCTTCTGCTTTGTTGTCACAGTG 720  
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780  
Qy 781 TGA 783  
Db 781 TGA 783

RESULT 3  
US-07-969-703B-1  
; Sequence 1, Application US/07969703B  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/969,703B  
; FILING DATE: 19921023  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 783 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: MOUSE  
; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS

TITLE OF INVENTION: CONTAINING ACCESSORY  
MOLECULE LIGAND, GENES AND  
THEIR USE FOR IMMUNO-  
MODULATION AND TREATMENT OF  
MALIGNANCIES

LOCATION: 1..783  
US-07-969-703B-1

Query Match 97.1%; Score 760.6; DB 3; Length 783;  
Best Local Similarity 98.2%; Pred. No. 1.1e-179;  
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACTGGAGTCCCATCAGC-60  
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCGTGGCACTGGAGTCCCATCAGC 60  
QY 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120  
DB 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120  
QY 121 CTTTTCCTGCTGATCTTCATAGAGATTGGATAGAGTGAAGAGAGTAAACCTTCAT 180  
DB 121 CTTTTCCTGCTGATCTTCATAGAGATTGGATAGAGTGAAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTCTATTCATAAAGAGCTTAAAGATGCAAGAGAGAGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTCTATTCATAAAGAGCTTAAAGATGCAAGAGAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTCAGCAGACAG 420  
DB 361 ATTCAGCAGACAG 420  
QY 421 AAGAAAGAGATATATACATGAAAGCACTTGGTATGCTTGAAGAGAGAGAGAGAGAG 480  
DB 421 AAGAAAGAGATATATACATGAAAGCACTTGGTATGCTTGAAGAGAGAGAGAGAGAG 480  
QY 481 ACGGTTAAAG 540  
DB 481 ACGGTTAAAG 540  
QY 541 GAGCCTTCGAGTCAAGCGGCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATGGATCT 600  
DB 541 GAGCCTTCGAGTCAAGCGGCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATGGATCT 600  
QY 601 GAGAGATCTTACTCAAGCGGCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATGGATCT 660  
DB 601 GAGAGATCTTACTCAAGCGGCAATTCATCGTGGCCTCTGGCTGAAGCCAGCATGGATCT 660  
QY 661 TCTGTTCACTTGGCGGAGTGTTCATGATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 720  
DB 661 TCTGTTCACTTGGCGGAGTGTTCATGATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 781 TGA 783  
DB 781 TGA 783

RESULT 4  
US-08-982-272-2  
Sequence 2, Application US/08982272  
GENERAL INFORMATION:  
APPLICANT: Kipps, Thomas J.  
APPLICANT: Sharma, Sanjai  
APPLICANT: Cantwell, Mark  
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS

Query Match 97.1%; Score 760.6; DB 13; Length 783;  
Best Local Similarity 98.2%; Pred. No. 1.1e-179;  
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACTGGAGTCCCATCAGC 60  
DB 1 ATGATGAGAACATACAGCCAACTTCCCGCAGATCGTGGCACTGGAGTCCCATCAGC 60  
QY 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120  
DB 61 ATGAAATTTTATGATTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120  
QY 121 CTTTTCCTGCTGATCTTCATAGAGATTGGATAGAGTGAAGAGAGTAAACCTTCAT 180  
DB 121 CTTTTCCTGCTGATCTTCATAGAGATTGGATAGAGTGAAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTCTATTCATAAAGAGCTTAAAGATGCAAGAGAGAGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTCTATTCATAAAGAGCTTAAAGATGCAAGAGAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
DB 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTCAGCAGACAG 420

US-08-982-272-2



Db 361 ATTCAGCACAGTTGTAAGCGAAGCCAAACAGTAATGAGCATCCGTTCTACAGTGGCC 420  
Qy 421 AAGAAAGATATATACCATGAAGCAACTTGGTAATGCTTGAATAATGGGAACAGCTG 480  
Db 421 AAGAAAGATATATACCATGAAGCAACTTGGTAATGCTTGAATAATGGGAACAGCTG 480  
Qy 481 ACGGTTAAAGAGAGAGGACTTATATCTACACTCAAGTCACCTTCTGCTCTAATCGG 540  
Db 481 ACGGTTAAAGAGAGAGGACTTATATCTACACTCAAGTCACCTTCTGCTCTAATCGG 540  
Qy 541 GAGCCTTCGAGTCAAGCCCAATTCATCTGCGCCCTCTGGCTGAAGCCAGCATTTGATCT 600  
Db 541 GAGCCTTCGAGTCAAGCCCAATTCATCTGCGCCCTCTGGCTGAAGCCAGCATTTGATCT 600  
Qy 601 GAGAGAACTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 660  
Db 601 GAGAGAACTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 660  
Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGCTGCTTCTGCTTCTCAACCTG 720  
Db 661 TCTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGCTGCTTCTGCTTCTCAACCTG 720  
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Qy 781 TGA 783  
Db 781 TGA 783

RESULT 5  
US-08-234-580-1  
; Sequence 1, Application US/08234580  
; GENERAL INFORMATION:  
; APPLICANT: KEHRY, MERILYN R  
; APPLICANT: CASTLE, BRIAN E  
; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
; TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 100 NEW YORK AVE. N.W. SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/234,580  
; APPLICATION NUMBER: US/08/234,580  
; FILING DATE: 28-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MILLMAN, ROBERT A  
; REGISTRATION NUMBER: 36,217  
; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 818 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..795

US-08-234-580-1  
Query Match 97.1%; Score 760.6; DB 6; Length 818;  
Best Local Similarity 98.2%; Pred. No. 1.2e-179;  
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1. ATGATCGAAACATCAACCAACTTCTCCGATCTGCGGCACCTGGACTGCCATCAGC 60  
Db 13 ATGATGAAACATACAGCCACCTTCCCCAGATCCGTCGCACTGGACTTCCACCGAGC 72  
Qy 61 ATGAAATTTTATGATATTTTACTTACTGTTTCTTATCACCCTTATGATGATCTGTG 120  
Db 73 ATGAAGATTTTATGATATTTTACTTACTGTTTCTTATCACCCTTATGATGATCTGTG 132  
Qy 121 CTTTTTGTGTGATCTTCTATAGAGATTTGATAGGTCGAAGAGAGAGTAACCTTAT 180  
Db 133 CTTTTTGTGTGATCTTCTATAGAGATTTGATAGGTCGAAGAGAGAGTAACCTTAT 192  
Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAGAGAGAGGATCTTTATCC 240  
Db 193 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAGAGAGAGGATCTTTATCC 252  
Qy 241 TTGCTGAATCTGTAGGAGATGAGAAAGCAATTTGAAGACCTTTGTCAAGSATATAACGTTA 300  
Db 253 TTGCTGAATCTGTAGGAGATGAGAAAGCAATTTGAAGACCTTTGTCAAGSATATAACGTTA 312  
Qy 301 RACAAAG 360  
Db 313 AACAAAG 372  
Qy 361 ATTCAGCACAGCTTGTAAAGCGAAGCCAAACAGTAATGAGCATCCGTTCTACAGTGGCC 420  
Db 373 ATTCAGCACAGCTTGTAAAGCGAAGCCAAACAGTAATGAGCATCCGTTCTACAGTGGCC 432  
Qy 421 AAGAAAGGATATTTACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAACAGCTG 480  
Db 433 AAGAAAGGATATTTACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAACAGCTG 492  
Qy 481 ACGGTTAAAGAGAGAGGACTTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540  
Db 493 ACGGTTAAAGAGAGAGGACTTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 552  
Qy 541 GAGCCTTCGAGTCAAGCCCAATTCATCTGCGCCCTCTGGCTGAAGCCAGCATTTGATCT 600  
Db 553 GAGCCTTCGAGTCAAGCCCAATTCATCTGCGCCCTCTGGCTGAAGCCAGCATTTGATCT 612  
Qy 601 GAGAGAACTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 660  
Db 613 GAGAGAACTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGAGCAGCAG 672  
Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGCTGCTTCTGCTTCTCAACCTG 720  
Db 673 TCTGTTCACTTGGCGGAGTGTGTAATACAAAGCTGCTGCTTCTGCTTCTCAACCTG 732  
Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db 733 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 792  
Qy 781 TGA 783  
Db 793 TGA 795

RESULT 6  
US-07-969-703A-1  
; Sequence 1, Application US/07969703A  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 17

421 AGAAGAGATATATACCATGAAAGCACTTGGTAATGCTTGAATAATGGGAACAGCTG 480  
421 AGAAGAGATATATACCATGAAAGCACTTGGTAATGCTTGAATAATGGGAACAGCTG 480  
481 ACGTTAAAGAGAGAGAGACTCTATTATGCTACACCTCAAGTCACTTCTGCTCTATCGG 540  
481 ACGTTAAAGAGAGAGAGACTCTATTATGCTACACCTCAAGTCACTTCTGCTCTATCGG 540  
541 GAGCCTTCGAGTCAAGCCCAATTCATCGTGGGCTCTGGCTGAAGCCAGCAGTGGATCT 600  
541 GAGCCTTCGAGTCAAGCCCAATTCATCGTGGGCTCTGGCTGAAGCCAGCAGTGGATCT 600  
601 GAGAGATCTTACTCAAGGCGGCAAAATACCAAGTTCCTCCAGCTTTCGCGAGCAGCAG 660  
601 GAGAGATCTTACTCAAGGCGGCAAAATACCAAGTTCCTCCAGCTTTCGCGAGCAGCAG 660  
661 TCTCTTCACTTGGCGGAGTGTGTAATTAACAAGCTTGTCTCTGTTGTCAACAGTG 720  
661 TCTCTTCACTTGGCGGAGTGTGTAATTAACAAGCTTGTCTCTGTTGTCAACAGTG 720  
721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGTCTTCATCTTTTGGCTTACTCAACTC 780  
721 ACTGAAGCAAGCCCAAGTATCCACAGAGTGGTCTTCATCTTTTGGCTTACTCAACTC 780  
781 TGA 783  
781 TGA 783

Correspondence Address:  
Addressee: Immunex Corporation  
Street: 51 University Street  
City: Seattle  
State: Washington  
Country: USA  
Zip: 98101  
Computer Readable Form:  
Medium Type: Floppy disk  
Computer: IBM PC compatible  
Operating System: PC-DOS/MS-DOS  
Software: Patent In Release #1.0, Version #1.25  
Current Application Data:  
Application Number: US/07/969,703A  
Filing Date: 19921023  
Classification: 435  
Attorney/Agent Information:  
Name: Perkins, Patricia A.  
Registration Number: 34,693  
Reference/Docket Number: 2802-B  
Telecommunication Information:  
Telephone: 2065870606  
Telefax: 2065870606  
Information for Seq. ID. No. 1:  
Sequence Characteristics:  
Length: 783 base pairs  
Type: Nucleic Acid  
Strandedness: single  
Topology: linear  
Molecule Type: cDNA  
Hypothetical: NO  
Anti-Sense: NO  
Original Source:  
Organism: Mouse  
Immediate Source:  
Clone: CD40-L  
Feature:  
Name/Key: CDS  
Location: 1..783  
US-07-969-703A-1

Query Match 96.9%; Score 759; DB 3; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCAACATACAACTCTCCCGATCTCGGCACTGGACTGCCCATCAGC 60  
DB 1 ATGATGAACATACAGCACTCTCCCGATCTCGGCACTGGACTGCCCATCAGC 60  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACTCCCAATGATGGATCTG 120  
DB 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACTCCCAATGATGGATCTG 120  
QY 121 CTTTTCGTGTATCTTATCAAGATGGAATGATGATGATGATGATGATGATGAT 180  
DB 121 CTTTTCGTGTATCTTATCAAGATGGAATGATGATGATGATGATGATGATGAT 180  
QY 181 GAAGATTTTATTTATTAATAAAGCTTAAAGAGATGCAAAAGAGAGAGATCTTATCC 240  
DB 181 GAAGATTTTATTTATTAATAAAGCTTAAAGAGATGCAAAAGAGAGAGATCTTATCC 240  
QY 241 TTGCTGAACGTGAGGAGATGAGAGCAATTTGAAGCTTCTCAAGGATATAAGCTTA 300  
DB 241 TTGCTGAACGTGAGGAGATGAGAGCAATTTGAAGCTTCTCAAGGATATAAGCTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTGAGCAGACAGTTGTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
DB 361 ATTGAGCAGACAGTTGTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..780  
US-08-107-353-5

Query Match 96.9%; Score 759; DB 5; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 60  
DB 1 ATGATGAGAACATACAGCAACCTTCCCGAGATCGGTGGCACTTCCAGCGAGC 60  
QY 61 ATGAAATTTTATCTTACTTACTTCTTCTTATCACCCTTATCACCCTTATGATCTGGT 120  
DB 61 ATGAGATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATGATCTGGT 120  
QY 121 CTTTTTGTCTGATCTTTCATAGAAGATTGGATAAGTGTGAAGAGGAGAACTTTCAT 180  
DB 121 CTTTTTGTCTGATCTTTCATAGAAGATTGGATAAGTGTGAAGAGGAGAACTTTCAT 180  
QY 181 GAAGATTTTGTATTCATTAAGAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTGTATTCATTAAGAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
DB 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTGAGCAGCAGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
DB 361 ATTGAGCAGCAGCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 421 AAGAAAGAGATATTACCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 421 AAGAAAGAGATATTACCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 481 ACGGTTAAAG 540  
DB 481 ACGGTTAAAG 540  
QY 541 GAGCCTTCGAGTCAAGGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600  
DB 541 GAGCCTTCGAGTCAAGGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGGATCT 600  
QY 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTCTCCCGAGCTTTGGCAGCAGCAG 660  
DB 601 GAGAGATCTTACTCAAGCGGCAATACCCACAGTCTCCCGAGCTTTGGCAGCAGCAG 660  
QY 661 TCTGTTCACTTGGGGGAGTGTGAAATPACAGAGTGTGCTTCTGCTTTTGTCAACAGTG 720  
DB 661 TCTGTTCACTTGGGGGAGTGTGAAATPACAGAGTGTGCTTCTGCTTTTGTCAACAGTG 720  
QY 721 ACTGAAGCAAGCAAGTATTCACAGAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
DB 721 ACTGAAGCAAGCAAGTATTCACAGAGTGTGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
QY 781 TGA 783  
DB 781 TGA 783

RESULT 8  
US-08-477-733A-1

; Sequence 1, Application US/08477733A  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,733A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1...783  
US-08-477-733A-1

Query Match 96.9%; Score 759; DB 8; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAGACATACCAACAACTTCTCCCGATCTGGGCCACTGGAGTCCCATCAGC 60  
DB 1 ATGATGAGAACATACAGCAACCTTCCCGAGATCGGTGGCACTTCCAGCGAGC 60  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCCTTATCACCCTTATGATCTG 120

OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: IUS/98/484, 524

FILING DATE: 07/969.703  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA: 08/249,189  
 APPLICATION NUMBER: 07/805,723  
 FILING DATE: May 24, 1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA: 07/969.703  
 APPLICATION NUMBER: 07/969.703  
 FILING DATE: October 23, 1992  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA: 07/805,723  
 APPLICATION NUMBER: 07/805,723  
 FILING DATE: December 5, 1991  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA: 07/783,707  
 APPLICATION NUMBER: 07/783,707  
 FILING DATE: October 25, 1991  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia A.  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2802  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 2065870430  
 TELEFAX: 2065870506  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 783 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: gDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: MOUSE  
 IMMEDIATE SOURCE:  
 CLONE: CD40-L  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..783  
 -84-624-1  
 PS-08-48A-624-1

DB 8: Length 783;

Query Match	96.9%	Score:759;	DB 8;	Length 783;
Best Local Similarity	98.1%	Pred. NO: 2.9e-179;		
Matches 768; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;

QY	1	ATGATCGAACAATACAGCAAACTTCTCCCGATCTGCGGCCACCTGGAGTCGCCCATCAGC	60
DB	1	ATGATAGAAACATACAGCCAACTTCCCCAGATCGTGGCAACTGGACTTCGACGAGC	60
QY	61	ATGAAATATTTTAGTATTACTTACTGTGTTCTTATCACCACCAATGATTGGATCTGTG	120
DB	61	ATGAAGATTTTATGTATTACTTACTGTGTTCTTATCACCCAATGATTGGATCTGTG	120
QY	121	CTTTTTCGTGTGATCTTTCATAGAAGATTGGATAAGGTGGAAGAGAACTTAACCTTCAT	180
DB	121	CTTTTTCGTGTGATCTTTCATAGAAGATTGGATAAGGTGGAAGAGAACTTAACCTTCAT	180
QY	181	GAAGATTTTGTTATTCATAAAAAGCTAAAGAGATGCAACAAGAGGAAAGGATCTTTTATCC	240
DB	181	GAAGATTTTGTTATTCATAAAAAGCTAAAGAGATGCAACAAGAGGAAAGGATCTTTTATCC	240
QY	241	TGTCGTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGAGATATAAGCTTA	300
DB	241	TGTCGTGAACCTGTAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGAGATATAAGCTTA	300
DB			

DEPT. 9

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1  US-08-484-624-1
2  Sequence 1, Application US/08484624
3  GENERAL INFORMATION:
4  APPLICANT: ARMITAGE, RICHARD
5  APPLICANT: FLOW, WILLIAM
6  APPLICANT: SPRIGGS, MELANIE
7  APPLICANT: SRINIVASAN, SUBHASHI
8  APPLICANT: GIBSON, MARYLOU
9  TITLE OF INVENTION: NOVEL CYTOK
10 NUMBER OF SEQUENCES: 24
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: IMMUNEX CORPORATION
13 STREET: 51 UNIVERSITY STREET
14 CITY: SEATTLE
15 STATE: WASHINGTON
16 COUNTRY: USA
17 ZIP: 98101
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: Apple Macintosh

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|||||
Db 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGGTGATGAGGATCCTCAA 360
Qy 361 ATTGAGCACACGTTGTAAAGGAGAGCCCAACAGTATGAGGATCGTGTCTACAGTGGCC 420
Db 361 ATTGAGCACACGTTGTAAAGGAGAGCCCAACAGTATGAGGATCGTGTCTACAGTGGCC 420
Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGGACTCTATTATGCTTACACTCAAGTCAAGTCTTCTGCTCAATCGG 540
Db 481 ACGGTTAAAGAGAGGACTCTATTATGCTTACACTCAAGTCAAGTCTTCTGCTCAATCGG 540
Qy 541 GAGCCTTCGAGTCAAGCCCAATTCATCGTGGCTCTGGCTGAAGCCAGCATGGATCT 600
Db 541 GAGCCTTCGAGTCAAGCCCAATTCATCGTGGCTCTGGCTGAAGCCAGCATGGATCT 600
Qy 601 GAGAGAACTTTACTCAAGCGGCGCAAAATACCCACAGTTCCTCCAGCTTTGCGAGCAG 660
Db 601 GAGAGAACTTTACTCAAGCGGCGCAAAATACCCACAGTTCCTCCAGCTTTGCGAGCAG 660
Qy 661 TCTGTTCACTTGGCGGAGTGTGAATTACAGCTGCTTCTGCTTCTGCTCAAGCTG 720
Db 661 TCTGTTCACTTGGCGGAGTGTGAATTACAGCTGCTTCTGCTTCTGCTTCTCAAGCTG 720
Qy 721 ACTGAAGCAAGCAAGTGCATCCAGAGTTCGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGCATCCAGAGTTCGCTTCTCATCTTTGGCTTACTCAAACTC 780
Qy 781 TGA 783
Db 781 TGA 783

```

RESULT 10

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US-08-770-981-1
: Sequence 1, Application US/08770981
: GENERAL INFORMATION:
: APPLICANT: FANSLAW, RICHARD
: APPLICANT: SPRIGGS, MELANIE
: APPLICANT: SRINIVASAN, SUBHASHINI
: APPLICANT: GIBSON, MARYLOU
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: IMMUNEX CORPORATION
: STREET: 51 UNIVERSITY STREET
: CITY: SEATTLE
: STATE: WASHINGTON
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple Operating System 7.1
: SOFTWARE: Microsoft Word for Apple, version 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08770, 981
: FILING DATE: 20-DEC-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/477, 733
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/249, 189
: FILING DATE: May 24, 1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969, 703
: FILING DATE: October 23, 1992
: CLASSIFICATION: 435

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/805, 723
: FILING DATE: December 5, 1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/783, 707
: FILING DATE: October 25, 1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia A.
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2802-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 2065870430
: TELEFAX: 2065870606
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 783 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: MOUSE
: IMMEDIATE SOURCE:
: CLONE: CD40-L
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..783
: US-08-770-981-1

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Query Match 96.9%; Score 759; DB 11; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACAACTCTCCCGATCTCGCGCACCTGGAGTCCGCCATCAGC 60
Db 1 ATGATCGAAACATACAGCCAACTTCCCGCAGATCCGTTGGCAACTGGACTTCCAGCGAGC 60
Qy 61 ATGAAATTTTATGATTTACTTCTCTCTTATCACCCTTATCACCCTTATGATGATCTGTG 120
Db 61 ATGAAATTTTATGATTTACTTCTCTCTTATCACCCTTATCACCCTTATGATGATCTGTG 120
Qy 121 CTTTTCGTGTGATCTTCATAGAGATTTGATAGTTCGAGAGAGAGTAACTTTCAT 180
Db 121 CTTTTCGTGTGATCTTCATAGAGATTTGATAGTTCGAGAGAGAGTAACTTTCAT 180
Qy 181 GAAGATTTTGTATTATCAATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTATCAATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Db 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300
Qy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 ATTGAGCACACGTTGTAAAGGAGAGCCCAACAGTATGAGGATCGTGTCTACAGTGGCC 420
Db 361 ATTGAGCACACGTTGTAAAGGAGAGCCCAACAGTATGAGGATCGTGTCTACAGTGGCC 420
Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAGCTG 480
Qy 481 ACGGTTAAAGAGAGGAGTCTTATGCTTACACTCAAGTCAAGTCTTCTGCTCAATCGG 540
Db 481 ACGGTTAAAGAGAGGAGTCTTATGCTTACACTCAAGTCAAGTCTTCTGCTCAATCGG 540

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QY 541 GAGCCTTCAGTCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
Db 541 GAGCCTTCAGTCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
QY 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTCTCTCTCTCTCTCTCT 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTCTCTCTCTCTCTCTCT 720
QY 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 TGA 783
Db 781 TGA 783

```

RESULT 11

```

US-09-088-913-1
; Sequence 1, Application US/09088913
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,913
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,624
; FILING DATE:
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MOUSE
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
; US-09-088-913-1.

Query Match 96.9%; Score 759; DB 14; Length 783;
Best Local Similarity 98.1%; Pred. No. 2.9e-179;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGCGCCACTGACTGGCCATCAGC 60
Db 1 ATGATAGAAACATACACCAAACTTCTCCCGAGATCCCGGATCGGTGGCAACTGGACTTCCAGCAGC 60
QY 61 ATGAAATTTTATGTTATTTACTTACTTCTTCTTCTTATCACCACAAATGATGTGATCTGTG 120
Db 61 ATGAAGATTTTATGTTATTTACTTACTTCTTCTTCTTATCACCACAAATGATGTGATCTGTG 120
QY 121 CTTTTCGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGGAGGAAGTAAACCTTCAT 180
Db 121 CTTTTCGCTGTATCTTCATAGAGATTGGATAGGTGCGAAGGAGGAAGTAAACCTTCAT 180
QY 181 GAAGATTTTGTATTCAATAAAAGCTAAAGAGATGCAACAAAGGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCAATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
QY 241 TTGCTGAACTGTAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACCTTA 300
Db 241 TTGCTGAACTGTAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATAACCTTA 300
QY 301 AACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ATTGCAGCACACGTTGTAGCGAAGCCCAACAGTATGAGCATCGGTTCTACAGTGGGCC 420
Db 361 ATTGCAGCACACGTTGTAGCGAAGCCCAACAGTATGAGCATCGGTTCTACAGTGGGCC 420
QY 421 AGAAGAGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCTG 480
Db 421 AGAAGAGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGGAAACAGCTG 480
QY 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GAGCCTTCGAGTCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
Db 541 GAGCCTTCGAGTCAACGCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCAATGGATCT 600
QY 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
Db 601 GAGAGAATCTTACTAAGCGGCAATACCCACAGTTCCTCCAGCTTTGGAGCAGCAG 660
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTCTCTCTCTCTCTCTCTCT 720
Db 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAGCTGGTCTCTCTCTCTCTCTCTCTCT 720
QY 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 ACTGAAGCAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 781 TGA 783

```

Db 781 TGA 783

RESULT 12

US-09-322-021-1

Sequence 1, Application US/09322021

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: Microsoft Word for Apple, version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09322,021

FILING DATE:

CLASSIFICATION:

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/249,189

FILING DATE:

CLASSIFICATION:

Prior APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

CLASSIFICATION:

Prior APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: MOUSE

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783

US-09-322-021-1

Query Match 96.9%; Score 759; DB 17; Length 783;

Best Local Similarity 98.1%; Pred. No. 2.9e-179;

Matches 766; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60

Db 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60

Qy 61 ATGAAATTTTATGTATTTTACTTCTTTTCTTATCACCRAATGATTGGATCTGTG 120

Db 61 ATGAAGATTTTATGTATTTTACTTCTTTTCTTATCACCRAATGATTGGATCTGTG 120

Qy 121 CTTTTTGTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAGTAAGTAACCTTCA 180

Db 121 CTTTTTGTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAGTAAGTAACCTTCA 180

Qy 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAGAGAGAGAGATCTTTATCC 240

Db 181 GAAGATTTTGTATTATATAAAGCTAAAGAGATGCAACAAGAGAGAGAGATCTTTATCC 240

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300

Db 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300

Qy 301 AACAAAG 360

Db 301 AACAAAG 360

Qy 361 ATTCAGCACACAGTTGTAAAGCGAAGCCAAACAGTAATGCAGCATCCGTTTCTACAGTGGCC 420

Db 361 ATTCAGCACACAGTTGTAAAGCGAAGCCAAACAGTAATGCAGCATCCGTTTCTACAGTGGCC 420

Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTTGGTAATGCTTGAAGATGGGAAGAGAGAG 480

Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTTGGTAATGCTTGAAGATGGGAAGAGAGAG 480

Qy 481 ACGGTTAAAG 540

Db 481 ACGGTTAAAG 540

Qy 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGCCCTCTGGCTGAAGCCAGCAGTGGATCT 600

Db 541 GAGCCTTCGAGTCAACGCCCATTCATCTCGCCCTCTGGCTGAAGCCAGCAGTGGATCT 600

Qy 601 GAGAGATCTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGCAGCAGAG 660

Db 601 GAGAGATCTTACTCAAGCGGCGCAATACCCACAGTTCTCCAGCTTTGGCAGCAGAG 660

Qy 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGTGCTTCTGTTGTCAACGTG 720

Db 661 TCTGTTCACTTGGCGGAGTGTGTAATTAACAAGCTGTGCTTCTGTTGTCAACGTG 720

Qy 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780

Db 721 ACTGAAGCAAGCCCAAGTGATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780

Qy 781 TGA 783

Db 781 TGA 783

RESULT 13

US-09-322-021A-1

Sequence 1, Application US/09322021A

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: FANSLAW, WILLIAM

APPLICANT: SPRIGGS, MELANIE

APPLICANT: SRINIVASAN, SUBHASHINI

APPLICANT: GIBSON, MARYLOU

TITLE OF INVENTION: NOVEL CYTOKINE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/322.021A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-09-322-021A-1

Query Match 96.9%; Score 759; DB 17; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	1	ATGATCGAACAATACAAACAACTCTCCCGCATCTCGCGCACTGGCACTGCCCATCAGC	60
DB	1	ATGATGAGAAACATACAGCCAACTCTCCCGCATCTCGCGCACTGGCACTGCCCATCAGC	60
QY	61	ATCAAAATTTTATGTATTTACTTACTGTCTTATACCCCAATGATTGGATCTGTG	120
DB	61	ATCAAAATTTTATGTATTTACTTACTGTCTTATACCCCAATGATTGGATCTGTG	120
QY	121	CTTTTTCGTGTATCTTCATAGAGATTGGATAGGTGGAAGAGAACTTCAAT	180
DB	121	CTTTTTCGTGTATCTTCATAGAGATTGGATAGGTGGAAGAGAACTTCAAT	180
QY	181	GAGATTTTCTATTATCAAAAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC	240
DB	181	GAGATTTTCTATTATCAAAAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC	240
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAGACCTTGTCAAGATATAACGTTA	300
DB	241	TTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAGACCTTGTCAAGATATAACGTTA	300

QY	301	ARCAAGAAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGAGGTGATGAGGATCCTCAA	360
DB	301	ARCAAGAAGAGAAAAAGAAACAGCTTTGAAATGCAAGAGAGGTGATGAGGATCCTCAA	360
QY	361	ATTGAGCAGCACGTTTGTAAAGCAAGCCCAACAGTAATGAGCATCGTTCTACAGTGGGCC	420
DB	361	ATTGAGCAGCACGTTTGTAAAGCAAGCCCAACAGTAATGAGCATCGTTCTACAGTGGGCC	420
QY	421	AGAGAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG	480
DB	421	AGAGAAGGATATATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG	480
QY	481	ACGTTTAAAGAGAGAGAGACTCTATTATGCTACACTCAAGTACACTTCTGCTCTAATCGG	540
DB	481	ACGTTTAAAGAGAGAGAGACTCTATTATGCTACACTCAAGTACACTTCTGCTCTAATCGG	540
QY	541	GAGCCTTCGAGTCAAGCCCATTCATCGTCGGCTCTCGCTCAAGCCCAAGCAGTGGATCT	600
DB	541	GAGCCTTCGAGTCAAGCCCATTCATCGTCGGCTCTCGCTCAAGCCCAAGCAGTGGATCT	600
QY	601	GAGAGATCTTACTCAAGCGGCAATACCCAGTTCCTCCAGCTTTCGCGAGCAGCAG	660
DB	601	GAGAGATCTTACTCAAGCGGCAATACCCAGTTCCTCCAGCTTTCGCGAGCAGCAG	660
QY	661	TCGTTTCACTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTTCTGTTGTCAACGTG	720
DB	661	TCGTTTCACTTGGCGGAGTGTGTTGAATTACAAGCTGGTCTTCTGTTGTCAACGTG	720
QY	721	ACTGAAGCAAGCCCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC	780
DB	721	ACTGAAGCAAGCCCAAGTATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAACTC	780
QY	781	TGA 783	
DB	781	TGA 783	

RESULT 14  
US-09-365-940-1  
Sequence 1, Application US/09365940  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANLOW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,940  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992



CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-09-365-940A-1

Query Match 96.9%, Score 759; DB 17; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 60  
Db 1 ATGATGAAGACATACAGCACTTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 60

Qy 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTATFACCCCAATGATGATCTGTG 120  
Db 61 ATGAAGATTTTATGATTTACTTACTCTTTTCTTATFACCCCAATGATGATCTGTG 120

Qy 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAGATTAACCTTCAT 180  
Db 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAGATTAACCTTCAT 180

Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
Db 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240

Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTGGAAGACCTTGTCAAGGATATAACGTTA 300  
Db 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTGGAAGACCTTGTCAAGGATATAACGTTA 300

Qy 301 AACAAAG 360  
Db 301 AACAAAG 360

Qy 361 ATTGAGCAGACAGTTGTGAAGCGAGCCCAACAGTAAATGAGAGATCGTTCTACAGTGGCC 420  
Db 361 ATTGAGCAGACAGTTGTGAAGCGAGCCCAACAGTAAATGAGAGATCGTTCTACAGTGGCC 420

Qy 421 AAGAAAGGATATTACCATGAAAGCAACTTGGTAATGCTTTGAAATGGGAAACAGCTG 480  
Db 421 AAGAAAGGATATTACCATGAAAGCAACTTGGTAATGCTTTGAAATGGGAAACAGCTG 480

Qy 481 ACGGTTAAAG 540  
Db 481 ACGGTTAAAG 540

Db 481 ACGGTTAAAG 540

Qy 541 GAGCCTTCAGTCAACGCCCATTCATCTCGGCCTCTGGCTCAAGCCAGCATTCGATCT 600  
Db 541 GAGCCTTCAGTCAACGCCCATTCATCTCGGCCTCTGGCTCAAGCCAGCATTCGATCT 600

Qy 601 GAGAGAATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGCAG 660  
Db 601 GAGAGAATCTTACTCAAGCGCGCAATACCCACAGTTCCTCCAGCTTTGGCAGCAGCAG 660

Qy 661 TCTGTTCACTTGGCGGAGTGTTCGAATACAAAGCTGCTCTCTGTTGTCACAGTG 720  
Db 661 TCTGTTCACTTGGCGGAGTGTTCGAATACAAAGCTGCTCTCTGTTGTCACAGTG 720

Qy 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780

Qy 781 TGA 783  
Db 781 TGA 783

RESULT 15  
US-09-365-940A-1  
Sequence 1, Application US/09365940A  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, Richard, J.  
APPLICANT: FANSLAW, III, William, C.  
APPLICANT: SPRIGGS, Melanie, K.  
TITLE OF INVENTION: METHOD OF TREATING AN UNDESIRE IMMUNE RESPONSE BY BLOCKING TH  
TITLE OF INVENTION: OF CD40 LIGAND TO CD40  
FILE REFERENCE: 2802-K  
CURRENT APPLICATION NUMBER: US/09/365,940A  
CURRENT FILING DATE: 1999-08-02  
PRIOR APPLICATION NUMBER: 08/249,189  
PRIOR FILING DATE: 1994-05-24  
PRIOR APPLICATION NUMBER: 07/969,703  
PRIOR FILING DATE: 1992-10-23  
PRIOR APPLICATION NUMBER: 07/805,723  
PRIOR FILING DATE: 1991-12-05  
PRIOR APPLICATION NUMBER: 07/783,707  
PRIOR FILING DATE: 1991-10-25  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 783  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(783)  
OTHER INFORMATION:  
US-09-365-940A-1

Query Match 96.9%, Score 759; DB 17; Length 783;  
Best Local Similarity 98.1%; Pred. No. 2.9e-179;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATCGAAACATCAACAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC 60  
Db 1 atgataaacaacatacagcacaacctccccagatccgagcaactggacttccagcagc 60

Qy 61 ATGAAATTTTATGATTTACTTACTCTTTTCTTATFACCCCAATGATGATCTGTG 120  
Db 61 atgaagattttatgtatttacttactgttttcttattcaccacaaatgatggatctgtg 120

Qy 121 CTTTTGCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAGATTAACCTTCAT 180  
Db 121 ctttttgcgtgtatcttcataagaatctgataagaatctgataagaatctgataagaatcttccat 180

Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGAGAGAGAGATCTTTATCC 240

Thu May 30 05:46:13 2002

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181 gaagattttgtattcataaaagctaaagagatgcaacaagagagagatctttatcc 240
241 TTGCTGAAGTGTGAGGAGTGAAGGCAATTTGAAGACCTTTGTCAAGGATATTAACGTTA 300
241 ttgctgaagctgtgagagatgagaaggcaatttgaagaccttgcaggatataacgtta 300
301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
301 aacaaagagagagagagagagagagagagagagagagagagagagagagagagagag 360
361 ATTGCAGCAGCTTGTATACCCAGCCAGCCAGCTAATGAGCATCGTTCTACAGTGGGCC 420
361 attgcagcacagctgtgtatgccagccagccagctaatgagcatcgtttctacagtgggcc 420
421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTTGAAAATGGGAAACAGCTG 480
421 aagaaaggatatttatccatgaaagcaacttggtaatgctttgaaaatgggaaacagctg 480
481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
481 acggttaaagagagagagagagagagagagagagagagagagagagagagagagagag 540
541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCTCTGCTGAAGCCAGCATTTGGATCT 600
541 gagccttcgagtcacgcccatctcatcgctggctctgctgaagccagcatTTGGATCT 600
601 GAGAGAATCTTACTCAAGGCGGCAATFACCCAGTTCCTCCAGCTTTGCCGAGCAGCAG 660
601 gagagaatcttactcaaggcgcaatfaccagttcctccagctttgccgagcagcag 660
661 TCTGTTCACTTGGCGGAGTGTGTTGAATTAAGCTGGTCTGCTGTTGTTGTTCAACGTTG 720
661 tctgttcacttggcgagtggttgaattaaagctggctgctgctgctgctgctgctgctg 720
721 ACTGAAGCAAGCCAGAGTATCCAGAGTTGGCTTCTATCTTTTGGCTTACTCAAACTC 780
721 actgaagcaagccagagtattccagagttggcttctatcttttggcttactcaaaactc 780
781 TGA 783
781 tga 783

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Search completed: May 30, 2002, 05:23:00  
Job time: 18659 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:39:00 ; Search time 627.19 Seconds  
(without alignments)  
1310.273 Million cell updates/sec

Title: US-08-982-272-5  
Perfect score: 783  
Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

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- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	759	96.9	1250	5	US-09-053-375B-821
2	582.8	74.4	1816	5	US-09-053-375B-226
3	582.8	74.4	1816	5	US-09-442-384B-457
4	315	40.2	508	5	US-09-911-904-131
5	146.2	18.7	2395	5	US-09-875-453A-9
6	38.4	4.9	45698	6	US-10-105-299-12515
7	38.4	4.9	65566	5	US-09-830-706B-37
8	38	4.9	476	6	US-10-027-632-187249
9	38	4.9	476	6	US-10-027-632-187250
10	37.6	4.8	685	6	US-10-027-632-35082
11	37.6	4.8	349	5	US-09-721-544-11180
12	37	4.7	1758	6	US-10-071-192-29
13	36.6	4.7	341	5	US-09-789-189-555
14	36.6	4.7	57649	6	US-10-105-299-9151
15	36.6	4.7	57649	6	US-10-105-299-10646
16	36.6	4.7	57649	6	US-10-105-299-14274
17	36.2	4.6	2430	6	US-10-105-694-1
18	36.2	4.6	2430	6	US-10-105-695-1
19	35.2	4.6	2430	6	US-10-106-014-1
20	36	4.6	1379	6	US-10-027-632-199307
21	35.8	4.6	598	6	US-10-027-632-207524
22	35.8	4.6	2580	6	US-10-027-632-258659
23	35.6	4.5	626	6	US-10-027-632-239684
24	35.6	4.5	712	6	US-10-106-698-1404
25	35.6	4.5	1640	6	US-10-106-698-499
26	35.6	4.5	1665	5	US-09-919-002-8655

## ALIGNMENTS

RESULT 1  
US-09-053-375B-821  
; Sequence 821, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 821  
; LENGTH: 1250  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-053-375B-821

Query Match	96.9%	Score 759;	DB 5;	Length 1250;
Best Local Similarity	98.1%	Pred. No. 2.8e-184;		
Matches	768;	Conservative	0;	Mismatches 15;
		Indels	0;	Gaps
QY	1	ATGATCGAATAACAACTTCTCCCGATCTGCGGCACCTGGAGTCCCATCAGC	60	Sequence 219364,
				Sequence 219365,
Db	13	atgataaataacacagccacacccacagatcggtgcaactggacttcacagcagc	72	Sequence 233265,
				Sequence 111808,
QY	61	ATGAAATTTTATCTATTTACTTCTCTTCTTATCACCACCAATGATTGATCTGTG	120	Sequence 141134,
				Sequence 380, App
Db	73	atgaagattttatgtatttatttacttcttcttccatcccaaatgattgattctgtg	132	Sequence 270, App
				Sequence 362, App
QY	121	CTTTTGTCTGTATCTTCTATAGAGATGGAAGTGTGAAGAGAGAGAGAGAGAGAG	180	Sequence 85186, A
				Sequence 85187, A
Db	133	ctttttgtctgtatttcttcatagagattggaagtcgaagaggaagaaacattcat	192	Sequence 46525, A
				Sequence 46526, A
QY	181	GAAGATTGTGTTTATTAATAAAGCTTAAGAGATGCAACAAAGAGAGAGAGAGAG	240	Sequence 200394,
				Sequence 317028,
Db	193	gaagattttgtatttcttcaaaagcgttaagagatgcaacaaaggaaggaattctatcc	252	Sequence 317029,
				Sequence 228875,
QY	241	TTGCTGAATCTGTGAGAGATGAGAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA	300	Sequence 233425,
Db	253	ttgctgaactgtgagagagatggaagcctttgaagaccttgcgaagataataagctta	312	
QY	301	ACAAAG	360	
Db	313	acaaagaag	372	
QY	361	ATTGAGCAGCACCTTGTGAAGCAAGCAACATATGACGATCCGTTCTACAGTGGGCC	420	

Thu May 30 05:46:15 2002

Db 373 attgagcacacgttgtaagcgaggaagccaaagtaagcagcatcgcttctacatgagcc 432  
 QY 421 AAGAAAGGATATATACCATGAAAGCAAGCACTTGGTAAATGCTTGAATGGGAAACAGCTG 480  
 Db 433 aagaagagattatataccatgaagcaacttggttaagcttgaaatgggaaacagctg 492  
 QY 481 ACGGTTAAAGAGAGGAGCTCTATATGCTACACTCAAGTCAAGTCTGCTCTAAATCGG 540  
 Db 493 acggttaaaagagaagactctatgtctacactcaagtcacactctctctaaatcg 552  
 QY 541 GAGCCTTCGAGTCAACGCCCATTCATCTGCTGGCCCTCTGGCTGAAGCCAGCAGATGGATCT 600  
 Db 553 gagccttcgagtcacagccattcatcgctggcctctgctgaagccagcagtgatct 612  
 QY 601 GAGAGATCTTACTCAAGGGGGCAATACCCAGCTTCTCCAGCTTTGGCAGCAGCAG 660  
 Db 613 gagagatcttactcaagggcggaataaccacagctctccacagcttgcgagcagcag 672  
 QY 661 TCTGCTTCACTTGGCGGAGGTGTTGAATTAACAAGCTGGTCTCTGCTGTTCTCAACG 720  
 Db 673 tctgttcaactggcgagtggtttgaattacaagctgggtctctgtgttgcaacg 732  
 QY 721 ACTGAAGCAAGCAAGTGATCCAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780  
 Db 733 actgaagcaagccaagtgtatccacagagttggtctctctcttcttggcttactcaaac 792  
 QY 781 TGA 783  
 Db 793 tga 795

RESULT 2  
 US-09-053-375B-226  
 ; Sequence 226, Application US/09053375B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenchik, Alex  
 ; APPLICANT: Bibilashvili, Robert  
 ; TITLE OF INVENTION: Nucleic Acid Arrays  
 ; FILE REFERENCE: CLON-006  
 ; CURRENT APPLICATION NUMBER: US/09/053, 375B  
 ; CURRENT FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 1543  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 226  
 ; LENGTH: 1816  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-053-375B-226

Query Match 74.4%; Score 582.8; DB 5; Length 1816;  
 Best Local Similarity 84.7%; Pred. No. 3.1e-139;  
 Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;  
 QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGGACTGCCATCAGC 60  
 Db 40 atgacgaacatacaaccaacttctcccgatctgagccactgagccatcagc 99  
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGCAATGATGATCTGTG 120  
 Db 100 atgaaattttattgtatttacttactgttttcttataccacagatgattggttcagca 159  
 QY 121 CTTTGTGCTGATCTATCTATAGAGATTTGGATAAGGTGCGAAGGAGGAGTAAACCTTCAT 180  
 Db 160 ctttgtgctgtatcttca tagaaggttggaagaagataagaagataaagaaatcttcat 219  
 QY 181 GAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACAAAGAGAGAGGATCTTTATCC 240  
 Db 220 gaagatttttattatcatgaacacgatacagagatgcaacacagagagagaaatcttctatoc 279  
 QY 241 TTGCTGAAGTGTGAGGAGATGAGGAGCAATTTGAGACCTTGTCAAGGATATTAACCTTA 300  
 Db 280 ttactgaactgtgagagattaaagccagcttggaaggtcttggaaggaataaattta 339

QY 301 AACAAAGAGA---CAAAAAAGAAACAGCTTGAATGCAAAAGAGGTGATGAGATCCT 357  
 Db 340 aacaaagggagacagaagaagaacagcttggaaatgcaaaaggtgatcagaatcct 399  
 QY 358 CAATTTGACGACACAGCTTGTAAAGCGAAGCAACAGTAAATGAGCATCGTTCTACAGTGG 417  
 Db 400 caaatgcygcacatgctcaatgaagtggccagcagtaaaacaacatctgtgttaccagtcg 459  
 QY 418 GCCAAGAAAGGATATATACCATGAAAGCAACTTGGTAAATGCTTGAATGGGAAACAG 477  
 Db 460 gctgaaaaaggatactacacattgagcaacaacttggtaaccctggaataatgggaaacag 519  
 QY 478 CTGACGTTAAAGAGAGAGACTCTATTATGCTACACTCAAGTCAAGTCTGCTCTTAAT 537  
 Db 520 ctgacgcttaaaagacaagactctattatctatgcccacagtcacactctgttcccaat 579  
 QY 538 CGGAGGCTTCGAGTCAACGCCCATTCATCTGCTGGCTGCTGAGCCAGCAGCATTTGGA 597  
 Db 580 cggaagcttcgagtcgaagctccattattatagccagcctctgctaaagtcccccgtaga 639  
 QY 598 TCTGAGAGAACTTACTCAAGGGCGCAATACCCAGCTTCTCCAGCTTTCCGAGCAG 657  
 Db 640 ttcgagagaacttactcagagctgcaaataccacacagttccgcaaacacttgcgggcaa 699  
 QY 658 CAGCTGTTCACTTGGCGGAGTGTGTTGAATTAACAAGCTGGTCTGCTCTGTTGTTCAAC 717  
 Db 700 caatccattcacttgggagagatttgaattgcaaccaggtcttcggtgttgcatt 759  
 QY 718 GTGACTGAAGCAAGCTGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAA 777  
 Db 760 gtgactgatccaaagcgaagtggcctgagccatggcactggtcttcacgtcttcttactcaaa 819  
 QY 778 CTCTGA 783  
 Db 820 ctctga 825

RESULT 3  
 US-09-442-384B-457  
 ; Sequence 457, Application US/09442384B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenchik, Alex  
 ; APPLICANT: Lukashev, Matvey  
 ; TITLE OF INVENTION: Hematology/Immunology Array  
 ; FILE REFERENCE: CLON-006CIP15  
 ; CURRENT APPLICATION NUMBER: US/09/442, 384B  
 ; CURRENT FILING DATE: 1999-11-17  
 ; PRIOR APPLICATION NUMBER: 09/053, 375  
 ; PRIOR FILING DATE: 1998-03-31  
 ; NUMBER OF SEQ ID NOS: 830  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 457  
 ; LENGTH: 1816  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-442-384B-457

Query Match 74.4%; Score 582.8; DB 5; Length 1816;  
 Best Local Similarity 84.7%; Pred. No. 3.1e-139;  
 Matches 666; Conservative 0; Mismatches 117; Indels 3; Gaps 1;  
 QY 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGCGGCCACTGGACTGCCATCAGC 60  
 Db 40 atgacgaacatacaaccaacttctcccgatctgagccactgagccatcagc 99  
 QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGCAATGATGATCTGTG 120  
 Db 100 atgaaattttattgtatttacttactgttttcttataccacagatgattggttcagca 159  
 QY 121 CTTTGTGCTGATCTATCTATAGAGATTTGGATAAGGTGCGAAGGAGGAGTAAACCTTCAT 180



Thu May 30 05:46:15 2002

Qy	1	ATATCGAAACATACAAACCAATTTCTCCCGATCTGGGCCACTGGACATGCCCATCAGC	60
Db	1939	atgatcgaaacatacaaaccaactctcccgatctcgccactggactgcccatacgc	1998
Qy	61	ATGAAATATTTATGTPATTTACTTACTGTTTCTTTATCACCCAAATGATGGATCTGTG	120
Db	1999	atgaaaattttatgtatttactactgtttttcttataccccagatgattgggtcagca	2058
Qy	121	CTTTTTCCTGTGATCTTCATAGAAGATGGATAAAGTTCGAAGAGGAAGTAAACCTTCAT	180
Db	2059	ctttttgctgtgtattcttcatagaaggctggacaaggtaagatgaaccacaagcctttat	2118
Qy	181	GAA	183
Db	2119	taa	2121

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RESULT      6
US-10-105-299-12515/c
; Sequence 12515, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12515
; LENGTH: 45698
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-105-299-12515

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Query Match	4.9%	Score 38.4;	DB 6;	Length 45698;
Best Local Similarity	50.5%;	Pred. No. 8.4;	91;	Indels 0;
Matches 93;	Conservative	0;	Mismatches	0;
Qy 217	AACAAAGGAGAGGATCTTTATCCCTTGCTGAACGTGTCAGGAGATGCAAGGCAATTTGAA	276		
Db 42407	AACAAAAAAAAAAAAAAAACTTCATGCTTCATCATAGGGTTATTTATGAAAAAGAA	42348		
Qy 277	GACCTTGTCAAGGATATACGTTTAAACAAAGCAAGAAAAAGAAACAGCTTTGAAATG	336		
Db 42347	GAATTTGGAAACAATATATAATTTAACCAAAAAGAGGTTGTTAATAATACACTATAGTATT	42288		
Qy 337	CAAAAGGGTGTATGAGGATCCTCAAATTGCGACACACGTTGTAAAGCAAGCCACAGTAAT	396		
Db 42287	TATGGATATATATAATTTCAGCCATATAAACACAGACTATGTAGCAACATTAATAAGTTTT	42228		
Qy 397	GCAG 400			
Db 42237	GAAG 42224			

RESULT 7  
US-09-830-706B-37/c  
: Sequence 37, Application US/09830706B  
: GENERAL INFORMATION:  
: APPLICANT: TOJII, SHINGO  
: APPLICANT: YANO, MINORU  
: APPLICANT: TAMAI, KATSUYUKI  
: TITLE OF INVENTION: THIOREDUXIN REDUCTASE II  
: FILE REFERENCE: 5865-71965  
: CURRENT APPLICATION NUMBER: US/09/830,706B  
: CURRENT FILING DATE: 2002-01-29  
: PRIOR APPLICATION NUMBER: PCT/JF99/05983  
: PRIOR FILING DATE: 1999-10-28  
: PRIOR APPLICATION NUMBER: JP 1998-310422  
: NUMBER OF SEQ ID NOS: 38  
: PRIOR FILING DATE: 1998-10-30

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 66566
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (31417)
; OTHER INFORMATION: n is un
US-09-830-706B-37

```

Query Match 4.9%; Score 38.4; DB 5; Length 66566;  
Best Local Similarity 60.6%; Pred. No. 9.4;  
Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

[illegible]

RESULT 8

```

US-10-027-632-187249
; Sequence 187249, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187249
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-187249

```

[illegible]



TELEFAX: 303/863-0223  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1758 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1...1758  
FEATURE:  
NAME/KEY: W = A or T  
LOCATION: 1136  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-10-071-192-29

Query Match 4.7%; Score 37; DB 6; Length 1758;  
Best Local Similarity 47.2%; Pred. No. 7;  
Matches 109; Conservative 1; Mismatches 121; Indels 0; Gaps 0:

QY 155 AGGTCGAAGAGGAGGAGGATCTTTATCCCTGCTGAACTGTGAGGAGATGAGAAGGCAATTG 274  
DB 1043 AGATGTAGAAGATTGAAGAAGCCATAGTTGCTGCTGAGAAAACCAAGAGATGAGATAA 1102  
QY 215 GCAACAAAGGAGAGGAGGATCTTTATCCCTGCTGAACTGTGAGGAGATGAGAAGGCAATTG 274  
DB 1103 AAGAACTAAAGGAGCTCAACGATTTGTTGAAGAMGGTTTAAAGATGATATACGAAATGG 1162  
QY 275 AAGACCTTGTCAAGGATATAACGTTAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334  
DB 1163 ATACTGTTGTACAGAATTTGAAGCAAGAAATCTGAGAGAGAGAGAGAGAGAGAGAGAG 1222  
QY 335 TCCAAAGAGGTGAAGGAGATCTCAATTCGAGGACACGTTGTAGACGAAG 385  
DB 1223 TTGAAGCTCCTAGGAGCGCTACTGAACTCAAGAAATTAGATGTAAGGAAG 1273

RESULT 13  
US-09-789-189-555/c  
Sequence 555, Application US/09789189  
GENERAL INFORMATION:  
APPLICANT: Lelias, Jean-Michel  
TITLE OF INVENTION: Human Polynucleotides and Polypeptides  
FILE REFERENCE: 25436/1720  
CURRENT APPLICATION NUMBER: US/09/789,189  
CURRENT FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/183452  
PRIOR FILING DATE: 2000-02-18  
NUMBER OF SEQ ID NOS: 2005  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 555  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-789-189-555

Query Match 4.7%; Score 36.6; DB 5; Length 341;  
Best Local Similarity 53.1%; Pred. No. 5.3;  
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0:

QY 203 AGCTAAGAGATGCAACAAAGGAGAGGATCTTTATCTGCTGAACTGTGAGGAGATGA 262  
DB 278 AGGTGAGGGGTGGATATGAGGAGGAAATTTGTAATGCAAGGGGAGGTTAAGTGAAGA 219  
QY 263 GAAGGCAATTTGAAGACCTTGTCAAGATATATACGTTTAAACAAGAGAGAGAGAGAGAA 322  
DB 218 TATTGTGATTGATAG 159  
QY 323 ACAGCTTTGAAATGCAAGAGAGGATGATG 349

APPLICANT: Verna, Ron  
APPLICANT: Yang, Fei  
APPLICANT: Yim, Kenneth  
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
FROM A cDNA Library of Fetal Liver-Spleen  
FILE REFERENCE: 728CIP  
CURRENT APPLICATION NUMBER: US/09/721,544  
CURRENT FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 09/515,128  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 09/034,341  
PRIOR FILING DATE: 1998-02-13  
NUMBER OF SEQ ID NOS: 24489  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 11180  
LENGTH: 349  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-721-544-11180

Query Match 4.8%; Score 37.6; DB 5; Length 349;  
Best Local Similarity 56.5%; Pred. No. 3;  
Matches 70; Conservative 0; Mismatches 54; Indels 0; Gaps 0:

QY 256 GAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAGAGAGAA 315  
DB 133 gatagagcagccattcagactttgtgagcaaatcagaaacaaattatttaca 192  
QY 316 AAGAAACAGCTTTGAAATGCAAGAGGTTGATGAGAGATCCTCAATTCGACACACGTT 375  
DB 193 ggtgaccagggcattgttgagaactaatggaagatgatccagcagggcagaagaagct 252  
QY 376 GTAA 379  
DB 253 gaaa 256

RESULT 12  
US-10-071-192-29  
Sequence 29, Application US/10071192  
GENERAL INFORMATION:  
APPLICANT: Hunter, Shirley Wu  
Sim, Gek-kee  
Weber, Eric R.  
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND  
APPARATUS TO COLLECT SUCH PROTEINS  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SHERIDAN ROSS P.C.  
STREET: 1560 BROADWAY, SUITE 1200  
CITY: DENVER  
STATE: CO  
COUNTRY: U.S.A.  
ZIP: 80202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/071,192  
FILING DATE: 07-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/171,156  
FILING DATE: 1998-10-09  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303/863-9700



Search completed: May 30, 2002, 05:39:58  
Job time: 16772 sec

Db 158 AGTTGTCAGAAAATAAAAGATGTAATG 132

## RESULT 14

US-10-105-299-9151

; Sequence 9151, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9151

; LENGTH: 57649

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-299-9151

Query Match 4.7%; Score 36.6; DB 6; Length 57649;  
Best Local Similarity 54.0%; Pred. No. 26;  
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 161 AAGAGGAAGTAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACA 220

Db 48584 aaggacaataaaccttttataaaattttctctataaaaaaaatcacactgtacaa 48643

Qy 221 AAGGAGAAGGATCTTTATCTTGTGTAAGTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280

Db 48644 atttagatagaacattatcaatgctcagattttataaaatgggaacagaaagactaaagc 48703

Qy 281 TTGTCAGGATATAACGTT 299

Db 48704 tagcgaaggaaacgtacatt 48722

## RESULT 15

US-10-105-299-10646

; Sequence 10646, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10646

; LENGTH: 57649

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-299-10646

Query Match 4.7%; Score 36.6; DB 6; Length 57649;  
Best Local Similarity 54.0%; Pred. No. 26;  
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 161 AAGAGGAAGTAACCTTCATGAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACA 220

Db 48584 aaggacaataaaccttttataaaattttctctataaaaaaaatcacactgtacaa 48643

Qy 221 AAGGAGAAGGATCTTTATCTTGTGTAAGTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280

Db 48644 atttagatagaacattatcaatgctcagattttataaaatgggaacagaaagactaaagc 48703

Qy 281 TTGTCAGGATATAACGTT 299

Db 48704 tagcgaaggaaacgtacatt 48722



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:32 ; Search time 139.75 Seconds  
(without alignments)  
1376.251 Million cell updates/sec

Title: US-08-982-272-5

Perfect score: 783

Sequence: 1 ATGATCGAACAATACCA.....TTGGTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760.6	97.1	818	1	US-08-431-055-1
2	760.6	97.1	818	4	US-08-858-197-1
3	759	96.9	783	1	US-08-446-922-5
4	759	96.9	783	2	US-08-249-189-1
5	759	96.9	783	2	US-08-484-624A-1
6	759	96.9	783	2	US-08-477-733B-1
7	759	96.9	783	3	US-09-088-913A-1
8	759	96.9	783	4	US-08-769-819-1
9	759	96.9	783	5	US-08-770-974-1
10	759	96.9	783	5	PCT-US93-10034-5
11	631.4	80.6	878	2	US-08-249-189-22
12	631.4	80.6	878	2	US-08-484-624A-22
13	631.4	80.6	878	2	US-08-477-733B-22
14	631.4	80.6	878	3	US-09-088-913A-22
15	631.4	80.6	878	4	US-08-769-819-22
16	631.4	80.6	878	4	US-08-770-974-22
17	582.8	74.4	786	1	US-08-446-922-3
18	582.8	74.4	786	5	PCT-US93-10034-3
19	582.8	74.4	840	1	US-07-940-605A-1
20	582.8	74.4	840	1	US-08-184-422-7
21	582.8	74.4	840	1	US-08-360-923A-1
22	582.8	74.4	840	1	US-08-431-055-3
23	582.8	74.4	840	2	US-08-690-096-1
24	582.8	74.4	840	2	US-08-249-189-11
25	582.8	74.4	840	2	US-08-484-624A-11
26	582.8	74.4	840	2	US-08-477-733B-11
27	582.8	74.4	840	3	US-08-763-995-1

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Sequence 7, Appli  
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Sequence 11, Appli  
Sequence 3, Appli  
Sequence 15, Appli  
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## ALIGNMENTS

RESULT 1

US-08-431-055-1.

; Sequence 1, Application US/08431055

; Patent No. 5817516

; GENERAL INFORMATION:

; APPLICANT: KEHRY, MERILYN R

; APPLICANT: CASTLE, BRIAN E

; TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

; DIFFERENTIATING B CELLS, AND USES THEREOF

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX

; STREET: 100 NEW YORK AVE. N.W. SUITE 600

; CITY: WASHINGTON

; STATE: D.C.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,055

; FILING DATE: 28-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/234,580

; FILING DATE: 28-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLMAN, ROBERT A

; REGISTRATION NUMBER: 36,217

; REFERENCE/DOCKET NUMBER: 1011.1030000/RAM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 818 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 13..795

US-08-431-055-1

Query Match 97.1%; Score 760.6; DB 1; Length 818;  
Best Local Similarity 98.2%; Pred. No. 1.6e-220;

Thu May 30 05:46:12 2002

us-08-982-272-5.rni

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Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATGAAACATACACCAACTTCTCCCGATCTGCGCACTGGGACCTCCCATCAGC 60
Db 13 ATGATAGAACATACAGCAACCTTCCCGAGATCGGCACTGGGACCTCCAGCAGC 72
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCCCTATACCCAAATGATGGATCTGTG 120
Db 73 ATGAGATTTTATGATTTACTTACTGTTTCCCTATACCCAAATGATGGATCTGTG 132
QY 121 CTTTTCCTGCTGATCTTATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180
Db 133 CTTTTCCTGCTGATCTTATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 192
QY 181 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATCAACAAAGAGAGAGTCTTTATCC 240
Db 193 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATCAACAAAGAGAGAGTCTTTATCC 252
QY 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGATATAACGTTA 300
Db 253 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGATATAACGTTA 312
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 313 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
QY 361 ATTGCAGCACACCTGTTGAAGCAAGCCACAGTAATGCAAGAGTCCGTTTACAGTGGCC 420
Db 373 ATTGCAGCACACCTGTTGAAGCAAGCCACAGTAATGCAAGAGTCCGTTTACAGTGGCC 432
QY 421 AAGAAAGATATATACCATGAAAGCAACTTGTGATGCTTGAAGAGTGGAAACAGCTG 480
Db 433 AAGAAAGATATATACCATGAAAGCAACTTGTGATGCTTGAAGAGTGGAAACAGCTG 492
QY 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 493 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
QY 541 GAGCCTTCGAGTCAAGCCCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 553 GAGCCTTCGAGTCAAGCCCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
QY 601 GAGAGAACTTACTCAAGCGGCAATACCAAGTCTTCCCAAGTCTTCCCAAGTCTTCC 660
Db 613 GAGAGAACTTACTCAAGCGGCAATACCAAGTCTTCCCAAGTCTTCCCAAGTCTTCC 672
QY 661 TCTGTTCACTTGGCGGAGTGTGTTGAATACAAGTGTGCTGCTGCTGCTGCTGCTGCT 720
Db 673 TCTGTTCACTTGGCGGAGTGTGTTGAATACAAGTGTGCTGCTGCTGCTGCTGCTGCT 732
QY 721 ACTGAAGCAAGCAAGTATCCACAGATGCTGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 733 ACTGAAGCAAGCAAGTATCCACAGATGCTGCTTCTCATCTTTTGGCTTACTCAAACTC 792
QY 781 TGA 783
Db 793 TGA 795
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RESULT 2  
US-08-858-197-1  
Sequence 1, Application US/08858197  
Patent No. 6297052  
GENERAL INFORMATION:  
APPLICANT: KEHR, MERILYN R  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
DIFFERENTIATING B CELLS, AND USES THEREOF  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON

```
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/858,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,580  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 818 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13...795  
US-08-858-197-1
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Query Match 97.1%; Score 760.6; DB 4; Length 818;  
Best Local Similarity 98.2%; Pred. No. 1.6e-220;  
Matches 769; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 ATGATGAAACATACACCAACTTCTCCCGATCTGCGCACTGGGACCTCCCATCAGC 60  
Db 13 ATGATAGAACATACAGCAACCTTCCCGAGATCGGCACTGGGACCTCCAGCAGC 72  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCCCTATACCCAAATGATGGATCTGTG 120  
Db 73 ATGAGATTTTATGATTTACTTACTGTTTCCCTATACCCAAATGATGGATCTGTG 132  
QY 121 CTTTTCCTGCTGATCTTATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180  
Db 133 CTTTTCCTGCTGATCTTATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 192  
QY 181 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATCAACAAAGAGAGAGTCTTTATCC 240  
Db 193 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATCAACAAAGAGAGAGTCTTTATCC 252  
QY 241 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGATATAACGTTA 300  
Db 253 TTGCTGAACCTGTGAGAGATGAGAGGCAATTTGAGACCTTGTCAAGATATAACGTTA 312  
QY 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
Db 313 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372  
QY 361 ATTGCAGCACACCTGTTGAAGCAAGCCACAGTAATGCAAGAGTCCGTTTACAGTGGCC 420  
Db 373 ATTGCAGCACACCTGTTGAAGCAAGCCACAGTAATGCAAGAGTCCGTTTACAGTGGCC 432  
QY 421 AAGAAAGATATATACCATGAAAGCAACTTGTGATGCTTGAAGAGTGGAAACAGCTG 480  
Db 433 AAGAAAGATATATACCATGAAAGCAACTTGTGATGCTTGAAGAGTGGAAACAGCTG 492  
QY 481 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Db 493 ACGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
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Oy 541 GAGCCTTCAGTCAACGCCCATTCATCGTGGCCCTCTGCTGAAGCCCGCAGCATTTGGATCT 600
Db 553 GAGCCTTCAGTCAACGCCCATTCATCGTGGCCCTCTGCTGAAGCCCGCAGCATTTGGATCT 612
Oy 601 GAGAGAATCTTACTCAAGCGGCGCAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 660
Db 613 GAGAGAATCTTACTCAAGCGGCGCAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 672
Oy 661 TCTGTTCACTTTGGCGGAGTGTGGAATTACAAGCTGTGCTTCTGTTTGTCAACGTG 720
Db 673 TCTGTTCACTTTGGCGGAGTGTGGAATTACAAGCTGTGCTTCTGTTTGTCAACGTG 732
Oy 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 780
Db 733 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACTC 792
Oy 781 TGA 783
Db 793 TGA 795

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# RESULT 3

```

US-08-446-922-5
; Sequence 5, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 1..780
US-08-446-922-5

Query Match 96.9%; Score 759; DB 1; Length 783;
Best Local Similarity 98.1%; Pred. No. 4.8e-220;
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGGCCGACCTGGACTGGCCCATCAGC 60
Db 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTTGGACTTCCACGAGC 60
Oy 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
Db 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
Oy 121 CTTTGTGCTGTATCTTTCATAGAGATTGGATAAGTTCGAAGAGAGTAACCTTCAT 180
Db 121 CTTTGTGCTGTATCTTTCATAGAGATTGGATAAGTTCGAAGAGAGTAACCTTCAT 180
Oy 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 181 GAAGATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Oy 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGSATATACGTTA 300
Db 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGSATATACGTTA 300
Oy 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Oy 361 ATTGCAGCACACGTTGTAAAGCGAGCCCAACAGTAAATGAGATCCGTTCTACAGTGGCC 420
Db 361 ATTGCAGCACACGTTGTAAAGCGAGCCCAACAGTAAATGAGATCCGTTCTACAGTGGCC 420
Oy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAAATGCTTGAATAATGGAAACAGCTG 480
Oy 481 ACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 ACGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 541 GAGCCTTCAGTCAACGCCCATTCATCGTGGCCCTCTGCTGAAGCCCGCAGCATTTGATCT 600
Db 541 GAGCCTTCAGTCAACGCCCATTCATCGTGGCCCTCTGCTGAAGCCCGCAGCATTTGATCT 600
Oy 601 GAGAGAATCTTACTCAAGCGGCGCAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 660
Db 601 GAGAGAATCTTACTCAAGCGGCGCAATACCCACAGTTTCTCCAGCTTTGGCAGCAGCAG 660
Oy 661 TCTGTTCACTTTGGCGGAGTGTGGAATTACAAGCTGTGCTTCTGCTTGTCTCAACGTG 720
Db 661 TCTGTTCACTTTGGCGGAGTGTGGAATTACAAGCTGTGCTTCTGCTTGTCTCAACGTG 720
Oy 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Db 721 ACTGAAGCAAGCAAGTGAATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAACTC 780
Oy 781 TGA 783
Db 781 TGA 783

RESULT 4
US-08-249-189-1
; Sequence 1, Application US/08249189
; Patent No. 5961974
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE

```

APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,189  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-249-189-1

Query Match 96.9%; Score 759; DB 2; Length 783;  
Best Local Similarity 98.1%; Pred. No. 4.8e-220;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 1 ATGATCGAAACATACACCAACTCTCCCGATCTGCGGCACTGGACTGCCCATCAGC 60  
DB 1 ATGATGAAACATACAGCCAACTCTCCCGAGATCCGTCGCACTGGACTTCCAGCGAGC 60  
QY 61 ATGAAATTTTATGTATTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 120  
DB 61 ATGAAATTTTATGTATTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG 120  
QY 121 CTTTTCGTCTGTATCTTCATAGAGATGGATAGGTCGGAAGAGAACTTTCAT 180  
DB 121 CTTTTCGTCTGTATCTTCATAGAGATGGATAGGTCGGAAGAGAACTTTCAT 180

QY 181 GAAGATTTTCTATTCATAAAAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTCTATTCATAAAAAAGCTAAAGAGATGCAACAAGAGAGAGATCTTTATCC 240  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACTTGTCAAGGATATAAGCTTA 300  
DB 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACTTGTCAAGGATATAAGCTTA 300  
QY 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATCAAAAGAGGTGATGAGGATCTCAA 360  
DB 301 AACAAAGAGAGAAAAAGAAACAGCTTTGAAATCAAAAGAGGTGATGAGGATCTCAA 360  
QY 361 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATGCAGCATCCGTTCTACAGTGGCC 420  
DB 361 ATTGCAGCACACGTTGTAAGCGAAGCAACAGTAATGCAGCATCCGTTCTACAGTGGCC 420  
QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGTATGCTTGAAATGGGAAACAGCTG 480  
DB 421 AAGAAAGGATATTATACCATGAAAGCAACTTGTATGCTTGAAATGGGAAACAGCTG 480  
QY 481 ACGGTTAAAGAGAGAGACTCTATTATGCTTACACTCAAGTCACCTTCTCTTAATCGG 540  
DB 481 ACGGTTAAAGAGAGAGACTCTATTATGCTTACACTCAAGTCACCTTCTCTTAATCGG 540  
QY 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCTCTGGCTGAAGCCAGCAGTGGATCT 600  
DB 541 GAGCCTTCGAGTCAACGCCCAATTCATCGTGGCTCTGGCTGAAGCCAGCAGTGGATCT 600  
QY 601 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTGGGAGCAGCAG 660  
DB 601 GAGAGATCTTACTCAAGCGGCAAAATACCCACAGTTCCTCCAGCTTGGGAGCAGCAG 660  
QY 661 TCTGTTCACTTGGCGGAGTCTTGAATTAACAAGCTGGTCTCTGTTTGTCAAGCTG 720  
DB 661 TCTGTTCACTTGGCGGAGTCTTGAATTAACAAGCTGGTCTCTGTTTGTCAAGCTG 720  
QY 721 ACTGAAGCAAGCCAGTGTATCCACAGATTCGCTTCTCATCTTTGGCTTACTCAACTC 780  
DB 721 ACTGAAGCAAGCCAGTGTATCCACAGATTCGCTTCTCATCTTTGGCTTACTCAACTC 780  
QY 781 TGA 783  
DB 781 TGA 783  
RESULT 5  
US-08-484-624A-1  
Sequence 1, Application US/08484624A  
Patent No. 5962406  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,624A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,733

FILING DATE: June 07, 1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/969,703

FILING DATE: October 23, 1992

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/805,723

FILING DATE: December 5, 1991

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/783,707

FILING DATE: October 25, 1991

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: MOUSE

IMMEDIATE SOURCE:

CLONE: CD40-L

FEATURE:

NAME/KEY: CDS

LOCATION: 1..783

US-08-484-624A-1

Query Match 96.9%; Score 759; DB 2; Length 783;

Best Local Similarity 98.1%; Pred. No. 4.8e-220;

Matches 768; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60

DB 1 ATGATGAAACATACACCAAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60

QY 61 ATGAAATTTTATGATTTATCTACTGTTTCTTATCACCACCAATGATTCGATCTGTG 120

DB 61 ATGAAATTTTATGATTTATCTACTGTTTCTTATCACCACCAATGATTCGATCTGTG 120

QY 121 CTTTTCCTGCTATCTTCATAGAGATTGGATAAGGTGCGAAGAGAGTAAACCTTCAT 180

DB 121 CTTTTCCTGCTATCTTCATAGAGATTGGATAAGGTGCGAAGAGAGTAAACCTTCAT 180

QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240

DB 181 GAAGATTTTGTATTCATATAAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240

QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATAAGTTA 300

DB 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATAAGTTA 300

QY 301 AACAAAG 360

DB 301 AACAAAG 360

QY 361 ATTGCAGCACACGTTGTAAAGCGAAGCCAAACAGTAAATGACAGATCCGTTTCTACAGTGGCC 420

DB 361 ATTGCAGCACACGTTGTAAAGCGAAGCCAAACAGTAAATGACAGATCCGTTTCTACAGTGGCC 420

QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAANAATGGGAACAGCTG 480

DB 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAANAATGGGAACAGCTG 480

QY 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTGCTCTAATCGG 540

DB 481 ACGGTTAAAGAGAGAGGACTCTATTATGCTTACACTCAAGTCACTTCTGCTCTAATCGG 540

QY 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGATCT 600

DB 541 GAGCCTTCGAGTCAACGCCCATTCATCGTGGCCCTCTGGCTGAAGCCAGCATTTGATCT 600

QY 601 GAGAGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCACAGCTTTGCCAGCAGCAG 660

DB 601 GAGAGAATCTTACTCAAGCGCGCAATATCCACAGTTCTCCACAGCTTTGCCAGCAGCAG 660

QY 661 TCTGTTCACTTGGCGGAGTGTTCGAATTACAAGCTGGTCTTCTGTCTTCTCAACGTG 720

DB 661 TCTGTTCACTTGGCGGAGTGTTCGAATTACAAGCTGGTCTTCTGTCTTCTCAACGTG 720

QY 721 ACTGAAGCAAGCAAGTATGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAATC 780

DB 721 ACTGAAGCAAGCAAGTATGATCCACAGAGTTGGCTTCTCATCTTTTGGCTTACTCAAATC 780

QY 781 TGA 783

DB 781 TGA 783

# RESULT 6

US-08-477-733B-1

; Sequence 1, Application US/08477733B

; Patent No. 5981724

; GENERAL INFORMATION:

; APPLICANT: ARMITAGE, RICHARD

; APPLICANT: FANSLAW, WILLIAM

; APPLICANT: SPRIGGS, MELANIE

; APPLICANT: SRINIVASAN, SUBHASHINI

; APPLICANT: GIBSON, MARYLOU

; APPLICANT: MORRIS, ARVIA E.

; APPLICANT: MCGREW, JEFFERY

; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: IMMUNEX CORPORATION

; STREET: 51 UNIVERSITY STREET

; CITY: SEATTLE

; STATE: WASHINGTON

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,733B

; FILING DATE: June 07, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/249,189

; FILING DATE: May 24, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,703

; FILING DATE: October 23, 1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/805,723

||||| GAGCCCTCGAGTCAACGCCCATTCATCGTGGCGCTCTGGCTGAAGCCAGCAGTGGATCT 600  
QY 601 GAGAGATCTTACTCAAGCGGCAAAATACCCAGATTCTCCAGCTTTGCGAGCAGCAG 660  
Db 601 GAGAGATCTTACTCAAGCGGCAAAATACCCAGATTCTCCAGCTTTGCGAGCAGCAG 660  
QY 661 TCTGTTCCACTTGGCGGAGTGTGTAATTACAAGCTGGTCTCTCTGTTGTTGTCACAGTG 720  
Db 661 TCTGTTCCACTTGGCGGAGTGTGTAATTACAAGCTGGTCTCTCTGTTGTTGTCACAGTG 720  
QY 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGCTTACTCAAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGAGTTGGCTTCTCATCTTTGCTTACTCAAACTC 780  
QY 781 TGA 783  
Db 781 TGA 783  
RESULT 7  
US-09-088-913A-1  
; Sequence 1, Application US/09088913A  
; Patent No. 6087329  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple Macintosh  
; SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,913A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/484,624  
; FILING DATE:  
; APPLICATION NUMBER: 08/477,733  
; FILING DATE: June 07, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-477-733B-1  
Query Match 96.98; Score 759; DB 2; Length 783;  
Best Local Similarity 98.18; Pred. No. 4.8e-220;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGCATCTCGGCGCACTGACTGCCCATCAGC 60  
Db 1 ATGATGAGAACAATACAGCAACCTTCCCGCCAGATCCGCTGGCACTGGCACTTCCAGCGAGC 60  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTGGATCTGTG 120  
Db 61 ATGAAAGATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATTGGATCTGTG 120  
QY 121 CTTTGTGCTGTATCTTATAGAGATTTGGATAGAGTTCGAGAGGAGTAACCTTCAT 180  
Db 121 CTTTGTGCTGTATCTTATAGAGATTTGGATAGAGTTCGAGAGGAGTAACCTTCAT 180  
QY 181 GAAGATTTTGTATTATATAAAGAGCTTAAGAGATGCAACAAAGAGAGAGGATCTTTATCC 240  
Db 181 GAAGATTTTGTATTATATAAAGAGCTTAAGAGATGCAACAAAGAGAGAGGATCTTTATCC 240  
QY 241 TTGCTCAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300  
Db 241 TTGCTCAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300  
QY 301 AACAAAG 360  
Db 301 AACAAAG 360  
QY 361 ATTGCAGCACAGCTTGTGAAGCGAAGCAACAGTAAATGACAGCTTGTCAAGTGGGCC 420  
Db 361 ATTGCAGCACAGCTTGTGAAGCGAAGCAACAGTAAATGACAGCTTGTCAAGTGGGCC 420  
QY 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATCTGTAATGGGAAACAGCTG 480  
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATCTGTAATGGGAAACAGCTG 480  
QY 481 ACGGTTAAAG 540  
Db 481 ACGGTTAAAG 540  
QY 541 GAGCCTTCGAGTCAACGCCCATTCATGCTGGCGCTCTGGCTGAAGCCAGCAGTGGATCT 600



LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-09-088-913A-1

Query Match 96.98; Score 759; DB 3; Length 783;  
Best Local Similarity 98.18; Pred. No. 4.8e-220;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 60  
Db 1 ATGATGAAACATCAACCAAACTTCTCCCGATCTGGCGCACTGGACTGCCCATCAGC 60

Qy 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTATGATGGATCTGTG 120  
Db 61 ATGAAATTTTATGATTTTACTTACTGTTTCTTATCACCCTTATGATGGATCTGTG 120

Qy 121 CTTTTGCTGTGATCTTTCATAGAGATGGATAGGTCGAGAGAGTAACCTTCAT 180  
Db 121 CTTTTGCTGTGATCTTTCATAGAGATGGATAGGTCGAGAGAGTAACCTTCAT 180

Qy 181 GAAGATTTGTTATCATAAAAAGCTTAAGAGATGCAACAAGAGAGGATCTTATCC 240  
Db 181 GAAGATTTGTTATCATAAAAAGCTTAAGAGATGCAACAAGAGAGGATCTTATCC 240

Qy 241 TTGCTGAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300  
Db 241 TTGCTGAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300

Qy 301 AACAAAGAGAGAGAGAGAGAGAGCTTTGAATGCAAGAGGATGAGATCCTCAA 360  
Db 301 AACAAAGAGAGAGAGAGAGAGAGCTTTGAATGCAAGAGGATGAGATCCTCAA 360

Qy 361 ATTGAGCAGACGTTGTAAAGCAAGCCCAACAGTATGATGAGATCGCTTACAGTGGCC 420  
Db 361 ATTGAGCAGACGTTGTAAAGCAAGCCCAACAGTATGATGAGATCGCTTACAGTGGCC 420

Qy 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG 480  
Db 421 AAGAAAGGATATTATACCATGAAAGCAACTTGGTAATGCTTGAATAATGGAAACAGCTG 480

Qy 481 ACGGTTAAAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540  
Db 481 ACGGTTAAAGAGAGGACTCTATTATGCTACACTCAAGTCACCTTCTGCTCTAATCGG 540

Qy 541 GAGCCTTCAGTCAAGCGCCATTTCATGCTGCGCCTCTCGCTGAAGCCAGCATTTGATCT 600  
Db 541 GAGCCTTCAGTCAAGCGCCATTTCATGCTGCGCCTCTCGCTGAAGCCAGCATTTGATCT 600

Qy 601 GAGAGAACTTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGGAGCAGCAG 660  
Db 601 GAGAGAACTTTACTCAAGCGCGCAATACCCACAGTCTCTCCAGCTTTGGGAGCAGCAG 660

Qy 661 TCTGTTCACTTTGGGCGGAGTGTGTAATTAAGCTGCTGCTCTGCTGTTGTCAACGTG 720  
Db 661 TCTGTTCACTTTGGGCGGAGTGTGTAATTAAGCTGCTGCTCTGCTGTTGTCAACGTG 720

Qy 721 ACTGAAGCAAGCAAGTATCCACAGATGCTGCTCTCTATCTTTGGCTTACTCAACTC 780  
Db 721 ACTGAAGCAAGCAAGTATCCACAGATGCTGCTCTCTATCTTTGGCTTACTCAACTC 780

Qy 781 TGA 783  
Db 781 TGA 783

RESULT 8  
US-08-769-819-1  
: Sequence 1, Application US/08769819  
: Patent No. 6264951  
: GENERAL INFORMATION:  
: APPLICANT: ARMITAGE, RICHARD  
: APPLICANT: FANLOW, WILLIAM  
: APPLICANT: SPRIGGS, MELANIE  
: APPLICANT: SRINIVASAN, SUBHASHINI  
: APPLICANT: GIBSON, MARYLOU  
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
: NUMBER OF SEQUENCES: 24  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: IMMUNEX CORPORATION  
: STREET: 51 UNIVERSITY STREET  
: CITY: SEATTLE  
: STATE: WASHINGTON  
: COUNTRY: USA  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: Apple Macintosh  
: OPERATING SYSTEM: Apple Operating System 7.1  
: SOFTWARE: Microsoft Word for Apple, version 5.1a  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08769,819  
: FILING DATE: 19-DEC-1996  
: CLASSIFICATION: 424  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/484,624  
: FILING DATE: 07-JUN-1995  
: APPLICATION NUMBER: 08/249,189  
: FILING DATE: May 24, 1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/969,703  
: FILING DATE: October 23, 1992  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/805,723  
: FILING DATE: December 5, 1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/783,707  
: FILING DATE: October 25, 1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Perkins, Patricia A.  
: REGISTRATION NUMBER: 34,693  
: REFERENCE/DOCKET NUMBER: 2802-E  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 2065870430  
: TELEFAX: 2065870606  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 783 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: CDNA  
: HYPOTHETICAL: NO  
: ANTI-SENSE: NO  
: ORIGINAL SOURCE:  
: ORGANISM: MOUSE  
: IMMEDIATE SOURCE:  
: CLONE: CD40-L  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..783  
US-08-769-819-1

Thu May 30 05:46:12 2002

Query Match 96.9%; Score: 759; DB 4; Length 783;  
Best Local Similarity 98.1%; Pred. No. 4.8e-220;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATGTCGGCCACTGGAGTCCCATCAGC 60  
DB 1 ATGATGAGAACATACAGCCCACTTCCCGCAGATCGTGGCACTGGAGTCCCATCAGC 60  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
QY 121 CTTTTGTCTGTATCTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180  
DB 121 CTTTTGTCTGTATCTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATATATAAAGCTTAAGAGATGAACAAAGGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTGTATATATAAAGCTTAAGAGATGAACAAAGGAGAGATCTTTATCC 240  
QY 241 TTCTGTAACCTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300  
DB 241 TTCTGTAACCTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTCACACACAGCTGTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
DB 361 ATTCACACACAGCTGTAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 421 AAGAGAGATATATACATGAAAGCAACTTGTATGCTTACACTCAAGTCACTTCTGCTTAATCGG 540  
DB 421 AAGAGAGATATATACATGAAAGCAACTTGTATGCTTACACTCAAGTCACTTCTGCTTAATCGG 540  
QY 541 GAGCCTTCAGTCAAGCGCCATTCATGCTGGCCCTGCTGGCTGAAGCCAGCAGTGGATCT 600  
DB 541 GAGCCTTCAGTCAAGCGCCATTCATGCTGGCCCTGCTGGCTGAAGCCAGCAGTGGATCT 600  
QY 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGAGTTCCTCCAGCTTTGCGAGCAGAG 660  
DB 601 GAGAGATCTTACTCAAGCGGCAATATACCCAGAGTTCCTCCAGCTTTGCGAGCAGAG 660  
QY 661 TCTGTTCACTTGGCGGAGTGTGAAATACAGCTGGTCTGCTTTTCTCAAGCTG 720  
DB 661 TCTGTTCACTTGGCGGAGTGTGAAATACAGCTGGTCTGCTTTTCTCAAGCTG 720  
QY 721 ACTGAGCAAGCAAGTGTATCAGAGTGGCTTCTATCTTTTGGCTTACTCAAACTC 780  
DB 721 ACTGAGCAAGCAAGTGTATCAGAGTGGCTTCTATCTTTTGGCTTACTCAAACTC 780  
QY 781 TGA 783  
DB 781 TGA 783

RESULT 9  
US-08-770-974-1  
; Sequence 1, Application US/08770974.  
; Patent No. 6290972  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANLOW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,974  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELEPHONE: 2065870430  
TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MOUSE  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..783  
US-08-770-974-1

Query Match 96.9%; Score: 759; DB 4; Length 783;  
Best Local Similarity 98.1%; Pred. No. 4.8e-220;  
Matches 768; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATGTCGGCCACTGGAGTCCCATCAGC 60  
DB 1 ATGATGAGAACATACAGCCCACTTCCCGCAGATCGTGGCACTGGAGTCCCATCAGC 60  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 61 ATGAAATTTTATGATTTACTTACTTCTTATCACCACCAATGATGGATCTGTG 120  
QY 121 CTTTTGTCTGTATCTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180  
DB 121 CTTTTGTCTGTATCTTCATAGAGATTTGATAGAGTTCGAAGAGAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGAACAAAGGAGAGATCTTTATCC 240



RESULT 11  
US-08-249-189-22  
Sequence 22, Application US/08249189  
Patent No. 5961974  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, WILLIAM  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple operating  
SOFTWARE: Microsoft Word for App  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/249,18  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
ORIGINAL SOURCE:  
STRAIN: Murine CD40-L trimer  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 15..92  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..857  
FEATURE:  
NAME/KEY: mat\_peptide

RESULT 12  
US-08-484-624A-22  
; Sequence 22: Application US/08484624A  
; Patent No.: 5962406  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA

ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/484,624A

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELEPHONE: 2065870430  
TELEFAX: 2065870606

INFORMATION FOR SEQ. ID. NO. 22:  
SEQUENCE CHARACTERISTICS:

LENGTH: 878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE: Murine CD40-L trimer

FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 15..92

FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..857

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 93..857

US-08-484-624A-22

Query Match 80.6%; Score 631.4; DB 2; Length 878;  
Best Local Similarity 99.8%; Pred. No. 2e-181;  
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	151	GATAGGTCGAAGAGGAGTAACTTCATCAAGATTGTTATTCATATAAAGCTAAAG	210
Db	225	GATAGGTCGAAGAGGAGTAACTTCATCAAGATTGTTATTCATATAAAGCTAAAG	284
Qy	211	AGATGCAACAAGGAGGAGTCTTATCTGCTGAACTGTGAGGAGATGAGAGGCAA	270
Db	285	AGATGCAACAAGGAGGAGTCTTATCTGCTGAACTGTGAGGAGATGAGAGGCAA	344
Qy	271	TTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGAGAAAAAAGACGCTTT	330
Db	345	TTTGAAGACCTTGTCAAGGATATACGTTAAACAAGAGAGAAAAAAGACGCTTT	404
Qy	331	GAATGCAACAAGGAGTGTGAGGATCTCAAAATTCAGCACACGTTGTAGGCAAGCCAA	390
Db	405	GAATGCAACAAGGAGTGTGAGGATCTCAAAATTCAGCACACGTTGTAGGCAAGCCAA	464

Qy	391	AGTAATGAGCATCCGTTCTACAGTGGGCCAAGAAAGATATTATACCATGAAAAGCAAC	450
Db	465	AGTAATGAGCATCCGTTCTACAGTGGGCCAAGAAAGATATTATACCATGAAAAGCAAC	524
Qy	451	TTGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGAGTCTATATGTC	510
Db	525	TTGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGAGTCTATATGTC	584
Qy	511	TACACTCAAGTCACCTTCTGCTCTAAATCGGGAGCCTTCGAGTCAAGGCCCATTCATCTGC	570
Db	585	TACACTCAAGTCACCTTCTGCTCTAAATCGGGAGCCTTCGAGTCAAGGCCCATTCATCTGC	644
Qy	571	GGCCTCTGGCTGAAGCCAGCAGTTCGATCTGAGAGAAATCTTACTCAAGCGGCAATACC	630
Db	645	GGCCTCTGGCTGAAGCCAGCAGTTCGATCTGAGAGAAATCTTACTCAAGCGGCAATACC	704
Qy	631	CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTTGGGCGGAGTGTGTAATTA	690
Db	705	CACAGTTCCTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTTGGGCGGAGTGTGTAATTA	764
Qy	691	CAAGCTGGTCTTCTGCTTTGTTGTTCAAGCTGACTGAAGCAAGCCAAAGTATCCACAGATT	750
Db	765	CAAGCTGGTCTTCTGCTTTGTTGTTCAAGCTGACTGAAGCAAGCCAAAGTATCCACAGATT	824
Qy	751	GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA	783
Db	825	GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA	857

RESULT 13  
US-08-477-733B-22  
Sequence 22, Application US/08477733B  
Patent No. 5981724  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, MARYLOU  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,733B  
FILING DATE: June 07, 1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:

Query Match	80.68;	Score 631.4;	DB 2;	Length 878;	
Best Local Similarity	99.88;	pred No 2e-181;			
Matches 632;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps
151	QY	GATAAGGTCTGAAGAGAAAGTAAACCTTCATGAGAGATTTTGTATTATCAAAAAAGCTAAAG	210		
225	Db	GATAAGGTCTGAAGAGAAAGTAAACCTTCATGAGAGATTTTGTATTATCAAAAAAGCTAAAG	284		
211	QY	AGATGCAACAAGAGAGAGAGATCTTTATCCCTTGCTGAACCTGTGAGGAGATGAGAAAGCAA	270		
285	Db	AGATGCAACAAGAGAGAGAGATCTTTATCCCTTGCTGAACCTGTGAGGAGATGAGAAAGCAA	344		
271	QY	TTTGAAGACCTTGTCAAGGATATACGTTTAAACAAGAGAGAAAGAAAGAAACAGCTTT	330		
345	Db	TTTGAAGACCTTGTCAAGGATATACGTTTAAACAAGAGAGAGAAAGAAAGAAACAGCTTT	404		
331	QY	GAATATGCAAAAGAGGTGATGAGGATCCTCAAATTTGCACGACACAGCTTGTAAAGCGCAAC	390		
405	Db	GAATATGCAAAAGAGGTGATGAGGATCCTCAAATTTGCACGACACAGCTTGTAAAGCGCAAC	464		
391	QY	AGTAATGCAAGCATTCTTCACGTGGCGCAAGAAAGGATATTATACCATGAAAAAGCAAC	450		
465	Db	AGTAATGCAAGCATTCTTCACGTGGCGCAAGAAAGGATATTATACCATGAAAAAGCAAC	524		
451	QY	TTGGTAAATGCTTGAARAATGGGAACAAGCTGACGGTTAAAGAGAAGCACTTATTATGTC	510		
525	Db	TTGGTAAATGCTTGAARAATGGGAACAAGCTGACGGTTAAAGAGAAGCACTTATTATGTC	584		
511	QY	TACACTCAAGTCACTTCCTCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTC	570		
585	Db	TACACTCAAGTCACTTCCTCTCTAATCGGGAGCCTTCGAGTCAACGCCCATTCATCGTC	644		
571	QY	GGCCTCTGGCTGAAGCCCGACCATTTGGATCTGAGAGAACTTTACTCAAGGGCGCAATACC	630		
645	Db	GGCCTCTGGCTGAAGCCCGACCATTTGGATCTGAGAGAACTTTACTCAAGGGCGCAATACC	704		
631	QY	CACAGTTCCTCCAGCTTTTCGGAGCAGCACTGTCTTCACTTTGGCGGAGTGTTTGAATTA	690		
705	Db	CACAGTTCCTCCAGCTTTTCGGAGCAGCACTGTCTTCACTTTGGCGGAGTGTTTGAATTA	764		
691	QY	CAAGCTGGTGGTCTTCTGTGTTTGTTCACAGTGAAGCAAGCAAGTGAATCCACAGAGTT	750		

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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..857
US-08-982-913A-22

Query Match      80.6%; Score 631.4; DB 3; Length 878;
Best Local Similarity 99.8%; Pred. No. 2e-181;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATATAAAGCTAAAG 210
DB 225 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATATAAAGCTAAAG 284
QY 211 AGATCAACAAGAGAGAGTATTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 270
DB 285 AGATCAACAAGAGAGAGTATTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGCTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGAGCTTT 404
QY 331 GAAATGCAAGAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 390
DB 405 GAAATGCAAGAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 464
QY 391 AGTAATGCAAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 450
DB 465 AGTAATGCAAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 524
QY 451 TTGGTAATGCTTGAAGAGTAAAGTGGGAGAGTAAAGAGAGAGAGAGAGAGAGCTTTATGTC 510
DB 525 TTGGTAATGCTTGAAGAGTAAAGTGGGAGAGTAAAGAGAGAGAGAGAGAGAGCTTTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATGCTC 570
DB 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATGCTC 644
QY 571 GGCCTCTGGCTGAAGCCAGAGTGGATCTGAGAGAACTTACTCAAGCGGCAAAATACC 630
DB 645 GGCCTCTGGCTGAAGCCAGAGTGGATCTGAGAGAACTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTTCTCCAGCTTTGGAGAGCAGTCTGTCTACTTGGCGGAGTGTGAAATTA 690
DB 705 CACAGTTCTCCAGCTTTGGAGAGCAGTCTGTCTACTTGGCGGAGTGTGAAATTA 764
QY 691 CAAGCTGCTGCTTCTGCTTGTCTCAAGCTGACTGAAGCAAGCCCAAGTATCCACAGAGTT 750
DB 765 CAAGCTGCTGCTTCTGCTTGTCTCAAGCTGACTGAAGCAAGCCCAAGTATCCACAGAGTT 824
QY 751 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 783
DB 825 GGCCTCTCATCTTTTGGCTTACTCAAACTCTGA 857

RESULT 15
US-08-769-819-22
; Sequence 22, Application US/08769819
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA

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; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Murine CD40-L trimer
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 15..92
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..857
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..857
US-08-769-819-22

Query Match      80.6%; Score 631.4; DB 4; Length 878;
Best Local Similarity 99.8%; Pred. No. 2e-181;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 151 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATATAAAGCTAAAG 210
DB 225 GATAGGTCGAGAGAGTAAACCTTCATGAAGATTTTGTATTCATATAAAGCTAAAG 284
QY 211 AGATCAACAAGAGAGAGTATTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 270
DB 285 AGATCAACAAGAGAGAGTATTTATCTTGTCTGAACCTGTGAGGAGATGAGAAGCAA 344
QY 271 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGCTTT 330
DB 345 TTTGAAGACCTTGTCAAGGATATAACGTTAAACAAGAGAGAGAGAGAGAGCTTT 404
QY 331 GAAATGCAAGAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 390
DB 405 GAAATGCAAGAGGTGATGAGGATCTCAAAATTCAGACACAGCTTGTAGGCGAAGCCCAAC 464
QY 391 AGTAATGCAAGGTGATGAGGATCTCAAAATTCAGACAGGATATATACCATGAGAGCCCAAC 450

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Thu May 30 05:46:12 2002

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|||||
Db 465 AGTAATGACGATCCGTTCTACAGTGGCCAAAGAAAGGATATTATACCATGAAAAGCAAC 524
QY 451 TTGGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGACTCTATTATGTC 510
Db 525 TTGGTAATGCTTGAATAATGGGAACAGCTGACGGTTAAAGAGAGGACTCTATTATGTC 584
QY 511 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 570
Db 585 TACACTCAAGTCACCTTCTGCTCTAATCGGAGCCTTCGAGTCAACGCCCATTCATCGTC 644
QY 571 GGCCTCTGGCTGAAGCCCAAGCAATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 630
Db 645 GGCCTCTGGCTGAAGCCCAAGCAATTTGATCTGAGAGATCTTACTCAAGCGGCAAAATACC 704
QY 631 CACAGTTCTCCAGCTTTGCGAGCAGAGTCTGTTCACCTTGGCGGAGTGTTCGAATTA 690
Db 705 CACAGTTCTCCAGCTTTGCGAGCAGAGTCTGTTCACCTTGGCGGAGTGTTCGAATTA 764
QY 691 CAAGCTGGTCTTCTGTTGTTTGTCAACGTGACTGAAGCAAGCCAGTATCCACAGAGTT 750
Db 765 CAAGCTGGTCTTCTGTTGTTTGTCAACGTGACTGAAGCAAGCCAGTATCCACAGAGTT 824
QY 751 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 783
Db 825 GGCTTCTCATCTTTTGGCTTACTCAAACTCTGA 857
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Search completed: May 30, 2002, 02:51:38  
Job time: 11602 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:48:59 ; Search time 6499.83 Seconds  
(without alignments)  
2530.567 Million cell updates/sec

Title: US-08-982-272-6  
Perfect score: 786  
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTCA 786

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	GenEmbl.:
1: gb_ba.:	187864 Sequence 3
2: gb_htg.:	AR044779 Sequence
3: gb_in.:	AR076926 Sequence
4: gb_om.:	AR078316 Sequence
5: gb_ov.:	AR08419 Sequence
6: gb_pat.:	AR08419 Sequence
7: gb_ph.:	AR103375 Sequence
8: gb_pl.:	AR106246 Sequence
9: gb_pr.:	AR169232 Sequence
10: gb_ro.:	AR171647 Sequence
11: gb_sts.:	AR171647 Sequence
12: gb_sy.:	AR171647 Sequence
13: gb_un.:	AR171647 Sequence
14: gb_vi.:	AR171647 Sequence
15: em_ba.:	AR171647 Sequence
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18: em_in.:	AR171647 Sequence
19: em_mu.:	AR171647 Sequence
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21: em_or.:	AR171647 Sequence
22: em_ov.:	AR171647 Sequence
23: em_pat.:	AR171647 Sequence
24: em_ph.:	AR171647 Sequence
25: em_pl.:	AR171647 Sequence
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29: em_vi.:	AR171647 Sequence
30: em_htg_hum.:	AR171647 Sequence
31: em_htg_inv.:	AR171647 Sequence
32: em_htg_other.:	AR171647 Sequence
33: em_htgo_inv.:	AR171647 Sequence

ALIGNMENTS

RESULT	1	786 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	187864	Sequence 3 from patent US 5716805.			
DEFINITION	Sequence 3 from patent US 5716805.				
ACCESSION	187864				
VERSION	187864.1	GI:3407804			
KEYWORDS	Unknown:				
SOURCE	Unknown:				
ORGANISM	Unknown:				
REFERENCE	1 (bases 1 to 786)				
AUTHORS	Srinivasan, S. and Spriggs, M.K.				
TITLE	Methods of preparing soluble, oligomeric proteins				
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;				
FEATURES	Location/Qualifiers				
source	1. 786				
BASE COUNT	250 a 168 c 168 g 200 t				
ORIGIN					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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Query Match 97.2%; Score 763.6; DB 6; Length 786;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;

JOURNAL    Patent: US 5817516-A    3    06-OCT-1998;  
FEATURES       Location/Qualifiers  
                1. .840  
                /organism="unknown"  
source                                  214 t  
  
BASE COUNT       263 a    182 c    181 g  
ORIGIN

Query Match	97.2%;	Score 763.6;	DB 6;	Length 840;
Best Local Similarity	98.2%;	Pred. No. 4.7e-193;		
Matches: 772; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

QY	1	ATGATAGAAACATACAGCCAACTTCTCCCCAGATCCGGTGCACACTGACATCTCCAGCGAC	80
DB	22	ATGATCGAAACATACAAACCAACTTCTCCCGGATCTGCGGCCACTGCACTGCCCATCAGC	81
QY	61	ATGAAGATTTTATGTATTTACTTGTCTTTTCTTATACCCAGATGATGSGTGACGA	120
DB	82	ATGAAATTTTATGTATTTACTTGTCTTTTCTTATCACCAGATGATGGGTGACGA	141
QY	121	CTTTTGTGTGTATCTTCATAGAGGTTGGACAAGATAGAAGATCAAGGAATCTTCAT	180
DB	142	CTTTTGTGTGTATCTTCATAGAGGTTGGACAAGATAGAAGATCAAGGAATCTTCAT	201
QY	181	GAAGATTTTGTATTCATCAAAACGATACAGAGATGCAACACAGAGAAAATCCTTATCC	240
DB	202	GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGAGAAAATCCTTATCC	261
QY	241	TTACTCAACTGTGAGGAGATTAAAACCACTTTGAAGCCTTTGTAAGGATATAATGTTA	300
DB	262	TTACTCAACTGTGAGGAGATTAAAACCACTTTGAAGCCTTTGTAAGGATATAATGTTA	321
QY	301	ACAAAGACGAGACGAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
DB	322	AACAAAGACGAGACGAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	381
QY	361	CAAAATCCGGCACATGTCATAAGTGAGGCCAGCATAAACCAATCTGTGTTACAGTGG	420
DB	382	CAAAATCCGGCACATGTCATAAGTGAGGCCAGCATAAACCAATCTGTGTTACAGTGG	441
QY	421	GCTGAAAGAGATCTACACCTTGACCAACTTGGTAACCTCGAAAAATGGGAAACAG	480
DB	442	GCTGAAAGAGATCTACACCTTGACCAACTTGGTAACCTCGAAAAATGGGAAACAG	501
QY	481	CTGACCGTTAAACACAGGACTCTATATATCTATGCCCAGTCACTCTGTGTTCCAA	540
DB	502	CTGACCGTTAAACACAGGACTCTATATATCTATGCCCAGTCACTCTGTGTTCCAA	561
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCTTAAGTCCCGCGTAGA	600
DB	562	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCCTCTGCTTAAGTCCCGCGTAGA	621
QY	601	TTGAGAGAAATCTTACTCAGAGTGCAAATACCCACAGTTTCGCCAAACCTTTGCGGGCAA	660
DB	622	TTGAGAGAAATCTTACTCAGAGTGCAAATACCCACAGTTTCGCCAAACCTTTGCGGGCAA	681
QY	661	CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGGTGCTTCGGTGTGTGTCAT	720
DB	682	CAATCCATTCACTTGGGAGGAGTATTTGAATGCAACAGGTGCTTCGGTGTGTGTCAT	741
QY	721	GTGACTGTATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAGTCTTGCCTTACTCAA	780
DB	742	GTGACTGTATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAGTCTTGCCTTACTCAA	801
QY	781	CTCTGA	786
DB	802	CTCTGA	807

RESULT	3	AR076926	LOCUS	840 bp	DNA	linear	PAT 31-AUG-2000
		AR076926	Sequence	11	from patent US 5961974.		

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Qy	1	ATGATAGAAACATACAGCAACCTTCCCCAGATCCGTGGCAACTGGACTTCACGAGGC	60		
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Qy	61	ATGAAGATTTTATGTATTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA	120		
Db	61	ATGAAATTTTATGTATTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA	120		
Qy	121	CTTTTTCGTGTATCTCTCATAGAGGTTGGACAAGATAGAAGATGAAGGAATCTTCAT	180		
Db	121	CTTTTTCGTGTATCTCTCATAGAGGTTGGACAAGATAGAAGATGAAGGAATCTTCAT	180		
Qy	181	GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCCTTATCC	240		
Db	181	GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCCTTATCC	240		
Qy	241	TTACTGAACTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300		
Db	241	TTACTGAACTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300		
Qy	301	AACAAAGAGGACGAGAAAGAAACAGCTTGAATGCAAAAAGGTGATCAGAATCCT	360		
Db	301	AACAAAGAGGACGAGAAAGAAACAGCTTGAATGCAAAAAGGTGATCAGAATCCT	360		
Qy	361	CAAAATTCGGGCACATCTCAATAGTGAAGGCGACAGTAAACAAACATCTGTTCACGTGG	420		
Db	361	CAAAATTCGGGCACATCTCAATAGTGAAGGCGACAGTAAACAAACATCTGTTCACGTGG	420		
Qy	421	GCTGAAAAGGATACTACACATGACACAACTTGGTAACCTCGAAAATGGGAAACAG	480		
Db	421	GCTGAAAAGGATACTACACATGACACAACTTGGTAACCTCGAAAATGGGAAACAG	480		
Qy	481	CTGACCGTTTAAAGACAAGGACTCTATTATCTATGTCGCAAGTCAACCTCTGTTCCAAT	540		
Db	481	CTGACCGTTTAAAGACAAGGACTCTATTATCTATGTCGCAAGTCAACCTCTGTTCCAAT	540		
Qy	541	CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCAGCTCTGGCTAAAGTCCCGCGTAGA	600		
Db	541	CGGGAAGCTTCGAGTCAAGCTCAATTTATAGCAGCTCTGGCTAAAGTCCCGCGTAGA	600		
Qy	601	TTGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAAACCTTCGGGGCAA	660		
Db	601	TTGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAAACCTTCGGGGCAA	660		
Qy	661	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCCAGTCTCGGTGTTTGTCAAT	720		
Db	661	CAATCCATTCACCTTGGGAGGAGTATTTGAATTCGAACCCAGTCTCGGTGTTTGTCAAT	720		
Qy	721	GTGACTGATCCAAAGCAAGTCAGGCAATGGCACTGGCTTCACGCTTCCTTGGCTTACTCAA	780		
Db	721	GTGACTGATCCAAAGCAAGTCAGGCAATGGCACTGGCTTCACGCTTCCTTGGCTTACTCAA	780		
Qy	781	CTCTGA 786			
Db	781	CTCTGA 786			
RESULT	2				
LOCUS	AR044779		840 bp	DNA	linear
DEFINITION	Sequence 3 from patent US 5817516.				
ACCESSION	AR044779				
VERSION	AR044779.1				
KEYWORDS	GI:5966244				

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 840) Kehry, M. and Castle, B.
TITLE	Methods for proliferating and differentiating B cells with high density membrane CD40 ligand

ACCESSION AR076926  
VERSION AR076926.1 GI:10003672  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)

Amitage,R.J., Fanslow,W.C. and Spriggs,M.K.  
Monoclonal antibodies to CD40 ligand, pharmaceutical composition

TITLE comprising the same and hybridomas producing the same  
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers

source  
1. 840

BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN /organism="unknown"

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACTTCCACCGAGC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACCTGGACTGCCATCAGC 105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ATGAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 106 ATGAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 CTTTTGCTGTATCTTTCATAGAGTTGGACAGATAGAGATGAAGATGAAGGAATCTTCAT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 166 CTTTTGCTGTATCTTTCATAGAGTTGGACAGATAGAGATGAAGATGAAGGAATCTTCAT 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 GAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 GAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTAAGGATATATGTTA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTAAGGATATATGTTA 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 346 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 CAATTTGCGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 406 CAATTTGCGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 421 GCTGAGAGAACTTACTACAGAGTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCA 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 646 TTCGAGAGAACTTACTACAGAGTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCA 705
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 661 CAATCCATTTCATTTGGGAGGAGTATTTGAATTCGAACACAGTGTCTCGGTGTTTCCAA 720
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Qy 706 CAATCCATTTCATTTGGGAGGAGTATTTGAATTCGAACACAGTGTCTCGGTGTTTCCAA 765
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 721 GTGACTGATCCAGCCAGTGAAGCCATGGCACTGCTTCAGTCTCTTTGGCTTACTCAA 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 766 GTGACTGATCCAGCCAGTGAAGCCATGGCACTGCTTCAGTCTCTTTGGCTTACTCAA 825
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 4

AR078316  
LOCUS AR078316  
DEFINITION Sequence 11 from patent US 5962406.  
ACCESSION AR078316  
VERSION AR078316.1 GI:10005062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)  
AUTHORS Amitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical  
composition containing the same  
JOURNAL Patent: US 5962406-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers

source  
1. 840

BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN /organism="unknown"

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACTTCCACCGAGC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTGCGGCACCTGGACTGCCATCAGC 105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ATGAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 106 ATGAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA 165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 CTTTTGCTGTATCTTTCATAGAGTTGGACAGATAGAGATGAAGATGAAGGAATCTTCAT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 166 CTTTTGCTGTATCTTTCATAGAGTTGGACAGATAGAGATGAAGATGAAGGAATCTTCAT 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 GAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGAGTCAACACAGAGAAAGATCCTTATCC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 GAAGATTTTATGTATTTACTTACTCTTTTCTTATCACCAGAGTCAACACAGAGAAAGATCCTTATCC 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTAAGGATATATGTTA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTAAGGATATATGTTA 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 346 AACAAAGAGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 CAATTTGCGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 406 CAATTTGCGGCACATGTCATAGTCAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 421 GCTGAGAGAACTTACTACAGAGTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCA 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 466 GCTGAGAGAACTTACTACAGAGTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCA 525
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 481 CTGACCGTTTAAAGACAAAGGACTCTTATTTATCTATGCCCAAGTCACCTCTCTGTTCCTCA 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 526 CTGACCGTTTAAAGACAAAGGACTCTTATTTATCTATGCCCAAGTCACCTCTCTGTTCCTCA 585
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 600
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 645
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCAAAACCTTGGGGCAA 660  
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QY 661 CAATCCATTCTCTGGAGGAGTATTTGAATTCGCAACAGTTCGGTCTGTTGTCAAT 720  
Db 706 CAATCCATTCTCTGGAGGAGTATTTGAATTCGCAACAGTTCGGTCTGTTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTTCGCACTGGCTTCACGCTCTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTTCGCACTGGCTTCACGCTCTTGGCTTACTCAAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 5  
AR085419  
LOCUS AR085419 840 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 11 from patent US 5981724.  
ACCESSION AR085419  
VERSION AR085419.1 GI:10012188  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40  
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGATCCGTCGCACTGGCTTCAGCAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCGCACTGGCACTCCATCAGC 105  
QY 61 ATGAGATTTTATGATTTACTTACTCTTTCTTATCACCAGATGATGGGTGACGA 120  
Db 106 ATGAAATTTTATGATTTACTTACTCTTTCTTATCACCAGATGATGGGTGACGA 165  
QY 121 CTTTTCCTGTCTATCTTCTATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTTCCTGTCTATCTTCTATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACAGAGGAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACAGAGGAAGATCTTATCC 285  
QY 241 TTACTGAACCTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
Db 286 TTACTGAACCTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345  
QY 421 GCTGAAAGAGGATACACCATGAGCAACACTTGGTAAACCTGGAAATGGGAAACAG 480

Db 466 GCTGAAAAAGGATACCTACACCATGAGCAACAACCTTGGTAAACCTGGAAAAATGGGAAACAG 525  
QY 481 CTGACCGTTTAAAGACAAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTTAAAGACAAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGGCTTAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGGCTTAAGTCCCGCGGTAGA 645  
QY 601 TTTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAA 660  
Db 646 TTTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGCGGCAA 705  
QY 661 CAATCCATTCTCTGGAGGAGTATTTGAATTCGCAACAGTTCGGTCTGTTGTCAAT 720  
Db 706 CAATCCATTCTCTGGAGGAGTATTTGAATTCGCAACAGTTCGGTCTGTTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTTCGCACTGGCTTCACGCTCTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTTCGCACTGGCTTCACGCTCTTGGCTTACTCAAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 6  
AR103375  
LOCUS AR103375 840 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 11 from patent US 6087329.  
ACCESSION AR103375  
VERSION AR103375.1 GI:12814963  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.  
TITLE CD40 ligand polypeptide  
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGATCCGTCGCACTGGCTTCAGCAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCGCACTGGCACTCCATCAGC 105  
QY 61 ATGAGATTTTATGATTTACTTACTCTTTCTTATCACCAGATGATGGGTGACGA 120  
Db 106 ATGAAATTTTATGATTTACTTACTCTTTCTTATCACCAGATGATGGGTGACGA 165  
QY 121 CTTTTCCTGTCTATCTTCTATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTTCCTGTCTATCTTCTATAGAGGTTGGCAAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACAGAGGAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACAGAGGAAGATCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
Db 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345  
QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTTCAATGCAAAAGGTGATCAGATCTCT 360

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Db 346 AACAAAGAGGACGAAGAAGAAAAACAGCTTGAATGCAAAAAGGTGATCAGAATCCT 405  
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Qy 361 CAAATGGCGGCACATGTCATAGTGGCCAGCCAGCAGTAAACAACATCTGTGTACAGTGG 420  
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Db 406 CAAATGGCGGCACATGTCATAGTGGCCAGCCAGCAGTAAACAACATCTGTGTACAGTGG 465  
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Qy 421 GCTGAAAAGGATGATACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 480  
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Db 466 GCTGAAAAGGATGATACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 525  
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Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 540  
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Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 585  
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Db 586 CGGGAAGCTTCCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645  
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Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTCTCGGTGTTCCTCAAT 765  
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Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGCTCAAGTCTTTCGCTTACTCAAA 780  
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Db 766 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGCTCAAGTCTTTCGCTTACTCAAA 825  
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Qy 781 CTCTGA 786  
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Db 826 CTCTGA 831

RESULT 7  
AR106246 AR106246 840 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 7 from patent US 6106832.  
DEFINITION AR106246  
ACCESSION AR106246  
VERSION AR106246.1 GI:12820776  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.  
TITLE Treatment of individuals exhibiting defective CD40L  
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60  
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Db 46 ATGATCGAACAATACACCAACTTCTCCCGATCTGGCCAGTGGACTGCCATCAGC 105  
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Qy 61 ATGAAGATTTTATGTTATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGCA 120  
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Db 106 ATGAAAATTTTATGTTATTTACTTACTGTTTCTTATCACCAGATGATGGGTACAGCA 165  
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Qy 121 CTTTTTGTGTTATCTTCAATAGAGGTTGGACAGATAGAGATGAAGAGGAATCTTCAT 180  
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Db 166 CTTTTTGTGTTATCTTCAATAGAGGTTGGACAGATAGAGATGAAGAGGAATCTTCAT 225  
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Qy 181 GAAGATTTTGTATTTCATGAAAAAGATACAGAGATGCAACACAGAGAGAAAGATCTTTATCC 240  
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Db 226 GAAGATTTTGTATTTCATGAAAAAGATACAGAGATGCAACACAGAGAGAAAGATCTTTATCC 285  
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Qy 241 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300  
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Db 286 TTACTGAATCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345  
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Qy 301 AACAAAGAGGACGAAGAAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCT 360  
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Db 346 AACAAAGAGGACGAAGAAGAAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCT 405  
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Qy 361 CAAATTTGGCGGCACATGTCATAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGG 420  
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Db 406 CAAATTTGGCGGCACATGTCATAGTGGCCAGCAGTAAACAACATCTGTGTACAGTGG 465  
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Qy 421 GCTGAAAAGGATGATACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 480  
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Db 466 GCTGAAAAGGATGATACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 525  
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Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 540  
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Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 585  
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Qy 541 CGGGAAGCTTCCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
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Db 586 CGGGAAGCTTCCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645  
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Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 660  
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Db 646 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCAA 705  
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Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTCTCGGTGTTCCTCAAT 765  
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Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGCTCAAGTCTTTCGCTTACTCAAA 780  
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Db 766 GTGACTGATCCAAAGCAAGTGGCCATGCGACTGCTCAAGTCTTTCGCTTACTCAAA 825  
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Qy 781 CTCTGA 786  
|||||  
Db 826 CTCTGA 831

RESULT 8  
AR169232 AR169232 840 bp DNA linear PAT 17-DEC-2001  
LOCUS Sequence 11 from patent US 6290972.  
DEFINITION AR169232  
ACCESSION AR169232  
VERSION AR169232.1 GI:17907047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and  
Gibson,M.G.  
TITLE Method of augmenting a vaccine response by administering CD40  
JOURNAL ligand  
FEATURES Patent: US 6290972-A 11 18-SEP-2001;  
Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60



SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A.  
TITLE Soluble and its use in B cell stimulation  
JOURNAL Patent: US 5540926-A 1 30-JUL-1996;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 263 a 182 c 181 g 214 t  
ORIGIN  
Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAACATACAGCCAACTTCCCGCAGATCCGTGGCAACTGGACTTCCACGGAGC 60  
Db 22 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGCGGCCACTGGACTGCCCATCAGC 81  
Qy 61 ATGAAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 120  
Db 82 ATGAAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 141  
Qy 121 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180  
Db 142 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 201  
Qy 181 GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 240  
Db 202 GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 261  
Qy 241 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300  
Db 262 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321  
Qy 301 AACAAAGAGGACCAAGAAACACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360  
Db 322 AACAAAGAGGACCAAGAAACACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 381  
Qy 361 CAAATTTGGGACATGTCTAATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
Db 382 CAAATTTGGGACATGTCTAATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 441  
Qy 421 GCTGAAAGAGGATACACACATGAGCAACACTTTGGTAAACCTGGAACATGGGAACAG 480  
Db 442 GCTGAAAGAGGATACACACATGAGCAACACTTTGGTAAACCTGGAACATGGGAACAG 501  
Qy 481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAGCTTCCCTTCTGTTCCTCAAT 540  
Db 502 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAGCTTCCCTTCTGTTCCTCAAT 561  
Qy 541 CGGGAAGCTTCAGGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
Db 562 CGGGAAGCTTCAGGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 621  
Qy 601 TTCGAGAGAACTTACTCAGAGCTCAAAATCCACAGTTCGCCCAAACTTGGCGGCA 660  
Db 622 TTCGAGAGAACTTACTCAGAGCTCAAAATCCACAGTTCGCCCAAACTTGGCGGCA 681  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCTGTTTCTCAAT 720  
Db 682 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCTGTTTCTCAAT 741  
Qy 721 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTTCACGCTTTCCTTACTCAA 780  
Db 742 GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTTCACGCTTTCCTTACTCAA 801  
Qy 781 CTCTGA 786  
Db 802 CTCTGA 807

RESULT 11  
LOCUS I27345 I27345 840 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 7 from patent US 5565321.  
ACCESSION I27345  
VERSION I27345.1 GI:1818121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs, M. K., Armitage, R. J., and Fanslow, W. C. III.  
TITLE Detection of mutations in a CD40 ligand gene  
JOURNAL Patent: US 5565321-A 7 15-OCT-1996;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN  
Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. No. 4.7e-193;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAACATACAGCCAACTTCCCGCAGATCCGTGGCAACTGGACTTCCACGGAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGCGGCCACTGGACTGCCCATCAGC 105  
Qy 61 ATGAAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 120  
Db 106 ATGAAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACAGATGATGGGTGACGA 165  
Qy 121 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180  
Db 166 CTTTTTGTGTGTATCTTATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAACACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 285  
Qy 241 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300  
Db 286 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345  
Qy 301 AACAAAGAGGACCAAGAAACACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360  
Db 346 AACAAAGAGGACCAAGAAACACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 405  
Qy 361 CAAATTTGGGACATGTCTAATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
Db 406 CAAATTTGGGACATGTCTAATAGTGAGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAGAGGATACACACATGAGCAACACTTTGGTAAACCTGGAACATGGGAACAG 480  
Db 466 GCTGAAAGAGGATACACACATGAGCAACACTTTGGTAAACCTGGAACATGGGAACAG 525  
Qy 481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAGCTTCCCTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCAGCTTCCCTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCAGGTCAAGCTCCATTTATAGCCAGCTTCCCTTAAAGTCCCGCGGTAGA 600  
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Qy 601 TTCGAGAGAACTTACTCAGAGCTCAAAATCCACAGTTCGCCCAAACTTGGCGGCA 660  
Db 646 TTCGAGAGAACTTACTCAGAGCTCAAAATCCACAGTTCGCCCAAACTTGGCGGCA 705  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCTGTTTCTCAAT 720  
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Db 706 CAATCCATTTCAGTGGAGGAGTATTTCAATTCGAACCAAGGTGCTTCGGTGTTCAT 765  
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 Db 766 GTGACTGATCCAAAGCAAGTGAAGCCAGTGGCTTCACGCTCTTCGCTTACTCAAA 825  
 QY 781 CTCTGA 786  
 Db 826 CTCTGA 831  
 RESULT 12  
 LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998  
 DEFINITION Sequence 1 from patent.US 5674492.  
 ACCESSION 167828  
 VERSION 167828.1 GI:2829950  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 840)  
 AUTHORS Armitage,R.J., Fanslow,W.C. III, Longo,D.L. and Murphy,W.J.  
 TITLE Method of preventing or treating disease characterized by  
 neoplastic cells expressing CD40  
 JOURNAL Patent: US 5674492-A 1 07-OCT-1997;  
 FEATURES Location/Qualifiers  
 source 1..840  
 BASE COUNT 266 a 185 c 175 g 214 t  
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 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
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 ACCESSION AX090039  
 VERSION AX090039.1 GI:13444004  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 879)  
 AUTHORS Ahuja,S.U. and Bonewald,L.U.  
 TITLE Cdx4 agonist compositions and methods of use  
 JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;  
 BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)  
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DEFINITION H.sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION Z15017.1
VERSION Z15017.1 GI:38483
KEYWORDS glycoprotein 39.
SOURCE human.
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REFERENCE 1 (bases 1 to 879)
AUTHORS Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
and Aruffo, A.
TITLE The human T cell antigen gp39, a member of the TNF gene family, is
a ligand for the CD40 receptor: expression of a soluble form of
gp39 with B cell co-stimulatory activity
EMBO J. 11 (12), 4313-4321 (1992)
JOURNAL 93049181
MEDLINE 2 (bases 1 to 879)
REFERENCE Hollenbaugh, D.L.
AUTHORS Direct Submission
TITLE Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
JOURNAL PRI, Seattle, WA, 98121
REFERENCE 3 (bases 1 to 879)
AUTHORS Hollenbaugh, D.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
COMMENT The original submission [1] reported 934bp.
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Query Match 97.2%; Score 763.6; DB 9; Length 879;
Best Local Similarity 98.2%; Pred. No. 4.7e-193;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCAACCTTCCGCCAGATCCGTGGCAACTGGACTTCCACCGAGC 60
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QY 781 CTCTGA 786
Db 802 CTCTGA 807
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Thu May 30 05:46:16 2002

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DEFINITION X67878.1 S50586  
ACCESSION X67878.1 GI:38411  
VERSION glycoprotein.  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1803)  
AUTHORS Spriggs, M.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development  
CORPORATION, 51 University Street, Seattle WA 98101, USA  
2 (bases 1 to 1803)  
AUTHORS Spriggs, M., Armitage, R.J., Strockbine, L., Clifford, K.N.,  
Macduff, B.M., Sato, T.A., Maliszewski, C.R. and Fanslow, W.C.  
TITLE Recombinant human CD40 ligand stimulates B cell proliferation and  
immunoglobulin E secretion  
J. Exp. Med. 176 (6), 1543-1550 (1992)  
JOURNAL 93094757  
MEDLINE Location/Qualifiers  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

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Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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LOCUS  
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ACCESSION  
VERSION  
KEYWORDS  
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GI:11695919  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 492)  
Smith T.P.L., Grosse W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Perte, G., Holt, I., Karamecheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.

TITLE  
JOURNAL  
MEDLINE  
COMMENT

Sequence evaluation of four pooled-tissue normalized bovine cdna libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
21180013  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

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BACKWARD: GTTTCCTCAGTCACGCG  
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Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smilchem@marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options.  
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QY 61 ATGAAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120  
DB 113 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGG 172  
QY 121 CTTTTCCTGTGATCTTCTATGAGAGTTGGCAAGATAGAGATGAAGAAATCTTTCAT 180  
DB 173 CTTTTCCTGTGATCTTCTATGAGAGTTGGCAAGATAGAGATGAAGAAATCTTTCAT 232  
QY 181 GAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 233 GAAGATTTTATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 292  
QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
DB 293 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 352  
QY 301 AACAAAGAGGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 346  
DB 353 AACAAAGAGGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 398  
RESULT 3  
AI982044 638 bp mRNA linear EST 07-MAY-2001  
LOCUS pat.pk0072.c9.f chicken activated T cell cDNA Gallus gallus cdna  
DEFINITION clone pat.pk0072.c9.f 5' similar to CD40 ligand, mRNA sequence.  
ACCESSION AI982044  
VERSION AI982044.1 GI:5885072  
KEYWORDS EST.  
SOURCE chicken.  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 638)  
Tirunagaru.V.G., Sofer,L., Cui,J. and Burnside,J.  
An expressed sequence tag database of T-cell-enriched activated  
chicken splenocytes: sequence analysis of 5251 clones  
Genomics 66 (2), 144-151 (2000)  
JOURNAL 20318616  
MEDLINE

/clone\_lib="MARC 3BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."  
BASE COUNT 163 a 103 c 104 g 122 t  
ORIGIN  
Query Match 45.7%; Score 359; DB 10; Length 492;  
Best Local Similarity 87.7%; Pred. No. 2.3e-71;  
Matches 392; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
QY 1 ATGATGAAACATACAGCAACCTCCCCAGATCCCGTGGCAACTGGCACTTCCAGCGAGC 60  
DB 46 ATGATGAAACATACAGCAACCTTCCTCCCGTGGCACTTCCAGCGAGC 105  
QY 61 ATGAAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120  
DB 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGG 165  
QY 121 CTTTTCCTGTGATCTTCTATGAGAGTTGGCAAGATAGAGATGAAGAAATCTTTCAT 180  
DB 166 CTTTTCCTGTGATCTTCTATGAGAGTTGGCAAGATAGAGATGAAGAAATCTTTCAT 225  
QY 181 GAAGATTTTATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 226 GAAGATTTTATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 285  
QY 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
DB 286 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345  
QY 301 AACAAAGAGGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360  
DB 346 AACAAAGAGGAGACGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 405  
QY 361 CAAATGCGGCACATGTCATGATGAGCGCCAGCAAGTAAACACATCTGTTTACAGTGG 420  
DB 406 CAGATAGCGGCACATGTCATGATGAGCGCCAGTAAACACATCTGTTTCCAGTGG 465  
QY 421 GCTGAAAGAGGATACCTACCATCAGC 447  
DB 466 GCCCCCAAGGATACCTACCATCAGC 492  
RESULT 2  
AW486605 398 bp mRNA linear EST 25-APR-2001  
LOCUS 75217 MARC 1BOV Bos taurus cdna 5', mRNA sequence.  
DEFINITION AW486605  
ACCESSION AW486605.1 GI:7056711  
VERSION AW486605.1  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 398)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Fahrenkrug,S.C., Bennett  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Perfeta,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and  
Keele,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cdna  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
JOURNAL 21180013  
MEDLINE  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA













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Query Match      6.0%; Score 47.2; DB 9; Length 797;
Best Local Similarity 39.6%; Pred. No. 1.3;
Matches 168; Conservative 37; Mismatches 215; Indels 4; Gaps 1;

QY 151 GACAAGATAGAAAGTAAAGCAATCTTCATCAAGCATTTTGTATTCAATGAAAGCAATACAG 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 GAAAWAAAAAAWTTWAAAAAAGAAAAAATTAATGAAAGGAAAGAAAAATTAAGGA 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 AGATGCAACACAGAGAAAGATCTTATCTTACTGAACTGTGAGGAGATTAAGAGCCAG 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 AAATTTAAAAAAGAAAAAGTAAATTTWATTTWARRAGGATTAATAAATAAAAAAATGTA 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 TTTGAAGCTTTGTGAAGGAT----ATAATGTTAAACAAAGAGAGAGAGAAAGAAAA 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 WAAGAGGAAAAAGAAAGATAAATAAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 327 CAGCTTTGAATGCAAAAGGTGATCAGAAATCTCAATTTGCGGCACATGTCTAATGTA 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 AAGTAWAGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGG 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 387 GCCCAGCAGTAACACATCTGTGTACAGTGGCTGAAAGAGTACTACACCATGAG 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 ARATGGAATAATGATTAATAAATAAATTAATAAATAAATAAATAAATAAATAAATAA 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 447 CAACAACCTTGTAACCCCTGGAAATGGAAACAGCTGACCGTTAAAGACAGAGCTCTA 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 AAATTAATAAATGAAAGAAAAAAGAAAAAAGAAAAAATTAATAAATAAATAAATAAATAA 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 507 TTATATCTATGCCCAAGTCATCTCTCTTCAATCGGGAAGCTTCAGTCAAGCTCCATT 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 TTGTMTTMMTMTWAGGMMMTTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMMTMM 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 TATA 570
    |||
Db 664 MMTA 667
    |||

RESULT 12
BG715238
LOCUS      602676117F1 NIH_MGC_96 845 bp mRNA linear EST 08-MAY-2001
DEFINITION mRNA sequence.
ACCESSION BG715238
VERSION    BG715238.1 GI:13994417
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 845)
           NIH-MGC http://mgi.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgaabs-remail.nih.gov
           Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
           cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
           Toshiyuki and Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10686 row: b column: 05
           High quality sequence stop: 830.
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         /tissue_type="hypothalamus"
         /lab_host="NIH_MGC_96"

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/tissue_type="hypothalamus"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
); Size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      284 a 151 c 228 g 182 t
ORIGIN

Query Match      6.0%; Score 47.2; DB 10; Length 845;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATG 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 TTCATACATTACAGTGGTTGGAATAAATAATCGGATGAATGGTTCGCGAGCAGAGTA 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 TTAACAAAGAGGAGAGAGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGAA 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 CTCAAAATACGTGGACCAATTTGCAGAAACAGCGAGAACTTCAAAAGAGCCAAATCAGGAG 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 CCTCAATTCGGGCACATGTCATTAAGTGAGGCGCAGCAGTAAACACATCTGTGTACAG 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 CAGTATGCAGAGGGGAGAGATGAGAGGGGCTGCCCGAGAAAGAGACATCTGGTCTGCAA 356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 TGGGCTGAAAAGGATACATACACATGAGCAACACTTTGGTAAACCTCGAAATGG 473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 CAGAAAAATGTTGAAGTGAAAAACGAAAAAGAAACAAACAGAAACACCTGGGAATGG 412
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
BG715238
LOCUS      603249012F1 NIH_MGC_96 845 bp mRNA linear EST 07-SEP-2001
DEFINITION mRNA sequence.
ACCESSION BG715238
VERSION    BG715238.1 GI:15494371
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 845)
           NIH-MGC http://mgi.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgaabs-remail.nih.gov
           Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
           cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
           Toshiyuki and Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11761 row: h column: 04
           High quality sequence stop: 740.
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     Location/Qualifiers
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         /organism="Homo sapiens"
         /db_xref="taxon:9606"
         /clone="IMAGE:5300787"
         /clone_lib="NIH_MGC_96"
         /tissue_type="hypothalamus"
         /lab_host="DH10B"
         /note="Organ: brain; Vector: pBluescriptR (modified

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insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
 Library."

BASE COUNT 296 a 159 c 226 g 192 t  
 ORIGIN

Query Match 6.08; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 50.08; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy	238	TCCTTACTGAAC	TGTGAGGAGATTAAAGCCAGCTTTGAAGGCTTTGTCAAGGATATATG	297
Db	144	TTCATACATTAC	AGTGGTGGATGAATGGGTTCCGGAGAGTAGATA	203
Qy	298	TTAAACAAGAGG	AGACGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAAT	357
Db	204	CTCAAAATACGT	GGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCCAATCAGGAG	263
Qy	358	CCTCAAAATGCG	GCACATGTCATAAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAG	417
Db	264	CAGTATGCAGAG	GGGAGATGAGAGGGCTGCCCGAGGAAAGACACATCTGGTCTGCAA	323
Qy	418	TGGGCTGAAAAA	GGATACACCATGAGCAACAACTTTGGTAACCCCTGGAAAAATGG	473
Db	324	CAGAAAAATGTT	GAGTGAAGTCAAAACGAAAGAAACAAACAGAAACACACCTGGAAATGG	379

Search completed: May 30, 2002, 01:00:13  
 Job time: 22223 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:23 ; Search time 680.87 Seconds  
(without alignments)  
1982.015 Million cell updates/sec

Title: US-08-982-272-6

Perfect score: 786

Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTCA 786

Scoring table:

IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1981.DAT.\*
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- 5: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1984.DAT.\*
- 6: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1985.DAT.\*
- 7: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1986.DAT.\*
- 8: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1987.DAT.\*
- 9: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1988.DAT.\*
- 10: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1989.DAT.\*
- 11: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1990.DAT.\*
- 12: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA1991.DAT.\*
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- 22: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA2001A.DAT.\*
- 23: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA2001B.DAT.\*
- 24: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	100.0	786	19	AAV39002
2	776.4	98.8	786	19	AAV39003
3	763.6	97.2	786	15	AA063959
4	763.6	97.2	786	15	AAV38997
5	763.6	97.2	786	19	AAV12852
6	763.6	97.2	840	14	AA041506
7	763.6	97.2	840	15	AA067123
8	763.6	97.2	840	16	AA050763
9	763.6	97.2	840	18	AAAT93782

10	763.6	97.2	840	19	AAV61063	Human CD40 ligand
11	763.6	97.2	840	20	AA027525	Human CD40-L codin
12	763.6	97.2	879	22	AA055539	Nucleotide sequenc
13	763.6	97.2	1816	23	AA051745	Human CD40 ligand
14	763.6	97.2	1816	23	AA086571	DNA encoding novel
15	762	96.9	840	15	AA057984	Genomic sequence o
16	760.6	96.8	840	18	AA058122	Human CD40L mutain
17	758.8	96.5	840	16	AA094091	Human CD40-L cDNA.
18	754	95.9	786	19	AAV39000	Exemplary CD40 lig
19	704.4	89.6	783	19	AAV42184	Exemplary nucleoti
20	648.2	82.5	1552	22	AA025525	Nucleotide sequenc
21	642.8	81.8	865	22	AA082933	HIV-1 gp120 V3 loo
22	642.8	81.8	906	22	AA082932	HIV-1 gp120 V3 loo
23	642.8	81.8	2209	22	AA082929	HIV-1 gp120-human
24	642.8	81.8	2252	22	AA082928	HIV-1 gp120-human
25	642	81.7	864	19	AAV39004	CD40 ligand gene u
26	638.2	81.2	1425	14	AA041516	Human CD40-L/Fc fu
27	638.2	81.2	1425	20	AA027534	Human CD40-L/Fc fu
28	637.2	81.1	929	18	AA027533	CDNA encoding yeas
29	637.2	81.1	929	20	AA027537	Human trimeric CD4
30	608.4	77.4	885	21	AA055540	Feline CD154 cDNA.
31	608.4	77.4	885	21	AA055541	Feline CD154 cDNA
32	605.4	77.0	780	21	AA055542	Feline CD154 cDNA
33	605.4	77.0	780	21	AA055543	Feline CD154 cDNA
34	584.4	74.4	783	15	AA063960	Mouse CD40-L type
35	584.4	74.4	783	19	AAV12853	CD40 ligand coding
36	584.4	74.4	783	20	AA027524	Mouse CD40-L codin
37	582.8	74.1	783	19	AAV38998	CD40 ligand gene u
38	582.8	74.1	818	19	AAV61062	Murine CD40 ligand
39	581.2	73.9	1878	21	AA055534	Canine CD154 cDNA.
40	581.2	73.9	1878	21	AA055535	Canine CD154 cDNA
41	580.2	73.8	782	14	AA041507	Murine CD40-L DNA.
42	578.2	73.6	780	21	AA055536	Canine CD154 cDNA
43	578.2	73.6	780	21	AA055537	Canine CD154 cDNA
44	570	72.5	783	19	AAV38999	Exemplary CD40 lig
45	560.4	71.3	783	19	AAV39001	Exemplary CD40 lig

ALIGNMENTS

RESULT 1

AAV39002

ID AAV39002 standard; DNA: 786 BP.

XX AC AAV39002;

XX AC AAV39002;

XX DT 23-SEP-1998 (first entry)

XX DE Exemplary CD40 ligand gene used in the course of the invention.

XX DE CD40 ligand; alteration; immunoreactivity; human cell;  
XX KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
XX KW autolimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX OS Chimeric - Mus sp.

XX OS Chimeric - Homo sapiens.

XX PN WO9826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX XX Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

XX XX





Db 421 gctgaaaggatgactacacacatgagcaacaacttggtgaacccctggaaatgggaaacag 480  
Qy 481 CTGACCGTTAAACACAGGACTCTATTATATCTATGTCGCCCAAGTCACCTTCTGTTCAT 540  
Db 481 ctgaccgttaaaagacaggaactattatctatgcccgaagtcacacctctgttccaat 540  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCTTAAGTCCCGGGTGA 600  
Db 541 cggaagcttcgagtcgaagctccatttatagccagcctctgctaaagtcccccggtaga 600  
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCTTCGGGGCAA 660  
Db 601 ttcgagagaaacttactcagagctgcaataaccacagttccgcgaacacctgcgggcaa 660  
Qy 661 CAATCCATTCACCTTGGGAGGAGTATTGAATGCAACAGGTGCTTCGGGTGTGTCAAT 720  
Db 661 caatccattcacttgggagagatttgattgaattgcaaccagtgcttcgggtgttgcatt 720  
Qy 721 GTGACTGATCAAGCAAGTCAAGTGGCACTGGCTTCAGTCTTGGCTTACTCAAA 780  
Db 721 gtgactgatccaagccaagtgagccatggcactggcactggcttcacgtctcttggcttactcaaa 780  
Qy 781 CTCCTGA 786  
Db 781 ctctga 786

RESULT 4  
AAV38997  
ID AAV38997 standard; DNA; 786 BP.  
XX AAV38997;  
XX  
XX  
DT 23-SEP-1998 (first entry)  
XX  
XX  
DE CD40 ligand gene used in the course of the invention.  
XX  
XX  
KW CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.  
XX  
XX  
OS Mus sp.  
XX  
XX  
PN WO9826061-A2.  
XX  
XX  
PD 18-JUN-1998.  
XX  
XX  
PF 08-DEC-1997; 97WO-US22740.  
XX  
XX  
PR 01-DEC-1997; 97US-0982272.  
PR  
PR 09-DEC-1996; 96US-0032145.  
XX  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
XX  
PI Cantwell M, Kipps TJ, Sharma S;  
XX  
XX  
XX WPI; 1998-348521/30.  
XX  
XX  
PT vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX  
XX  
PS Disclosure; Page 104; 167pp; English.  
XX  
XX  
XX The present sequence represents the CD40 ligand gene. The sequence is  
XX used to exemplify the method of the invention. The specification  
XX describes a method for altering the immunoreactivity of human cells  
XX which comprises introducing a gene encoding an accessory molecule  
XX ligand (AML) into the cells so that the AML is expressed on the surface  
XX of the cells. Vectors containing the AML genes can be used in gene  
XX therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
XX arthritis. They can also be used for vaccination to produce immunity  
XX against a virus cell, bacteria, protein, fungus or neoplasia.

XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;  
Query Match 97.2%; Score 763.6; DB 19; Length 786;  
Best Local Similarity 98.2%; Pred. No. 8.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCAACCTTCCCCAGATCCGCGGCAACTGGACCTTCCACCGAGC 60  
Db 1 atgatgaaacatacagcaaaccttcccccagatctggccactggactgcccacagc 60  
Qy 61 ATGAAGATTTTATGTATTACTTACTTCTTCTTATCACCACAGATGTTGGGTGACGA 120  
Db 61 atgaagatttttattgtatttacttactgttttcttctatcaccacagatgattgggtcagca 120  
Qy 121 CTTTTGCTGTGTATCTTCATAGAGTTGGCAAGATAGAAGATGAAGAAATCTTCAT 180  
Db 121 ctttttgcgtgtatcttctcatagaaagttggcaagatagaagatgaagggaattcttcat 180  
Qy 181 GAAGATTTTGTATTATGAAACGATTACAGATGCAACACAGGAGAAAGATCCTTATCC 240  
Db 181 gaagattttgtatttcatgaaacgatacacagatgcaacacagggagaaagatccttctacc 240  
Qy 241 TTTACTGACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATGTTA 300  
Db 241 ttactgaactgtgagagatactaaagccagtttgaagagcttggaaaggttgaagataataatgta 300  
Qy 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGATCCT 360  
Db 301 aacaaagaggagagcaagaagaaacagctttgaaatgcaaaaggtgatcagatcct 360  
Qy 361 CAATTCGGCACATGTCATAGTGAGGCCAGCAGTAAACACATCTGTGTACAGTGG 420  
Db 361 caaattgcgacatgtcataagtgaggccagcagtagtaaaacaacatctggttacagtgg 420  
Qy 421 GCTGAAAAGGATACTACACCATGAGCAACAACCTTGTGTACCTTGGAAATGGAAACAG 480  
Db 421 gctgaaaaggatactacacccatgagcaacaacttgtaaccttgaaaaatgggaaacag 480  
Qy 481 CTGACCGTTAAACACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCAT 540  
Db 481 ctgaccgttaaaagacagaggaactctattatctatctatgcccaagtcaccttctgtccaat 540  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTCCTTAAAGTCCCCGGGTAGA 600  
Db 541 cggaagcttcgagtcgaagctccatttatagccagcctctgctaaagtcccccggtaga 600  
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCCGCCAAACCTTCGGGGCAA 660  
Db 601 ttcgagagaaacttactcagagctgcaataaccacagttccgcgaacaccttgcgggcaa 660  
Qy 661 CAATCCATTCACCTTGGGAGGAGTATTGAATGCAACAGGTGCTTCGGGTGTGTCAAT 720  
Db 661 caatccattcacttgggagagatttgattgaattgcaaccagtgcttcgggtgttgcatt 720  
Qy 721 GTGACTGATCAAGCAAGTCAAGTGGCACTGGCTTCAGTCTTGGCTTACTCAAA 780  
Db 721 gtgactgatccaagccaagtgagccatggcactggcactggcttcacgtctcttggcttactcaaa 780  
Qy 781 CTCCTGA 786  
Db 781 ctctga 786

RESULT 5  
AAV12852  
ID AAV12852 standard; cDNA to mRNA; 786 BP.  
XX AAV12852;  
XX  
XX  
DT 13-MAY-1998 (first entry)  
XX





541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTTCCTTAAGTCCCGGTAGA 600  
586 cgggaagcttcagtcgaagctcatttatagccagcctctgcttaagtcctcccgtaga 645  
601 TTCGAGAGAATCTTACTCAGAGCTGCAATATCCACAGTTCGCCCAAACTTCGCGGCAA 660  
646 ttcgagagaatcttactcagagctgcaaataccacagttccgcaaaccttcgcgggcaa 705  
661 CAATCCATTCACCTGGGAGGAGTATTGTAATTCGAACACAGGCTTCGCTGTTTGTCAAT 720  
706 caatccattcactcgggagaggtatttgatgcaaccagtgcttcggtttgtcaat 765  
721 GTGACTGATCCAAAGCAAGTGCAGCCATGCGCTTCACGCTTCCTTGGCTTACTCACA 780  
766 gtgactgatccaaagcgaagtgagccatggcactggcttcacgttcctttggttactccaa 825  
781 CTCTGA 786  
826 ctctga 831

RESULT 7  
AA067123  
ID AA067123 standard; DNA; 840 BP.  
XX AA067123;  
AC AA067123;  
XX 23-MAR-1995 (first entry)  
DT CD40 ligand gene.  
DE CD40 ligand gene.  
XX  
KW Probe; primer: PCR; amplify; polymerase chain reaction; detection;  
mutation; CD40 ligand gene; IGM; ss.  
XX Synthetic.  
OS  
FH Key Location/Qualifiers  
FT CDS 46..831  
FT /\*tag= a  
FT /product= CD40 ligand  
XX  
PN WO9417196-A.  
XX  
PD 04-AUG-1994.  
XX  
PE 21-JAN-1994; 94WO-US00786.  
XX  
PR 22-JAN-1993; 93US-0009258.  
PR 20-JAN-1994; 94US-0184422.  
XX  
PA (IMMV ) IMMUNEX CORP.  
PI Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;  
PI Spriggs MK, Widmer MB;  
XX WPI; 1994-264109/32.  
DR P-PSDB; AAR57469.  
XX  
PT Method for detecting mutation in CD 40 ligand gene - comprises  
amplification of nucleic acid, and mutational analysis  
XX  
PS Disclosure: Page 22-24; 38pp; English.  
XX  
CC This sequence represents the CD40 ligand gene. Mutations within  
CC this gene were identified by the method of the invention. The  
CC method comprises isolating DNA from an individual and selectively  
CC amplifying the isolated DNA derived from the CD40 ligand gene. The  
CC amplification product is then analysed to determine if there is a  
CC mutation present and determining if a protein expressed from the  
CC ligand gene will bind CD40. The detection of mutations in the CD40  
CC ligand gene allows subsequent treatment of a syndrome resulting in  
CC elevated levels of serum Igm and diminished levels of other Ig  
CC isotypes, due to mutation in the CD40 ligand gene. ie. X-linked

29-APR-1993.  
23-OCT-1992; 92WO-US08990.  
25-OCT-1991; 91US-0783707.  
05-DEC-1991; 91US-0805723.  
(IMMV ) IMMUNEX CORP.  
Armitage RJ, Fanslow WC, Spriggs MK;  
WPI; 1993-152417/18.  
P-PSDB; AAR36701.  
New cytokine CD40-L as CD40 agonist and antagonist - is used for  
treating allergies, lupus, rheumatoid arthritis,  
graft-versus-host disease and insulin-dependent diabetes mellitus  
Claim 1; Fig 2; 80pp; English.  
This sequence encodes a human CD40-L polypeptide which binds to CD40.  
CD40-L is a type II membrane polypeptide which has an extracellular  
region at its C-terminus, a transmembrane region and an  
intracellular region at its N-terminus. A soluble form of CD40-L  
lacks the transmembrane domain. CD40-L activity is mediated by  
binding with CD40 and induces B cell proliferation and induction of  
antibody secretion, including IgE. Membrane bound CD40-L acts as a  
CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L  
can be used in a binding assay to detect cells expressing CD40.  
Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;  
Query Match 97.2%; Score 763.6; DB 14; Length 840;  
Best Local Similarity 98.2%; Pred. No. 8.6e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 ATGATAGAAACATACAGCAACCTTCCCGCCAGCTCGTGCAACTGGACATCCCGCGAGC 60  
DB 46 atgatgaacatacacaacaaacttctcccgatctgcggccactggactgcccacagc 105  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCACAGATGATTGGGTGAGCA 120  
DB 106 atgaatattttatgtatttacttactgttttcttaccacagatgattgggtgagca 165  
QY 121 CTTTTGCTGCTGATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180  
DB 166 cttttgctgctgcttcctcatagaaaggttggacaagatagaagatgaaggaatcttc 225  
QY 181 GAAGATTTTGTATTCATGAACGATACAGATGCAACACAGGAGAGATCCTTATCC 240  
DB 226 gaagattttgtatttcataagaaaggttggacaagatagaagatgaaggaatcttc 285  
QY 241 TTACTGAACCTGTCAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 ttactgaactgtgagagattaaagccagtttgaaggctttgtgaaggatataatgtta 345  
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAATGCCAAAAGGTGATCAGAACTCT 360  
DB 346 acaaaagagagagagaaagaaacagctttgaaatgcataaaggtatcagagatcct 405  
QY 361 CAATTCGGCCACATGTCATAAGTGAGCGCAGCAGTAAACACATCTGTGTACAGTGG 420  
DB 406 caaattcggccacatgtcctaagtgagggcagcagtaaaacaacatctgtttacagt99 465  
QY 421 GCTGAAAAGGATACTACCATGAGCAACAACTTGTGAACCTTGGAAAATGGGAACAG 480  
DB 466 gctgaaaaagatactacacatgagcaacaacttgtaacctggaaaatgggaaacag 525  
QY 481 CTGACCGGTTAAAGACAGAGGACTTATATATCTATGCCCAAGTCACCTCTGTCCAA 540  
DB 526 ctgaccggttaaaagacagagactctattatctatgcccaagtcacactctgttccaa 595

CC hyperIgM syndrome.

Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 97.2%; Score 763.6; DB 15; Length 840;  
Best Local Similarity 98.2%; Pred. No. 8.6e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0;

Qy	1	ATGTAGAAACATACAGCCAAACCTTCCCCAGATCGTGGCACTCGGACTTCCAGCGAGC	60
Db	46	atgctgaaacatacaaccaaaactctcccagatctgcggcaactggaatgcccatcagc	105
Qy	61	ATGAAGATTTTATGTATTACTTTACTTTCTTTCTTATCACCAGATGATGGGTGACGA	120
Db	106	atgaaaaattttatgtatttaacttaactgttttcttatcaccagatgatcgggtcagca	165
Qy	121	CTTTTTGCTGTGTATCTTCATAGAAGTTGGCAAGATAGAAGATGAAAGGAATCTTCAT	180
Db	166	cttttctgtgtatctctatagaaagtgtgacaagatagaagatgaaggaaatcttcatt	225
Qy	181	GAAGATTTTGTATTCATGAACGATACAGAGATGCAACACAGGACAAAGATCCTTATCC	240
Db	226	gaagattttgtattcatgaaaacgatacagagatgcaacacaggaagaagatccttatcc	285
Qy	241	TTACTGAACTGTGAGGAGATTAAGACGCCAGTTTGAAGGCTTTCTGAAGGATATAATGTGA	300
Db	286	ttactgaactgtgaggagataaaagccagtttgaaggcttttgaaggatataaagtta	345
Qy	301	AACAAAGAGGAGCGAAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
Db	346	aacaaagaggagacgaagaagaacacagcttttgaagtgcataaaggatcagaaatcct	405
Qy	361	CAAAATCCGGCACATGTCATAAGTGAAGCCAGCAGTAAACACACATCTGTGTACAGTGG	420
Db	406	caaatctgcgcacatg tca taagtggaggccagcagtaaaacaaca tctgtttcacagtgg	465
Qy	421	GCTGAAAAGAGTACTACACCATGAGCAACAACCTTGTAACCTCGAAAATGGGAACAG	480
Db	466	gctgaaaaaggatactacacatgagcaacaacttggtaacctggaaaatgggaaacag	525
Qy	481	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAGTCACCTTCGTTCCAAAT	540
Db	526	ctgacctttaaagacaaggactctatta tctatgccccagtcacctctctgttccaat	585
Qy	541	CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGA	600
Db	586	cgggaagcttcgagtcgaagctccattatagccagcctctgctctaaagtcctcccgtaga	645
Qy	601	TTCCAGAGATCTTTACTCAGAGTGCANAATACCACAGTTCCGCCAAAACCTTCGGGGCAA	660
Db	646	ttcgagagaacttactcagagtgcaaa taccacagtttcgcccaaaacttgcgggcaa	705
Qy	661	CAATCCATTCACTTGGGAGGAGTATTGAATTCACAACAGGTGCTTCGGTGTGTTGTCAAT	720
Db	706	caa tccattcactttgggaggagtatttgaattgcaaccagggtgcttcgggttctgccaat	765
Qy	721	GTGACTGATCCAAAGGAGGACATGAGCAGTGGCTTCACGTCCCTTTGGCTTACTCAA	780
Db	766	gtgactgataccaagcgaagtgagcca tggcacitggttcaagtcctttggcttactcaaa	825
Qy	781	CTCTGA 786	
Db	826	ctctga 831	

## RESULT 8

AA05763

ID	AAT05763	standard	DNA	840 BP.

XX AAT05763:

AC  
XX  
AA103703,

DT 18-MAR-1996 (first entry)

QY	361	CAAAATGGCGCACATGTCATAGTGAGCCGACGCTAAACAAACATCTGCTTACAGTGG	420
Db	382	caaatggcgccacatgtcataagtggccagcagtaaaacacacatctgtgttacagtgg	441
QY	421	GCTGAAAAGGATACATACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG	480
Db	442	gctgaaaaggatatacaccatgagcacaacttggtaacccctggaaaatggaaaacag	501
QY	481	CTGACCGTTTAAAGACAGGACTCTATTATATCTATGTCGCAAGTCACTCTCTGTTCCAAAT	540
Db	502	ctgacccgtttaaagacaagactctattatctatgcccgaagtcacctctgtttccaat	561
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCTAAAGTCCGCCGGTAGA	600
Db	562	cgggaagcttcgagtcgaagctcattatagccagcctctgctaaagtcctcccggtaga	621
QY	601	TTTCGACAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTCGCGGCA	660
Db	622	tttcgagagaaattctactagagctgcaaataccacagttccgccaaccttgcgggcaa	681
QY	661	CAATCCATTACATTTGGGAGGAGTATTGTAATGCAACAGGTGCTTCGGTGTTCAT	720
Db	682	caatccattcaattggaggagatttgattgaattgcaaccaggtgcttcggtttgttcaat	741
QY	721	GTGACTGATCCAGCCAAAGTACGATGCGACTGCGCTTCAGCTCCCTTGGCTTACTCAA	780
Db	742	gtgactgatccaaagccaagtggccatgagcactggcttcacgctccctttggttactcaa	801
QY	781	CTCTGA 786	
Db	802	ctctga 807	
RESULT 9			
AAT93782			
ID	AAT93782 standard; cDNA; 840 BP.		
XX			
AC	AAT93782;		
XX			
DT	16-FEB-1998 (first entry)		
XX			
DE	cDNA of CD40L, a novel cytokine ligand for CD40.		
XX			
KW	Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;		
KW	neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;		
KW	melanoma; carcinoma; ss.		
XX			
OS	Homo sapiens.		
XX			
FT	Key Location/Qualifiers		
FT	46..831		
FT	/*tag= a		
XX			
PN	US5674492-A.		
XX			
PD	07-OCT-1997.		
XX			
PF	21-DEC-1994; 9AUS-0360923.		
XX			
PR	23-DEC-1993; 93US-0172664.		
XX			
PA	(IMV) IMMUNEX CORP.		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX			
PI	Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;		
XX			
DR	WPI; 1997-502273/46.		
DR	P-PSDB; AAW34669.		
XX			
PT	Treating or preventing neoplastic disease associated with		
PT	CD40-expressing cells - particularly B-cell lymphoma, by		
PT	administration of CD40-binding protein, preferably antibody or		
PT	soluble CD40-ligand		

XX	Claim 3: Columns 19-22; 21pp: English.					
PS						
XX						
CC	The present sequence represents the cDNA sequence of a novel cytokine					
CC	ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,					
CC	which is expressed by activated CD4+ T cells, and causes B cell					
CC	proliferation and induction of antibody secretion. The protein can be					
CC	used to produce monoclonal antibodies, which in turn bind to					
CC	CD40-expressing cells. This inhibits binding of soluble CD40 to its					
CC	ligand CD40L. The monoclonal antibody against CD40L is used to inhibit					
CC	proliferation of neoplastic cells, and is particularly useful in treating					
CC	B-cell lymphoma (e.g. where induced after transplants or in other cases					
CC	of immune deficiency such as AIDS) and also melanoma or carcinoma. Since					
CC	the monoclonal antibodies inhibit neoplastic cells directly, they may not					
CC	need to be coupled to a toxin or radioisotope, avoiding toxic effects on					
CC	normal B cells.					
XX						
SQ	Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;					
Query Match 97.2%; Score 763.6; DB 18; Length 840;						
Best Local Similarity 98.2%; Pred. No. 8.6e-213;						
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;						
QY	1	ATGATAGAAACATACAGCCCACTTCCCCAGATCCGTCGCAACTGCACTTCCAGCGAGC	60			
Db	46	atgatcgaacatacaacaaactctcccgatctcgccgaactcgccgaactggactcccatcagc	105			
QY	61	ATGAAGATTTTATGTTTACTTACTTCTTCTTATACCCAGATGATTGGGTACGCA	120			
Db	106	atgaaaattttatgtatttacttactgttttttcttaccacccagatgattgggtcagca	165			
QY	121	CTTTTGTGTGTATCTTCATAGAGTTGGACAGATAGAGATGAAGAAATCTTCAT	180			
Db	166	cttttgtgtgtatcttcataagaaggttgacaagatagagaatgaaagaaatttcac	225			
QY	181	GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAGAAGATCTTATCC	240			
Db	226	gaagattttgtattcatgaaacgatacagagatgcaacacagggagaagatccctatcc	285			
QY	241	TTACTGAACGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300			
Db	286	ttactgaactgtgaggagattaaagccagtttgaggctttgtgaaggatataatgta	345			
QY	301	AACAAAGAGGAGACGACGAAGAAAGAAACAGCTTTGAAATCCAAAGGTGATCAGATCCT	360			
Db	346	aacaagagagagacgaagaagaaagaaacagctttgaaatcacaaggtgatcagaatcc	405			
QY	361	CAAAATTCGCGCACATGTCATAGTGAGCCAGCAGTAAACACATCTGTTTACAGTGG	420			
Db	406	caaatTCGCGCACATGTCATAGTGAGCCAGCAGTAAACACATCTGTTTACAGTGG	465			
QY	421	GCTGAAAAGGATACATACATGAGCAACACTTGTGAACCTTGAAATGGGAAACAG	480			
Db	466	gctgaaaaggatatacaccatgagcaacactgtgtaacccctggaaaatggaaaacag	525			
QY	481	CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCAAT	540			
Db	526	ctgaccgtttaaagacaagagacttattatctatgcccgaagtcacactctgttccaat	585			
QY	541	CGGGAAGCTTCGAGTCAAGCTTCATTTATAGCCAGCTCTGCTTAAGTCCCGGCTAGA	600			
Db	586	cgggaagcttcgagtcgaagctccatttatagccagcctctgcttaagtcctcccggtaga	645			
QY	601	TTCCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGTTCGCGCAACCTTCGCGGCAA	660			
Db	646	ttcgagagaaatcttactcagagctgcaataaccacagttccgccaaccttcgcggtcaa	705			
QY	661	CAATCCATTCACTTGGGAGGAGTATTGCAATGCAACACAGGTGCTTCGGTGTTCAT	720			
Db	706	caatccattcaactgggaggagatttgaaattgcaacaggtgcttcgggtgttcttcaat	765			
QY	721	GTGACTGATCCAAAGCAAGTGAAGTGGCACTGGCTTCACGCTCTTGGGCTTACTCAA	780			



601	TTCGAGAGAATCTTACTCAGACCTGCAAAATACCACACAGTTCCGCCAAAACCTTGCGGGCAA	666
Dd	ttcagagaaatcttactcagagtgcgaataaccacacagttccgccaaaacctgcgggcaa	705
Qy	CAATCCATTACCTTTGGGAGAGATTATTTGAATTTGCACACAGTGCTCGGTGGTTTGTCAAT	720
Dd	caatccattacattggaggagagatttgaaattgcacacagtgcttcgggtgttgtccaat	765
Qy	GTGACTGATCCAGCCAAAGTAGCCATGGCACCTGCTTACAGTCTTTGGCTTACTCAAA	780
Dd	gtgactgatccaagccaagttagcattgcaaccagtgcttcggtgttgtccaat	825
Qy	CTCTCGA 786	
Dd	ctctcga 831	
 RESULT 12		
AAF55539	standard; DNA; 879 BP.	
XX	AAF55539;	
XX	29-MAY-2001 (first entry)	
XX	Nucleotide sequence of human gp39 protein, a CD40 ligand.	
DE		
XX	gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;	
KW	osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;	
KW	ovariectomy; historectomy; lupus nephritis; Takayasu's arteritis;	
KW	Wegener's granulomatosis; nephritis; myositis; scleroderma;	
KW	thrombocytopenia; asthma; lung disease; cancer; ss.	
OS	Homo sapiens.	
XX		
FF	Key Location/Qualifiers	
FT	22..807	
FT	/tag= a	
FT	/product= "gp39"	
XX		
PN	WC200116180-A2.	
XX		
PD	08-MAR-2001.	
XX		
PF	24-AUG-2000; 2000WO-US23276.	
XX		
PR	27-AUG-1999; 99US-0151250.	
XX	(TEXA ) UNIV TEXAS SYSTEM;	
PA		
XX	Ahuja SS.; Bonewald LF;	
PI		
XX	WPI: 2001-169007/17.	
DR	P-PSDB; AAB67612.	
XX		
PT	CD40 agonist containing composition, used to reduce bone cell death	
PT	apoptosis associated with osteoporosis, osteonecrosis and inflammao	
PT	arthritis	
XX		
PS	Disclosure; Page 113; 118pp; English.	
XX		
CC	The present sequence encodes a gp39 protein. It is a CD40 ligand.	
CC	CD40 ligands are used for reducing osteoblast cell death or apoptosi	
CC	for treating or preventing bone loss in animals, preferably huma	
CC	at risk of, or undergoing, bone loss. The bone loss is associated wi	
CC	osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal	
CC	estrogen loss, estrogen loss due to ovariectomy, total hysterecto	
CC	lupus nephritis, Takayasu's arteritis; Wegener's granulomatosis,	
CC	anti-glomerular basement membrane nephritis, myositis, scleroderma,	
CC	idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructiv	
CC	lung disease, nephrotic/nephritic syndrome, or cancer. They may also	
CC	used to treat or prevent bone loss in a subject undergoing, or sched	

CC for, an organ or bone marrow transplant.

Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;  
XX  
SQ

Query Match 97.2%; Score 763.6; DB 22; Length 879;  
Best Local Similarity 98.2%; Pred. No. 8.8e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0;

Qy	1	ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTTGGCAGCTTGGCACTTCCAGGAGC	60
Db	22	atgatcgaacacatacaacaaactctccccgattctcgccactgctcgccactgagtcgccatcagc	81
Qy	61	ATGAAGATTTTATGTATTTACTTACTGTGTTTCTTCTATCACCAGATGATTGGGTCA	120
Db	82	atgsaaattttatgtatttacttactgttttcttatcaccagatgattgggtcagca	141
Qy	121	CTTTTTCCTGTGATCTTTCATAGAAGTTGGACAAGATGAAGATCAAAAGGAATCTTCAT	180
Db	142	ctttttctgtgtatcttcataagaagtttgacacaagatagaaggaatcttcatt	201
Qy	181	GAAGATTTTGTATCTATGTAACGATACAGAGATGCAACACAGGAGAAAGATCTTTATCC	240
Db	202	gaagattttgtattctatgaaaacgatacagagatgcaacacaggagaagaatccttatcc	261
Qy	241	TTACTGTAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTCTGAAGGATATAATGTTA	300
Db	262	ttactgtaacctgtgaggagataaagaccagtttgaaggcttctggaagatataatgttca	321
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Db	382	caaatctgaggacatgtcataagtgaggccagcagtaaaacaacactgtgttaccagtgg	441
Qy	421	GCTGAAAAGAGGATACTACACCATGAGCAACAACCTTGGTAAACCTGGAAAATGGGAACAG	480
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Qy	541	CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCGCTCTGCTTAAAGTCCCCCGGTAGA	600
Db	562	cgggaagcttcgagtcgaagcttcaattatagccagcctctgctctaagtcctccccggcaga	621
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Db	622	ttcgagagaatcttactcagagctgcaaaataccacagttccgcgcaaaccttgcgggcaa	681
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Db	682	caa'tccattcacttgggaggattttgaattgcaaccagggtcttcggtgtttgttccaat	741
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Db	742	gtgactgatccaagccaagtgagccatggcactggcttccagtccttcttggttactcaaa	801
Qy	781	CTCTGA 786	
Db	802	ctctga 807	

RESULT	13
AAA51745	
ID	AAA51745 standard; cDNA; 1816 BP.
XX	
AC	AAA51745;
XX	
DT	31-OCT-2000 (first entry)

XX Human CD40 ligand cDNA.

XX CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;

XX cell death inhibition; stress-induced; immunosuppressive; anti-thyroid;

XX anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;

XX ophthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;

XX dermatological; cytostatic; ss.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

XX CDS 40..825

XX /tag= a

XX /product= Human\_CD40\_ligand

XX WO200039283-A1.

XX

XX 06-JUL-2000.

XX

XX 22-DEC-1999; 99WO-US30930.

XX

XX 29-DEC-1998; 98US-0114106.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX

XX Newell MK, Wagner D, Newell E;

XX

XX WPI; 2000-452387/39.

XX P-PSDB; AAY96993.

XX

XX Inducing T cell receptor gene rearrangement for treating autoimmune

XX diseases comprises contacting T cells with a CD40-binding agent

XX

XX Disclosure; Page 46; 50pp; English.

XX

XX CD40 engagement on T cells can be used to induce T cell receptor

XX rearrangement and enhance T cell affinity for a particular antigen. CD40

XX engagement can be bought about by contacting CD40 with a CD40-binding

XX agent, e.g. human CD40 ligand. The CD40-binding agents can also be used

XX in methods for promoting T cell maturation, inhibiting T cell receptor

XX rearrangement, inhibiting environmental stress-induced cell death,

XX altering the specificity of a T cell towards an antigen, inducing T cell

XX reactivity towards an antigen or enhancing environmental stress-induced

XX cell death (all claimed). T cell affinity maturation towards a specific

XX antigen can be inhibited, especially for a self-antigen in an autoimmune

XX disease, which includes rheumatoid arthritis, uveitis, insulin-dependent

XX diabetes mellitus, haemolytic anaemias, rheumatic fever, Crohn's disease,

XX Guillain-Barre syndrome, psoriasis, thyroiditis, Grave's disease,

XX myasthenia gravis, glomerulonephritis, autoimmune hepatitis or systemic

XX lupus erythematosus. Inducing environmental stress-induced T cell death

XX is carried out in a cancerous T cell or a self-reactive T cell where the

XX environmental stress is a chemotherapeutic agent (claimed).

XX

XX Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;

XX

Query Match	97.2%	Score	763.6	DB	21	Length	1816
Best Local Similarity	98.2%	Pred. No.	1.2e-212				
Matches	772	Conservative	0	Mismatches	14	Indels	0
Gaps	0						
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Db	40	atgatcgaaacatacaaccaaacttctcccgactctcgcgcaatcgactggccatcagc	99				
Qy	61	ATGAAGATTTTTATGTATTTACTTACTGTTTTCTTATPACCCAGATGATTTGGGTACGCA	120				
Db	100	atgaaattttatgtatttacttactgttttcttattaccacagatgatgggtcagca	159				
Qy	121	CTTTTTCGTGTATCTTCATAGAAGTTGGACAAAGATAGAAGATGAAGAATCTTCAT	180				
Db	160	ctttttgcgtgattcttcataagaagttggacaaagataagaagatgaaagaaacttcac	219				



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ID	AAS86571	standard; cDNA; 1816 BP.
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AC	AAS86571.	
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DT	13-FEB-2002	(first entry)
XX		
DE	DNA encoding novel human diagnostic protein #2375.	
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KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.	
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OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
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PF	30-MAR-2001; 2001WO-US08631.	
XX		
PR	31-MAR-2000; 2000US-0540217.	
PR	23-AUG-2000; 2000US-0649167.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Drmanac RT, Liu C, Tang YT;	
XX		

WPI: 2001-639362/73.  
P-FSDb: ABG22384.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 1; SEQ ID NO 22375; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Sequence 1816 RP: 520 A; 461 C; 343 G; 492 T; 0 other;

Query Match	97.2%	Score 763.6	DB 23	Length 1816
Best Local Similarity	98.2%	Pred. No. 1.2e-212		
Matches	772	Conservative 0	Mismatches 14	Indels 0
Gaps	0			
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Db	40	atgatgaaacatatacaaccaacttctccgatctcgccactggaactgcccatacgc	99	
Qy	61	ATGAAGATTTTATGTPATTACTTACTGTTTTCTATACCCAGATGATTGGGTGACGA	120	
Db	100	atgaaaaatttatgtatttaactactgttttcttataccccagatgattgggcaaga	159	
Qy	121	CTTTTGTCTGTATCTTCATAGAAGGTTGGACAAGATAGAAGATGAAGAATFTTCAT	180	
Db	160	ctttttgctgtgatacttcataagaaggttgacaagatagaagatgaagaagaattctcat	219	
Qy	181	GAAGATTTTCTATTATGAAGCATACAGATGCCACACAGAGAAAGATCCTTATCC	240	
Db	220	gaagattttgattctatgaataacgatatacagatgatacaacagagagaagatccctatcc	279	
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Db	280	ttactgaactgtgagagattaaagccagtttgaggctttggaagataataatgta	339	
Qy	301	AACAAAGGAGAGACGAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT	360	
Db	340	aacaaaggagagcaagaagaagaaaacagctttgaaatgtaaaaggtgatcagaatcct	399	
Qy	361	CAAAATTCGGGCATATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTTCAGTGG	420	
Db	400	caaatggcgcatatgataagtgaggccagcagtaaacacatctctgtttcagtcgg	459	
Qy	421	GCTGAAGAAGGATACTACACCATGAGCAACAACCTTGTAACCTCGAAATATGGGAACAG	480	
Db	460	gctgaaaaaggaatactacacatagacaacaacttggtaacctggaaaaatgggaacag	519	
Qy	481	CTGACCGCTTAAAGACAAGGACTATTATATCTATGCCCAAGTCACTTCGTGTCGAAT	540	



Db 520 ctgacgcttaaaagacagagactctattatctatctatgcccgaagtcacotctctgttccaat 579  
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 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTTGGGGCAA 660  
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 Db 820 ctctga 825

## RESULT 15

AAQ57984  
 ID AAQ57984 standard; DNA; 840 BP.

XX AC AAQ57984;

DT 20-AUG-1994 (first entry)

XX DE Genomic sequence of human gp39.

KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation;  
 KW B-cell differentiation; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT 22..807  
 XX FT /\*tag= a

XX EP585943-A.

XX PD 09-MAR-1994.

XX PF 03-SEP-1993; 93EP-0114153.

XX PR 04-SEP-1992; 92US-0940605.

XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo AA, Hollenbaugh D, Ledbetter JN, Aruffo A;

XX DR WPI; 1994-076264/10.

XX DR P-PSDB; AAR59548.

XX PT New nucleic acid encoding human gp39 T cell antigen - which is a  
 PT ligand for the CD40 receptor, causing proliferation and  
 PT differentiation of B cells and some cancer cells

XX PS Claim 1; Fig 1; 39pp; English.

XX The complete nucleic acid sequence of human gp39 (hgp39) protein  
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are  
 CC presented in AAQ57984 and AAR59548 respectively and contd. in plasmid  
 CC CDm8-hgp39, deposited with the ATCC as E. coli, CDm8 MC1061/p3-hgp39  
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a  
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the  
 CC expression vector CD8-gp39.

XX Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;

Query Match 96.9%; Score 762; DB 15; Length 840;  
 Best Local Similarity 98.18; Pred. No. 2.5e-212;  
 Matches 771; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 Qy 781 CTCTGA 786  
 Db 802 ctctga 807

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:23:00 ; Search time 8356.06 Seconds  
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Listing first 45 summaries

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72: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	786	100.0	786	13	US-08-982-272-6 Sequence 6, Appli
2	776.4	98.8	786	13	US-08-982-272-7 Sequence 7, Appli
3	763.6	97.2	786	5	US-08-107-353-3 Sequence 3, Appli
4	763.6	97.2	786	13	US-08-982-272-1 Sequence 1, Appli
5	763.6	97.2	840	1	PCT-US94-00786-7 Sequence 7, Appli
6	763.6	97.2	840	1	PCT-US94-14767-1 Sequence 1, Appli
7	763.6	97.2	840	1	PCT-US97-11956-1 Sequence 1, Appli
8	763.6	97.2	840	3	US-07-805-723-10 Sequence 10, Appli
9	763.6	97.2	840	3	US-07-969-703A-11 Sequence 11, Appli
10	763.6	97.2	840	3	US-07-969-703B-11 Sequence 11, Appli
11	763.6	97.2	840	4	US-08-009-258-7 Sequence 7, Appli
12	763.6	97.2	840	5	US-08-172-664-1 Sequence 1, Appli
13	763.6	97.2	840	6	US-08-215-862-1 Sequence 1, Appli
14	763.6	97.2	840	6	US-08-234-580-3 Sequence 3, Appli
15	763.6	97.2	840	7	US-08-396-230-1 Sequence 1, Appli
16	763.6	97.2	840	8	US-08-477-733A-11 Sequence 11, Appli
17	763.6	97.2	840	8	US-08-484-624-11 Sequence 11, Appli
18	763.6	97.2	840	9	US-08-589-771-7 Sequence 7, Appli
19	763.6	97.2	840	10	US-08-677-762-1 Sequence 1, Appli
20	763.6	97.2	840	11	US-08-770-981-11 Sequence 11, Appli
21	763.6	97.2	840	14	US-09-088-913-11 Sequence 11, Appli
22	763.6	97.2	840	17	US-09-322-021-11 Sequence 11, Appli
23	763.6	97.2	840	17	US-09-322-021A-11 Sequence 11, Appli
24	763.6	97.2	840	17	US-09-365-940-11 Sequence 11, Appli
25	763.6	97.2	840	17	US-09-365-940A-11 Sequence 11, Appli
26	763.6	97.2	840	17	US-09-387-935-1 Sequence 1, Appli
27	763.6	97.2	840	17	US-09-388-079-1 Sequence 1, Appli
28	763.6	97.2	840	17	US-09-388-079A-1 Sequence 1, Appli
29	763.6	97.2	840	17	US-09-392-618-11 Sequence 11, Appli
30	763.6	97.2	840	17	US-09-399-106-11 Sequence 11, Appli
31	763.6	97.2	840	18	US-09-430-448-1 Sequence 1, Appli

		Matches	786;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ATGATGAAACATACAGCCAAACCTTCCCCAGATCCGTTGGCAACTGGACTTCCAGCGAGC	60								
Db	1	ATGATGAAACATACAGCCAAACCTTCCCCAGATCCGTTGGCAACTGGACTTCCAGCGAGC	60								
Qy	61	ATGAAGATTTTTATGATATTTACTTGTTTTTCTATCACCACCATGATGGGTCAGCA	120								
Db	61	ATGAAGATTTTTATGATATTTACTTGTTTTTCTATCACCACCATGATGGGTCAGCA	120								
Qy	121	CTTTTTCTGTGATCTTTCATAGAAGGTTGGCAAGATAGAAGATGAAGGAATCTTCAT	180								
Db	121	CTTTTTGCTGTGATCTTTCATAGAAGGTTGGCAAGATAGAAGATGAAGGAATCTTCAT	180								
Qy	181	GAAGATTTTGATTCATGAAGATACAGATGATCAACACAGGAGAAAGATCCCTATCC	240								
Db	181	GAAGATTTTGATTCATGAAGATGATCAACACAGGATGATCAACACAGGAGAAAGATCCCTATCC	240								
--Qy	241	TTACTGAACTCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA	300								
Db	241	TTACTGAACTCTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA	300								
Qy	301	ACAAAGAGGAGACGAGAAAGAAACAGCTTGAATGCAAAAGAGTGATCAGAACTCT	360								
Db	301	ACAAAGAGGAGACGAGAAAGAAACAGCTTGAATGCAAAAGAGTGATCAGAACTCT	360								
Qy	361	CAAAATGGCGCACATGTCATAAGTGAGCGCCAGCAGTAAACACACATCTGTGTTACAGTGG	420								
Db	361	CAAAATGGCGCACATGTCATAAGTGAGCGCCAGCAGTAAACACACATCTGTGTTACAGTGG	420								
Qy	421	GCTGAAAAGGATACTCACCATGAGCAACACTTGTTAACCCCTGGAAAATGGAAACAG	480								
Db	421	GCTGAAAAGGATACTCACCATGAGCAACACTTGTTAACCCCTGGAAAATGGAAACAG	480								
Qy	481	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCAAAGTCACCTTCTGTTCCAAT	540								
Db	481	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCAAAGTCACCTTCTGTTCCAAT	540								
Qy	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCCTTAAAGTCCCGCGGTAGA	600								
Db	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGCTCTGCCTTAAAGTCCCGCGGTAGA	600								
Qy	601	TTGCGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTCGGGCAA	660								
Db	601	TTGCGAGAGATCTTACTCAGAGCTGCAAAATCCACAGTTCGCGCAAACTTCGGGCAA	660								
Qy	661	CAATCCATTCACHTGGGAGGATTTTGAATGCAACAGCTGCTCGGTGTTTTGTCAAT	720								
Db	661	CAATCCATTCACHTGGGAGGATTTTGAATGCAACAGGATTTTGAATGCAACAGGTTGCTTCGGTGTGTTGTCAT	720								
Qy	721	GTGACTGATCCAAAGCAAGTGAGCCATGSCACTGGCTTCAGCTCCTTTGGCTTACTCAAA	780								
Db	721	GTGACTGATCCAAAGCAAGTGAGCCATGSCACTGGCTTCAGCTCCTTTGGCTTACTCAAA	780								
Qy	781	CTCTGA 786									
Db	781	CTCTGA 786									
RESULT 2											
us-08-982-272-7											
; Sequence 7, Application US/08982272											
; GENERAL INFORMATION:											
; APPLICANT: Kipps, Thomas J.											
; APPLICANT: Sharma, Sanjai											
; APPLICANT: Cantwell, Mark											
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS											
; TITLE OF INVENTION: CONTAINING ACCESSORY											
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND											
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-											
; TITLE OF INVENTION: MODULATION AND TREATMENT OF											
; TITLE OF INVENTION: MALIGNANCIES											
; NUMBER OF SEQUENCES: 44											

US-08-982-272-6  
Sequence 6, Application US/08982272  
GENERAL INFORMATION:  
APPLICANT: Kipps, Thomas J.  
APPLICANT: Sharma, Sanjai  
APPLICANT: Cantwell, Mark  
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
TITLE OF INVENTION: CONTAINING ACCESSORY  
TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
TITLE OF INVENTION: THEIR USE FOR IMMUNO-  
TITLE OF INVENTION: MODULATION AND TREATMENT OF  
TITLE OF INVENTION: MALIGNANCIES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette,  
MEDIUM TYPE: 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,272  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-982-272-6

Query Match 100.0%; Score 786; DB 13; Length 786;  
Best Local Similarity 100.0%; Pred. No. 1.8e-201;

Sequence 7, Appli  
Sequence 7, Appli  
Sequence 1, Appli  
Sequence 31, Appli  
Sequence 3, Appli  
Sequence 22375, A  
Sequence 373, App  
Sequence 457, App  
Sequence 1, Appli  
Sequence 5, Appli  
Sequence 6, Appli

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette.
;; MEDIUM TYPE: 1.44 Mb Storage
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/982,272
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/132145
;; FILING DATE: 12/9/96
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Guise, Jeffrey W.
;; REGISTRATION NUMBER: 34,613
;; REFERENCE/DOCKET NUMBER: 231/003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 786 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-982-272-7

Query Match          98.8%; Score 776.4; DB 13; Length 786;
Best Local Similarity 99.2%; Pred. No. 7.1e-199;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0:

QY 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGGAGATCCGTGGCAACTGGACTTCCAGCGAGC 60
QY 61 ATGAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACCATGATTTGGGTCAGCA 120
DB 61 ATGAGATTTTATGTTATTTACTTACTTCTTCTTATCACCACCATGATTTGGGTCAGCA 120
QY 121 CTTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
DB 121 CTTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAAGGAATCTTCAT 180
QY 181 GAAGATTTTGTATTCATGAACACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAACACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240
QY 241 TTACTGAAGTGTGAGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
DB 241 TTACTGAAGTGTGAGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
QY 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAATGTCAAAAGGTCATCAGATCCT 360
DB 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAATGTCAAAAGGTCATCAGATCCT 360
QY 361 CAAATTTGGCGCACATGTCATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 420
DB 361 CAAATTTGGCGCACATGTCATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 420
QY 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTTGGTAACCCCTGGAAAAATGGGAAACAG 480
DB 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTTGGTAACCCCTGGAAAAATGGGAAACAG 480

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette.
MEDIUM TYPE: 1.44 Mb Storage
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-982-272-7

QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCAT 540
DB 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTTCAT 540
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGA 600
DB 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGA 600
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAAAGCTTGGCGGCA 660
DB 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCACAGTTCGCCCAAAAGCTTGGCGGCA 660
QY 661 CAATCCATTCACTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTTCAT 720
DB 661 CAATCCATTCACTTGGGAGGAGTATTGAAATTCGAACAGGTGCTTCGGTGTTCAT 720
QY 721 GTGACTGATCCAAAGCCAAAGTGAGCCATGCGACTGCTTCACGCTCTTTGGCTTACTCAA 780
DB 721 GTGACTGATCCAAAGCCAAAGTGAGCCATGCGACTGCTTCACGCTCTTTGGCTTACTCAA 780
QY 781 CTCCTGA 786
DB 781 CTCCTGA 786

RESULT 3
US-08-107-353-3
; Sequence 3, Application US/08107353
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,353
; FILING DATE: 19930813
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..783
```

Thu May 30 05:46:19 2002

US-08-107-353-3

Query Match 97.2%; Score 763.6; DB 5; Length 786;  
Best Local Similarity 98.2%; Pred. No. 2.1e-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60  
DB 1 ATGATAGAACATACAGCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60  
QY 61 ATGAAGATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTTCAGCA 120  
DB 61 ATGAAGATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTTCAGCA 120  
QY 121 CTCTTTGCTGTGATCTTCATAGAGGTTGGCAAGATGAGAGTGAAGGAATCTTCAT 180  
DB 121 CTCTTTGCTGTGATCTTCATAGAGGTTGGCAAGATGAGAGTGAAGGAATCTTCAT 180  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAGATCCTTATCC 240  
DB 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAGATCCTTATCC 240  
QY 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
DB 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
QY 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCCT 360  
DB 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCCT 360  
QY 361 CAATTTGCGGCACATGTCATTAAGTGAGGCGACAGTAAACACATCTGTGTACAGTGG 420  
DB 361 CAATTTGCGGCACATGTCATTAAGTGAGGCGACAGTAAACACATCTGTGTACAGTGG 420  
QY 421 GCTGAAAAGGATACACACATGAGCAACCACTTGGTAAACCTTGGAAATGGGAACAG 480  
DB 421 GCTGAAAAGGATACACACATGAGCAACCACTTGGTAAACCTTGGAAATGGGAACAG 480  
QY 481 CTGACCGTTTAAAGACAGAGCTCTATTTATATCTATGCCCAGTCACTTCTGTTCAT 540  
DB 481 CTGACCGTTTAAAGACAGAGCTCTATTTATATCTATGCCCAGTCACTTCTGTTCAT 540  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 600  
DB 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA 600  
QY 601 TTCGAGAGATCTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGGGGCAA 660  
DB 601 TTCGAGAGATCTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGGGGCAA 660  
QY 661 CAATCCATTCATCTGGGAGGATTTGAATTCGACAGGTCGTCGCTGTTGTCAAT 720  
DB 661 CAATCCATTCATCTGGGAGGATTTGAATTCGACAGGTCGTCGCTGTTGTCAAT 720  
QY 721 GTGACTGATCCAGCCAAAGTGAGCCATGGCATGGCTTCAGCTCTCTTGGCTTACTCAA 780  
DB 721 GTGACTGATCCAGCCAAAGTGAGCCATGGCATGGCTTCAGCTCTCTTGGCTTACTCAA 780  
QY 781 CTCTGA 786  
DB 781 CTCTGA 786

RESULT 4  
US-08-982-272-1  
; Sequence 1, Application US/08982272  
; GENERAL INFORMATION:  
; APPLICANT: Kipps, Thomas J.  
; APPLICANT: Sharma, Sanjai  
; APPLICANT: Cantwell, Mark  
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
; CONTAINING ACCESSORY

TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
THEIR USE FOR IMMUNO-  
MODULATION AND TREATMENT OF  
MALIGNANCIES  
TITLE OF INVENTION: MALIGNANCIES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette,  
MEDIUM TYPE: 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,272  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELECOMMUNICATION INFORMATION:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-982-272-1

Query Match 97.2%; Score 763.6; DB 13; Length 786;  
Best Local Similarity 98.2%; Pred. No. 2.1e-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60  
DB 1 ATGATAGAACATACAGCAACCTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60  
QY 61 ATGAAGATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTTCAGCA 120  
DB 61 ATGAAGATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTTCAGCA 120  
QY 121 CTCTTTGCTGTGATCTTCATAGAGGTTGGCAAGATGAGAGTGAAGGAATCTTCAT 180  
DB 121 CTCTTTGCTGTGATCTTCATAGAGGTTGGCAAGATGAGAGTGAAGGAATCTTCAT 180  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAGATCCTTATCC 240  
DB 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGAGATCCTTATCC 240  
QY 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
DB 241 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
QY 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCCT 360  
DB 301 AACAAAGAGGAGACGAAAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCCT 360  
QY 361 CAATTTGCGGCACATGTCATTAAGTGAGGCGACAGTAAACACATCTGTGTACAGTGG 420  
DB 361 CAATTTGCGGCACATGTCATTAAGTGAGGCGACAGTAAACACATCTGTGTACAGTGG 420

Db 361 CAAATTCGGGCACATGTCTAAGTGGAGCCAGCAGTAAACAAACATCTGTCTACAGTGG 420  
Qy 421 GCTGAAAAGGATACACCATGAGCAACACTTGGTAAACCTCGGAAAATGGGAAACAG 480  
Db 421 GCTGAAAAGGATACACCATGAGCAACACTTGGTAAACCTCGGAAAATGGGAAACAG 480  
Qy 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGATGCCCCAAGTCACCTCTGTGTCCAAAT 540  
Db 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGATGCCCCAAGTCACCTCTGTGTCCAAAT 540  
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600  
Db 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600  
Qy 601 TTCGAGAGAACTTACTCAGAGTGCCTAAATACCCACAGTTCGCGCAACCTTGGCGGCA 660  
Db 601 TTCGAGAGAACTTACTCAGAGTGCCTAAATACCCACAGTTCGCGCAACCTTGGCGGCA 660  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTTGAATTTGCAACAGTGTCTCGGTGTTGTCAAT 720  
Db 661 CAATCCATTCACTTGGGAGGAGTATTTGAATTTGCAACAGTGTCTCGGTGTTGTCAAT 720  
Qy 721 GTGACTGATCCAAAGCAAGTGCAGTGGCACTGGCTTCACGTCTCTTTGGCTTACTCAA 780  
Db 721 GTGACTGATCCAAAGCAAGTGCAGTGGCACTGGCTTCACGTCTCTTTGGCTTACTCAA 780  
Qy 781 CTCTGA 786  
Db 781 CTCTGA 786

## RESULT 5

PCT-US94-00786-7

Sequence 7, Application PC/TUS9400786

GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD

APPLICANT: DAVISON, BARRY

APPLICANT: FANSHAW, WILLIAM

APPLICANT: RENSLOW, BLAIR

APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL

TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS

TITLE OF INVENTION: IN A CD40 LIGAND GENE

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple Operating System 7.1

SOFTWARE: MS Word for Apple 5.1, Version a

CURRENT APPLICATION DATA:

FILING DATE: PCT/US94/00786

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/009,258

FILING DATE: 01/22/93

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATRICIA ANNE

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2810-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 2065870430

TELEFAX: 2065870606

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
PCT-US94-00786-7

Query Match 97.2%; Score 763.6; DB 1; Length 840;

Best Local Similarity 98.2%; Pred. No. 2.le:195;

Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTGGCAACTGGACTTCCACGGAGC 60  
Db 46 ATGATCGAAACATACAGCAACAACTTCTCCCGATCTGGCCACCTGGACTGCCATCAGC 105  
Qy 61 ATGAAGATTTTATGATATTTACTTACTGTTTCTTATCACCAGATGATGGGTACGA 120  
Db 106 ATGAAATTTTATGATATTTACTTACTGTTTCTTATCACCAGATGATGGGTACGA 165  
Qy 121 CTTTGTGCTGTATCTTTCATAGAGGTTGGCAAGATAGAGATGAAAGGAATCTTCAT 180  
Db 166 CTTTGTGCTGTATCTTTCATAGAGGTTGGCAAGATAGAGATGAAAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAGATCCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAGATCCTTATCC 285  
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
Qy 301 ACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360  
Db 346 ACAAAGAGGAGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 405  
Qy 361 CAAATTCGGCACATGTCATAGTCAGCCAGCAGTCAACACATCTGTGTACAGTGG 420  
Db 406 CAAATTCGGCACATGTCATAGTCAGCCAGCAGTCAACACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTTGGTAAACCTGGAAAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTTGGTAAACCTGGAAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCAGAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTAGA 645  
Qy 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTTGGCGGCA 660  
Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTTGGCGGCA 705  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCCTCAAT 720  
Db 706 CAATCCATTCACTTGGGAGGAGTATTTGAATTTGCAACAGGTGCTTCGGTGTTCCTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGCAGTGCATGCTGCTTCACGTCTCTTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGCAGTGCATGCTGCTTCACGTCTCTTTGGCTTACTCAA 825  
Qy 781 CTCTGA 786

Db 826 CACTGA 831

RESULT 6  
PCT-US94-14767-1  
Sequence 1, Application PC/TUS9414767  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MURPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14767  
FILING DATE: December 21, 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
PCT-US94-14767-1

Query Match 97.2%; Score: 763.6; DB 1; Length 840;  
Best Local Similarity 98.2%; Pred No. 2.1e-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACCGCAGC 60  
Db 46 ATGATGAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACCGCAGC 105  
QY 61 ATGATGAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACCGCAGC 120  
Db 106 ATGATGAACATACACCAACCTTCCCGAGATCGGTGGCACTGGACATTCACCGCAGC 165

QY 121 CTTTTGCTGTGTATCTTCATAGAGGTTGGACAGATAGAGATCAAGGAATCTTCAT 180  
Db 166 CTTTTGCTGTGTATCTTCATAGAGGTTGGACAGATAGAGATCAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAGGATACAGATGCAACACAGGAGAAAGATCTTCATCC 240  
Db 226 GAAGATTTTGTATTCATGAAGGATACAGATGCAACACAGGAGAAAGATCTTCATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 300  
Db 286 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 345  
QY 301 AACAAAGAGAGAGACGAAGAAACACAGCTTTGAAATGCAAAAGGATGATCAGATCT 360  
Db 346 AACAAAGAGAGACGAAGAAACACAGCTTTGAAATGCAAAAGGATGATCAGATCT 405  
QY 361 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
Db 406 CAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAAAGGATACATACACCATGAGCAACAACTTGTGAACCTGGAAATGGAAACAG 480  
Db 466 GCTGAAAAAGGATACATACACCATGAGCAACAACTTGTGAACCTGGAAATGGAAACAG 525  
QY 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTCCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTTCTGTCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGTTAGA 645  
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAA 660  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGCAA 705  
QY 661 CAATCCATTCACTGGGAGGAGTATTTGAATGCAACAGGCTTCGCTGTTGTCAAT 720  
Db 706 CAATCCATTCACTGGGAGGAGTATTTGAATGCAACAGGCTTCGCTGTTGTCAAT 765  
QY 721 GTGACTGATCCCAAGCAAGTGAAGCATGCACTGGCTTCACTGCTTGGGTTACTCAA 780  
Db 766 GTGACTGATCCCAAGCAAGTGAAGCATGCACTGGCTTCACTGCTTGGGTTACTCAA 825  
QY 781 CACTGA 786  
Db 826 CACTGA 831

RESULT 7  
PCT-US97-11956-1  
Sequence 1, Application PC/TUS9711956  
GENERAL INFORMATION:  
APPLICANT: Immunex Corporation  
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.6  
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/11956  
FILING DATE: 09-JUL-1997  
CLASSIFICATION:



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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/677,762
;; FILING DATE: 10-JUL-1996
;; PRIOR APPLICATION NUMBER: USSN 08/763,995
;; FILING DATE: 12-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia A.
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2845-WO
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 840 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; CLONE: CD40-L
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 46...831
PCT-US97-11956-1

Query Match          97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGGCACTGCGCAACTGGACTTCCAGCGGAGC 60
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGGCACTGCGGCACTGGAGTCCCATCAGC 105
Oy 61 ATGAGATTTTATGTTATTTACTTACTTCTTTCTTATCACCAGATGATTTGGGTGACGA 120
Db 106 ATGAAATTTTATGTTATTTACTTACTTCTTTCTTATCACCAGATGATTTGGGTGACGA 165
Oy 121 CTTTTCGTCTGTATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGAATCTTCAT 180
Db 166 CTTTTCGTCTGTATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGAATCTTCAT 225
Oy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGGAAAGATCCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGGAGGAAAGATCCTTATCC 285
Oy 241 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGCAAGGATATAATGTTA 300
Db 286 TTACTGAATCTGAGGAGATTAAGCCAGTTTGAAGGCTTTGCAAGGATATAATGTTA 345
Oy 301 AACAAAGAGGACGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 360
Db 346 AACAAAGAGGACGACGAAGAAAGAAACAGCTTTGAAATGCAAAAGGTCAGAAATCCT 405
Oy 361 CAAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Oy 421 GCTGAAAGAGGATACCTACCATGAGCAACACTTGGTTAAACCTGGAAGGAAATGGGAAACAG 480
Db 466 GCTGAAAGAGGATACCTACCATGAGCAACACTTGGTTAAACCTGGAAGGAAATGGGAAACAG 525
Oy 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCCAGTCACTCTCTGTTCCCAAT 540
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCGCCAGTCACTCTCTGTTCCCAAT 585
Oy 541 CGGGAAGCTTCGAGTCAAGCTCCCAFTTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 600

;; Sequence 10, Application US/07805723
;; GENERAL INFORMATION:
;; APPLICANT: ARMITAGE, RICHARD
;; APPLICANT: FANSLAW, WILLIAM
;; APPLICANT: SPRIGGS, MELANIE
;; TITLE OF INVENTION: NOVEL CYTOKINE
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMMUNEX CORPORATION
;; STREET: 51 UNIVERSITY STREET
;; CITY: SEATTLE
;; STATE: WASHINGTON
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07805,723
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSTER, JEFFREY B.
;; REGISTRATION NUMBER: 32585
;; REFERENCE/DOCKET NUMBER: 2802
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 2065870430
;; TELEFAX: 2065870606
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 840 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; CLONE: CD40-L
US-07-805-723-10

Query Match          97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGGCACTGCGCAACTGGACTTCCAGCGGAGC 60
Db 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAA 660
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGGCAA 705
Oy 661 CAATCCATTTCACCTGGGAGAGATATTTGAATTTGCAACAGGTGCTTCGGTGTGTTGTCAT 720
Db 706 CAATCCATTTCACCTGGGAGAGATATTTGAATTTGCAACAGGTGCTTCGGTGTGTTGTCAT 765
Oy 721 GTGACTGATCCAAAGCAAGTGAAGTGGCACTGGCACTGGCTTTCAGCTGCTTTGGGTACTCAA 780
Db 766 GTGACTGATCCAAAGCAAGTGAAGTGGCACTGGCACTGGCTTTCAGCTGCTTTGGGTACTCAA 825
Oy 781 CTCCTGA 786
Db 826 CTCCTGA 831

RESULT 8
US-07-805-723-10
;; Sequence 10, Application US/07805723
;; GENERAL INFORMATION:
;; APPLICANT: ARMITAGE, RICHARD
;; APPLICANT: FANSLAW, WILLIAM
;; APPLICANT: SPRIGGS, MELANIE
;; TITLE OF INVENTION: NOVEL CYTOKINE
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMMUNEX CORPORATION
;; STREET: 51 UNIVERSITY STREET
;; CITY: SEATTLE
;; STATE: WASHINGTON
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07805,723
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSTER, JEFFREY B.
;; REGISTRATION NUMBER: 32585
;; REFERENCE/DOCKET NUMBER: 2802
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 2065870430
;; TELEFAX: 2065870606
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 840 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; CLONE: CD40-L
US-07-805-723-10

Query Match          97.2%; Score 763.6; DB 3; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGATAGAAACATACAGCAACCTTCCCGGCACTGCGCAACTGGACTTCCAGCGGAGC 60
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Thu May 30 05:46:19 2002

us-08-982-272-6.rnmp

46 ATGATCGAAACATACACAAACATCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105  
61 ATGAAGATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120  
106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 165  
121 CTTTTCGCTGTATCTTATGATAGAGTTGGACAGATGATGAAAGGATCTTCAT 180  
166 CTTTTCGCTGTATCTTATGATAGAGTTGGACAGATGATGAAAGGATCTTCAT 225  
181 GAAGATTTTGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
226 GAAGATTTTGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 285  
241 TTACTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
286 TTACTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345  
301 AACAAAGAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
346 AACAAAGAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405  
361 CAATTCGCGGCACATGTCATGATGATGATGATGATGATGATGATGATGATGAT 420  
406 CAATTCGCGGCACATGTCATGATGATGATGATGATGATGATGATGATGATGAT 465  
421 GCTGAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
466 GCTGAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525  
481 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
526 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585  
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCGTAAAGTCCCGGTAGA 600  
586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCGTAAAGTCCCGGTAGA 645  
601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAA 660  
646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAA 705  
661 CAATCACTTCACTTCGAGGAGATTTGAAATGCAACACAGTTCGCGTTCGTTGCAAT 720  
706 CAATCACTTCACTTCGAGGAGATTTGAAATGCAACACAGTTCGCGTTCGTTGCAAT 765  
721 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAGCTGCTTCGCTTACTCAAA 780  
766 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTCAGCTGCTTCGCTTACTCAAA 825  
781 CTCTGA 786  
826 CTTCTGA 831

RESULT 9  
US-07-969-703A-11  
Sequence 11, Application US/07969703A  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
TITLE OF INVENTION: NOVEL CYTOKINE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,703A  
FILING DATE: 19921023  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-07-969-703A-11  
Query Match 97.2%; Score 763.6; DB 3; Length 840;  
Best Local Similarity 98.2%; Pred. No. 2.1e-195; Indels 0; Gaps 0;  
Matches 772; Conservative 0; Mismatches 14

QY 1 ATGATGAAACATACAGCAACCTTCCCGAGATCCCGTGGCACTGGACTGCCCATCAGC 60  
DB 46 ATGATGAAACATACAGCAACCTTCCCGAGATCCCGTGGCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAGATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTGACGA 120  
DB 106 ATGAAATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTGACGA 165  
QY 121 CTTTTCGCTGTATCTTCTCATAGAGTTGGACAGATGATGAAAGGATCTTCAT 180  
DB 166 CTTTTCGCTGTATCTTCTCATAGAGTTGGACAGATGATGAAAGGATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 226 GAAGATTTTGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 285  
QY 241 TTACTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 286 TTACTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345  
QY 301 AACAAAGAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 346 AACAAAGAGGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405  
QY 361 CAATTCGCGGCACATGTCATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 406 CAATTCGCGGCACATGTCATGATGATGATGATGATGATGATGATGATGATGAT 465  
QY 421 GCTGAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 466 GCTGAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525  
QY 481 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
DB 526 CTGACCGTTTAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585

Qy 541 CGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
 Db 586 CGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 705  
 Qy 661 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTGTCTTGTCAAT 720  
 Db 706 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTGTCTTGTCAAT 765  
 Qy 721 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTTCAGTCTTGGTGGTCTTACTCAA 780  
 Db 766 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTTCAGTCTTGGTGGTCTTACTCAA 825  
 Qy 781 CTCTGA 786  
 Db 826 CTCTGA 831

RESULT 10  
 US-07-969-703B-11  
 ; Sequence 11, Application US/07969703B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; TITLE OF INVENTION: NOVEL CYTOKINE  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/969,703B  
 ; FILING DATE: 19921023  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2802-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 2065870430  
 ; TELEFAX: 2065870606  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 840 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORGANISM: Homo sapiens  
 ; IMMEDIATE SOURCE:  
 ; CLONE: CD40-L  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 46..831  
 ; US-07-969-703B-11

Query Match 97.2%; Score 763.6; DB 3; Length 840;  
 Best Local Similarity 98.2%; Pred. No. 2.1e-195;  
 Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTTGGCAACTGGACTTGGACTTCCAGCGAGC 60  
 Db 46 ATGATCGAAACATACAGCAACCTTCCCGCAGATCCGTTGGCAACTGGACTTGGACTTCCAGCGAGC 105  
 Qy 61 ATGAGAGATTTTATGATTTTACTTACTTGTCTTTTCTTATCACCAGATGATTGGGTACAGA 120  
 Db 106 ATGAAATTTTATGATTTTACTTACTTGTCTTTTCTTATCACCAGATGATTGGGTACAGA 165  
 Qy 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAAT 180  
 Db 166 CTTTTTGTCTGTATCTTATAGAGGTTGGACAGATAGAGATGAAGAAATCTTCAAT 225  
 Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCCCTTATCC 240  
 Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGAGAAAGATCCCTTATCC 285  
 Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
 Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345  
 Qy 301 AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 360  
 Db 346 AACAAAGAGGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 405  
 Qy 361 CAATTTGGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
 Db 406 CAATTTGGCGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
 Qy 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGAAAAATGGGAAACAG 480  
 Db 466 GCTGAAAAAGGATACCTACACCATGAGCAACAACTTGTGTAACCTCGAAAAATGGGAAACAG 525  
 Qy 481 CTGACCGTTTAAAGACAAGGACTCTATTATATATATATATATATATATATATATATATATATAT 540  
 Db 526 CTGACCGTTTAAAGACAAGGACTCTATTATATATATATATATATATATATATATATATATATAT 585  
 Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
 Db 586 CGGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
 Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA 705  
 Qy 661 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTTCGGTGTCTTGTCAAT 720  
 Db 706 CAATCCATTACTTGGGAGGAGTATTTGAATTGCAACAGGTGCTTTCGGTGTCTTGTCAAT 765  
 Qy 721 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTTCAGTCTTGGTGGTCTTACTCAA 780  
 Db 766 GTGACTGATCCAAAGCAAGTGGCCACTGGCTTTCAGTCTTGGTGGTCTTACTCAA 825  
 Qy 781 CTCTGA 786  
 Db 826 CTCTGA 831  
 RESULT 11  
 US-08-009-258-7  
 ; Sequence 7, Application US/08009258  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; APPLICANT: WIDMER, MICHAEL  
 ; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
 ; TITLE OF INVENTION: IN A CD40 LIGAND GENE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:

us-08-982-272-6.rnnp

Thu May 30 05:46:19 2002

ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/009,258  
FILING DATE: 19930122  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
us-08-009-258-7

Query Match 97.28; Score 763.6; DB 4; Length 840;  
Best Local Similarity 98.28; Pred. No. 2.1e-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 ATGATAGAAACATACAGCAACCTCCCGGCACTGGCACTGGCACTCCAGCGAGC 60  
DB 46 ATGATAGAAACATACAGCAACCTCCCGGCACTGGCACTGGCACTCCAGCGAGC 105  
QY 61 ATGATAGAAACATACAGCAACCTCCCGGCACTGGCACTGGCACTCCAGCGAGC 120  
DB 106 ATGATAGAAACATACAGCAACCTCCCGGCACTGGCACTGGCACTCCAGCGAGC 165  
QY 121 CTTTTCCTGCTATCTTCATAGAGGTGGCAAGATAGAGATGAAGGAATCTTCAT 180  
DB 166 CTTTTCCTGCTATCTTCATAGAGGTGGCAAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATAGAAAGATGACAGATGCAACACAGGAGAAAGATCTTATCC 240  
DB 226 GAAGATTTTGTATTCATAGAAAGATGACAGATGCAACACAGGAGAAAGATCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 300  
DB 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 345  
QY 301 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAATCAAAAGGTCATCAGATCTCT 360  
DB 346 AACAAAGAGGAGAGGAGAAAGAAACAGCTTTGAATCAAAAGGTCATCAGATCTCT 405  
QY 361 CAATTCGGCAGATGTCATAGTGGCCAGCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
DB 406 CAATTCGGCAGATGTCATAGTGGCCAGCAGCAGTAAACAAACATCTGTGTACAGTGG 465

QY 421 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAAACCTGGAAATGGAAACAG 480  
DB 466 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAAACCTGGAAATGGAAACAG 525  
QY 481 CTGACCGTTAAAGAGCAAGGACTCTATTATCTATGATCCCAAGTCACTTCTGTCCAAT 540  
DB 526 CTGACCGTTAAAGAGCAAGGACTCTATTATCTATGATCCCAAGTCACTTCTGTCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645  
QY 601 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTGCAGGCAA 660  
DB 646 TTGAGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTGCAGGCAA 705  
QY 661 CAATCCATTCACCTGGGAGAGTATTGAATTCGAACACAGGTCTTCGGTGTGTGTCAAT 720  
DB 706 CAATCCATTCACCTGGGAGAGTATTGAATTCGAACACAGGTCTTCGGTGTGTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGGCCATGCGCATGGCACTGGCTTCAGTCTTTCGCTTACTCAAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGGCCATGCGCATGGCACTGGCTTCAGTCTTTCGCTTACTCAAA 825  
QY 781 CTCCTGA 786  
DB 826 CTCCTGA 831

RESULT 12  
US-08-172-664-1  
Sequence 1, Application US/08172664  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MURPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)233-0644  
TELEFAX: (206)587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-172-664-1

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Query Match      97.2%; Score 763.6; DB 5; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACATCCAGCGAGC 60
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGCCACTGGACTGCCCATCAGC 105
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA 120
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA 165
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 CTTTTGCTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGGAATCTTCAT 180
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
166 CTTTTGCTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGGAATCTTCAT 225
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GAAGATTTTATGTATTTATGAAACAGATACAGATGCAACACAGAGAGAAAGATCTTATCC 240
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
226 GAAGATTTTATGTATTTATGAAACAGATACAGATGCAACACAGAGAGAAAGATCTTATCC 285
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 300
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
286 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 345
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
346 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 405
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CAATTCGGGCACATGTCATAGTCAGGCCAGCAGTAAACAAACATCTGCTTACAGTGG 420
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
406 CAATTCGGGCACATGTCATAGTCAGGCCAGCAGTAAACAAACATCTGCTTACAGTGG 465
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 GCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCTCGAAAAATGGGAAACAG 480
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 GCTGAAAAAGGATACTACACCATGAGCAACAACTTGGTAAACCTCGAAAAATGGGAAACAG 525
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACCTCTGTTCCAAAT 540
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
526 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAAGTCACCTCTGTTCCAAAT 585
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 600
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 645
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAAACTTGGCGGCAA 660
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
646 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAAACTTGGCGGCAA 705
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
661 CAATCCATTCCTTCTGGGAGGAGTATTTGAAATGCAACAGAGTGCCTGCGTCTTCTCAAT 720
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
706 CAATCCATTCCTTCTGGGAGGAGTATTTGAAATGCAACAGAGTGCCTGCGTCTTCTCAAT 765
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
721 GTGACTGATCCNAGCCAGTGGCCATGGCCTTCACGTCCTTTGGCTTACTCAA 780
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
766 GTGACTGATCCNAGCCAGTGGCCATGGCCTTCACGTCCTTTGGCTTACTCAA 825
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
781 CTCTGA 786
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
826 CTCTGA 831

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RESULT 13  
US-08-215-862-1

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; Sequence 1: Application US/08215862
; GENERAL INFORMATION:
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: Method of Diagnosing or Treating Hodgkin's
; TITLE OF INVENTION: Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Apple Macintosh System 7.1
; SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,862
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-08-215-862-1

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Query Match      97.2%; Score 763.6; DB 6; Length 840;
Best Local Similarity 98.2%; Pred. No. 2.1e-195;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACATCCAGCGAGC 60
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGCCACTGGACTGCCCATCAGC 105
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA 120
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATGGGTCAGCA 165
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 CTTTTGCTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGGAATCTTCAT 180
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
166 CTTTTGCTGTATCTTCATAGAGGTGGACAAGATAGAGATGAAGGAATCTTCAT 225
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 GAAGATTTTATGTATTTATGAAACAGATACAGATGCAACACAGAGAGAAAGATCTTATCC 240
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
226 GAAGATTTTATGTATTTATGAAACAGATACAGATGCAACACAGAGAGAAAGATCTTATCC 285
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 300
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
286 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGATATATGTTA 345
Qy      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360

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Thu May 30 05:46:19 2002

MOLECULE TYPE: DNA  
FEATURE: NAME/KEY: CDS  
LOCATION: 22...807  
US-08-234-580-3

Query Match 97.2%; Score 763.6; DB 6; Length 840;  
Best Local Similarity 98.2%; Pred. NO. 2.le-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

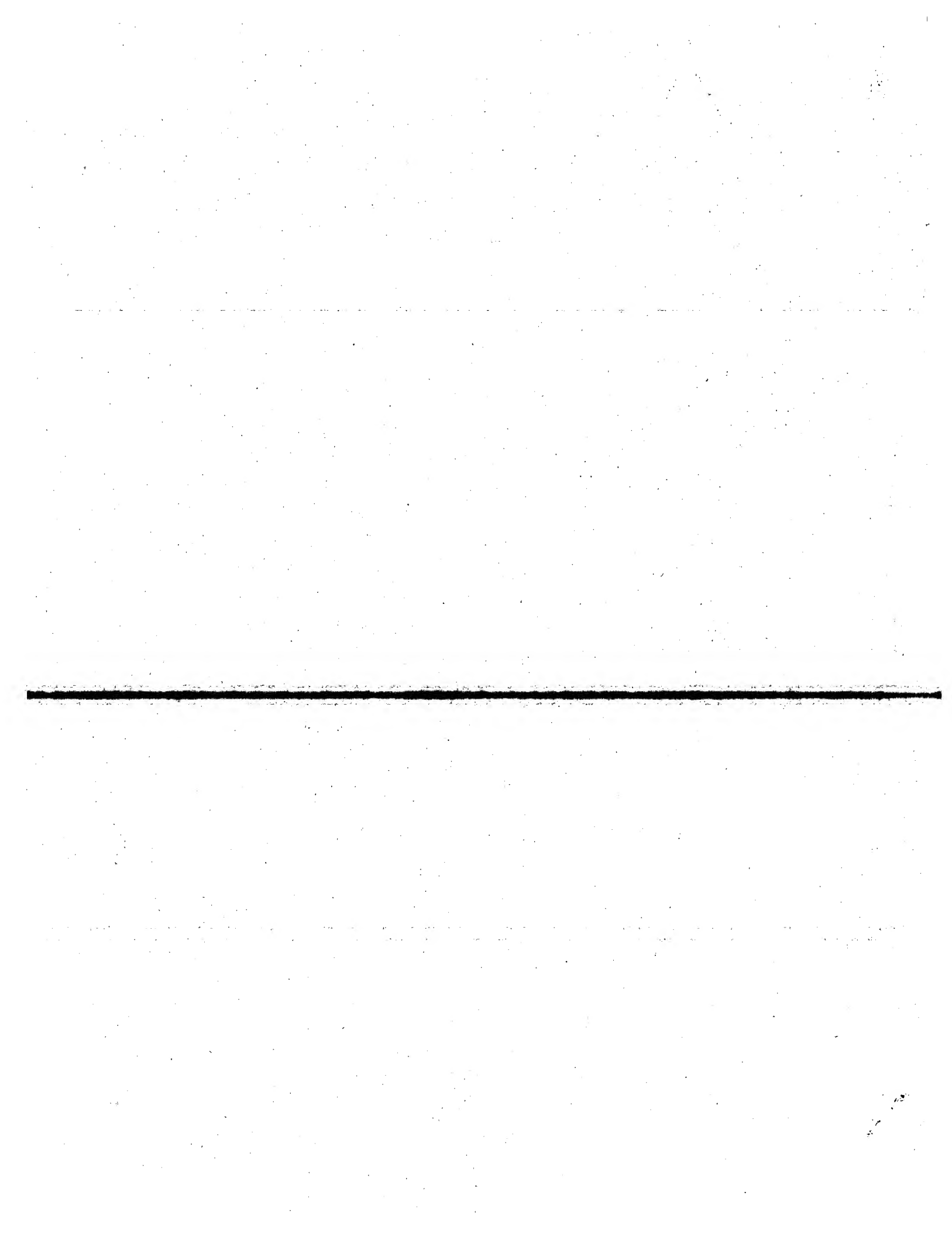
1 ATGATGAGAAACATACAGCCAACTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 60  
22 ATGATGAGAAACATACAGCCAACTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 81  
61 ATGATGAGAAACATACAGCCAACTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 120  
82 ATGATGAGAAACATACAGCCAACTTCCCCAGATCGGTGGCAACTGGACTTCCAGCGAGC 141  
121 CTCTTTGCTGTCATCTTATGATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGCA 180  
142 CTCTTTGCTGTCATCTTATGATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGCA 201  
181 GAAGATTTGCTGTCATCTTATGATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGCA 240  
202 GAAGATTTGCTGTCATCTTATGATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGCA 261  
241 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTCTGAAGGATATATGTTA 300  
262 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTCTGAAGGATATATGTTA 321  
301 AACAAAG 360  
322 AACAAAG 381  
361 CAATTTGCGGCACATGTCATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
382 .CAATTTGCGGCACATGTCATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441  
421 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAACTGGGAAATGGGAAACAG 480  
442 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAACTGGGAAATGGGAAACAG 501  
481 CTGACCGTTAAAGACAGAGGACTCTATTATATGATGATGATGATGATGATGATGATGATGAT 540  
502 CTGACCGTTAAAGACAGAGGACTCTATTATATGATGATGATGATGATGATGATGATGATGAT 561  
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGGTTAGA 600  
562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGGTTAGA 621  
601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTTCGGGGCAA 660  
622 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTTCGGGGCAA 681  
661 CAATTCATTCACCTTGGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 720  
682 CAATTCATTCACCTTGGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 741  
721 GTGACTCATCCAAAGCAAGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 780  
742 GTGACTCATCCAAAGCAAGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 801  
781 CTCTGA 786  
802 CTCTGA 807

RESULT 15  
US-08-396-230-1  
; Sequence 1, Application US/08396230  
; GENERAL INFORMATION:  
; APPLICANT: CAMPBELL, KIM A.

346 AACAAAG 405  
361 CAATTTGCGGCACATGTCATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
406 CAATTTGCGGCACATGTCATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465  
421 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAACTGGGAAATGGGAAACAG 480  
466 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAACTGGGAAATGGGAAACAG 525  
481 CTGACCGTTAAAGACAGAGGACTCTATTATATGATGATGATGATGATGATGATGATGATGAT 540  
526 CTGACCGTTAAAGACAGAGGACTCTATTATATGATGATGATGATGATGATGATGATGATGAT 585  
541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGGTTAGA 600  
586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTGCCTAAAGTCCCGGTTAGA 645  
601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTTCGGGGCAA 660  
646 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTTCGGGGCAA 705  
661 CAATTCATTCACCTTGGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 720  
706 CAATTCATTCACCTTGGGAGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 765  
721 CTGACTCATCCAAAGCAAGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 780  
766 GTGACTCATCCAAAGCAAGTGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 825  
781 CTCTGA 786  
826 CTCTGA 831

GENERAL INFORMATION: US/08234580  
APPLICANT: KEHRY, MERILYN R  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,580  
FILING DATE: 28-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011,1030000/RAM  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

Query Match	97.2%; Score 763.6; DB 7; Length 840;
Best Local Similarity	98.2%; Pred. No. 2.le-195;
Matches	772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY	1 ATGATGAACAACATACAGCCAACTTCCCACAGATCCGTGCACACTGGACITGCCAGCGAGC 60 
Ddb	46 ATGATCGAACAACATACACCANAATTCTCCCGATCTCGGCCACTGGCACTGCCCATCAGC 105 
QY	61 ATGAAGATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATTGGTCAGCA 120 
Ddb	106 ATGAAAATTTTATGTATTACTTACTTGTTTTCTTATCACCCAGATGATTGGTCAGCA 165 
QY	121 CTTTTTCGCTGTATCTTCATAGAAGTTGGACAAGATGAAGATGAAGAAATCTTCAT 180 
Ddb	166 CTTTTTCGCTGTATCTTCATAGAAGTTGGACAAGATGAAGATGAAGAAATCTTCAT 225 
QY	181 GAAGATTTTGTATTTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240 
Ddb	226 GAAGATTTTGTATTTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285 
QY	241 TTACTCAACTGTCAGAGAGATTAAAGCCACTTTTCAAGGCTTTCTGAAGGATATAATGTTA 300 
Ddb	286 TTACTCAACTGTCAGAGAGATTAAAGCCACTTTTGAAGGCTTTTGTGAAGGATATAATGTTA 345 
QY	301 AACAAAGAGGAGACGAAGAAAAAACACAGCTTTTGAATGCAAAAAGGTGTACAAATCCT 360 





GenCore version 4.5  
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OW nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:39:58 ; Search time 627.19 seconds  
(without alignments)  
1315.293 Million cell updates/sec

Title: US-08-982-272-6  
Perfect score: 786  
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	763.6	97.2	1816	5	US-09-053-375B-226 Sequence 226, App
2	763.6	97.2	1816	5	US-09-442-384B-457 Sequence 457, App
3	584.4	74.4	1250	5	US-09-053-375B-821 Sequence 821, App
4	360.6	45.9	508	5	US-09-911-904-131 Sequence 131, App
5	135	17.2	2395	5	US-09-875-453A-9 Sequence 9, Appli
6	45.6	5.8	569	1	PCT-US02-10421-202 Sequence 202, App
7	45.6	5.8	569	6	US-10-112-699-202 Sequence 202, App
8	44	5.6	2127	5	US-09-919-002-664 Sequence 664, App
9	39.4	5.0	234	5	US-09-540-210B-7000 Sequence 7000, Ap
10	38.2	4.9	230	5	US-09-540-210B-14649 Sequence 14649, A
11	38.2	4.9	620	6	US-10-027-632-35707 Sequence 35707, A
12	38.2	4.9	620	6	US-10-027-632-62305 Sequence 62305, A
13	38.2	4.9	620	6	US-10-027-632-297617 Sequence 297617, App
14	38	4.8	663	6	US-10-027-632-206146 Sequence 206146, App
15	38	4.8	663	6	US-10-027-632-206147 Sequence 206147, App
16	38	4.8	775	6	US-10-123-155-120 Sequence 120, App
17	37.6	4.8	1223197	6	US-10-027-632-179264 Sequence 179264, App
18	36.8	4.7	438	5	US-09-539-331D-26090 Sequence 26090, A
19	36.4	4.6	1751	6	US-10-105-299-1996 Sequence 1996, Ap
20	36.4	4.6	1751	6	US-10-106-698-239 Sequence 239, App
21	35.8	4.6	418	5	US-09-789-189-1323 Sequence 1323, Ap
22	35.8	4.6	10351	5	US-09-442-384B-628 Sequence 628, App
23	35.6	4.5	621	6	US-10-027-632-83794 Sequence 83794, A
24	35.6	4.5	621	6	US-10-027-632-83795 Sequence 83795, A
25	35.6	4.5	803	6	US-10-103-299-824 Sequence 824, App
26	35.2	4.5	646	5	US-09-919-002-11996 Sequence 11996, A

ALIGNMENTS

RESULT 1

US-09-053-375B-226  
; Sequence 226, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053.375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-226

Query Match 97.2%; Score 763.6; DB 5; Length 1816;  
Best Local Similarity 98.2%; Pred. No. 9e-195;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY	1	ATGATAGAACATACAGCCACCTTCCGCCAGATCGTGGCACTGGACTTCCAGCGAGC	60
DB	40	atgatcgaacatacaacaaacttctcccgatctcgccactggactgccccatcagc	99
QY	61	ATGAGATTTTATCTATTTACTTACTTCTTCTTCTTATCACCAGATGTTGGTTCAGCA	120
DB	100	atgaataatttatgtatttacttacttcttcttcttccaccagatgattgggctcagca	159
QY	121	CTTTTGTCTGTATCTTCTTATGAGAGTTGGACAAGATAGAGATGAAGAGTCTTCAT	180
DB	160	cttttctgtgtatcttctcagaagttggacaagatagaagaagaagaatcttcat	219
QY	181	GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCTTTATCC	240
DB	220	gaagattttgtattcagaac	279
QY	241	TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTTGAAGGATATATATGTTA	300
DB	280	ttactgaactgtgagagagattaaagccagtttgaggtcttctgtaagagataataatgta	339
QY	301	AACAAGAGGAGCAGGAAGAAACACAGCTTTGAATGCAAAAAGGTTGATCAGAAATCCT	360
DB	340	aacaagaggagacgaagaagaac	399
QY	361	CAAAATGGCGGCACATGTCTAATAAGTAGGCGCCACGATGAGTAAACACATCTGTGTACAGTGG	420

Sequence 12937, A  
Sequence 15838, A  
Sequence 732, App  
Sequence 84272, A  
Sequence 296495,  
Sequence 208277,  
Sequence 230025,  
Sequence 208276,  
Sequence 648, App  
Sequence 499, App  
Sequence 8655, Ap  
Sequence 128, App  
Sequence 210375,  
Sequence 282527,  
Sequence 254462,  
Sequence 268832,  
Sequence 90677, A  
Sequence 45221, A  
Sequence 45222, A

```

RESULT      2
US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; TITLE OF INVENTION: Hematocyte/Immunology Array
; FILE REFERENCE: CLON-008CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

```

Query Match	97.2%	Score	763.6	DB	5	Length	1816	
Best Local Similarity	98.2%	Pred. No.	98-195					
Matches	772	Conservative	0	Mismatches	14	Indels	0	Gaps
1	ATGATAGAAACATACACCAACCTTCCCCAGATCCGTGGCAACTGGACTTCCACGAGC	60						
40	atgattcgaaacatacaaccaactctcccgcatctcgccgacctggactgcccattcgcg	99						
61	ATGAAGATTTTTATGTATTTACTTGTGTTTTCTTATCACCAGATGATTGGGTACACA	120						
100	atgaaatatttatgtattacttactctgttttctctaccaccagatgaatgggtcagca	159						
121	CTTTTTGCTGTATCTTCTATAGAAAGTTTGGACAAGATAGACATCAAGGAATCTTCA	180						
160	ctttttgctgtatctcttcacgaagttggacaagatagaagatgaaggaattctcat	219						
181	GAAGATTTTGTATTCNTGAAACCATACAGAGTGCACACAGAGAAAAGATCCCTATCC	240						
220	gaagattttgtattcatgaaacatgatacagagatgcaacacagagagaagatccttatcc	279						
241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTCGAAGCCTTTGTGAGGATATAATGTTA	300						

280	Db	tlaci gaactgtagagatataaagccagtttgaagccttgtagaggataataagtcta	339
301	QY	ACAAAGAGGACCAAGAAAGAAACACAGCTTGAAATGCAAAAAGGTGATCAGAATCCT	360
340	Db	aacaagaggagacagadaagaaagaaaacagcttgaattgcaaaagtgatcagaatcct	399
361	QY	CAAAATGCGGCACATGTCATAAGTCAGGCCAGCAGTAACAACATCTGTCTACAGTGG	420
400	Db	caaatcgcgacatgtcataagttaggagccagcagtaaacacacactgtgttacagtgg	455
421	QY	GCTGAAAAAGGATACTTACACCATGAGCAACAACTTGGTAAACCCTGGAAATGGGAACAG	480
460	Db	gctgaaaaaggatactacaccatgagcaacaacttggtaaaccttggaatacggaacacag	519
481	QY	CTCAGCTTAAAGACAAAGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTTCCAAT	540
520	Db	ctgaccgtttaaagacaaagactctattatctatgcccgaagtccacttctgttcccaat	579
541	QY	CGGAGACTTCGAGTCAAGCTCCATTATAGCAGCCTCTGCCTTAAGTCCCCCGGTAGA	600
580	Db	cgggaagcttcgagtcaagctccattatagccagcctctgctaagctcccgcggtaga	639
601	QY	TTCCAGAGAACTCTTACTCAGAGCTGCAATACCACAGTTCCGCCAAACCTTCGCGGCAA	660
640	Db	ttcagagaaactcttactcagagctgcataaccacagttccgcgaacaccttgcggggcaa	699
661	QY	CAATCCATTCACCTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGTGTGTCAAAT	720
700	Db	caatccattacccttgggagagatttgaattgcaaccaggigtcttcgggtttgttccaat	759
721	QY	GTGACTGATCCAGCCAAAGTGAGCCATGGCAGCTTGCTTACGTCCTTTGGCTTACTCAAA	780
			819

```

RESULT      3
US-09-053-375B-821
, Sequence 821, Application US/09053375B
, GENERAL INFORMATION:
, APPLICANT: Chenchik, Alex
, APPLICANT: Bibilashvili, Robert
, TITLE OF INVENTION: Nucleic Acid Arrays
, FILE REFERENCE: CLON-006
, CURRENT APPLICATION NUMBER: US/09/053,375B
, CURRENT FILING DATE: 1998-08-31
, NUMBER OF SEQ ID NOS: 1543
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 821
, LENGTH: 1250
, TYPE: DNA
, ORGANISM: Mus musculus
US-09-053-375B-821

```

	Query Match	74.4%;	Score 584.4;	DB 5;	Length 1250;
	Best Local Similarity	84.9%;	Pred. No. 7.8e-147;		
	Matches 667;	Conservative	0;	Mismatches 116;	Indels 3; Gaps 1;
1	ATGATAGAAACATACAGCCAACTTCCCCGATGTCGGTGGCAACTGGGACTTCACGAGGC	60			
2					
3	atgataagaacatacagccaaccttccccagatcogtggcaactggactctccagcgagc	72			
4					
5					
6					
7					
8					
9					
10					
11					
12					
13	atgataagaacatacagccaaccttccccagatcogtggcaactggactctccagcgagc	72			
14					
15					
16					
17					
18					
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21					
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58					
59					
60					
61	ATGAAGATTTTATGTATTACTTACTGTTTTCTTTATCACCAGATGATGGGTACAGA	120			
62					
63					
64					
65					
66					
67					
68					
69					
70					
71					
72					
73	atgaagatttttatgtatttacttactgttttctctatcaccaccaaatgattgagactgtg	132			
74					
75					
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104					
105					

```

Db 133 ctttttgcgtgtatcttcataagaagattggataaggtcgaagaggaagtaaaccttcatt 192
Qy 181 GAAGATTGTTGTTATTCATGAACAGTACAGAGATCCACACAGAGGAAAGATCCCTTATCC 240
Db 193 gaaagatttgcattcattataaaagagctaaagagagtgcaacaagaaggagaggtacttatacc 252
Qy 241 TTACTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
Db 253 ttgcgaactgtgagagatgagaaggaatttgagaccccttgtaagagataaagcgtta 312
Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAATGCAAAAGGTCATCAGAAATCCT 360
Db 313 acaaaagaaga---gaaaaagaacacagcttgtaagtgaagagagagagatccct 369
Qy 361 CAATTTGGCGGACATGTCATAGTCAGGCGACGACGTAACAAACATCTGTGTTACAGTGG 420
Db 370 caaattgcagcacagctgtgaaggaagcccaacagtaataatgcagcaccgttctacagtg 429
Qy 421 GCTGAAAAGGATACACACATGAGCAACAACTTGGTAACCCCTGGAAATGGGAAACAG 480
Db 430 gccaaagaagatattacacatgaaagcaacttgtaagtctgaaatgggaaacag 489
Qy 481 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGTCACCAAGTCACTCTGTTCCAA 540
Db 490 ctgacggttaaaagaagaagactctattatgtctacactcaagtcacactctctctaat 549
Qy 541 CGGGAAGCTTCAGTCAAGCTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTGA 600
Db 550 cgggagccttcagtcacagcccatctcatcgtcggcccttcggtgaagccacagcagtg 609
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCAAACTTTCGCGGCA 660
Db 610 tctgagaactctactcaagcggaacataccacagttctccacagcttgcagcag 669
Qy 661 CAATCCATTCACTCGGAGGAGTATTGAATGCAACAGGTCGTCGCTGTTGTTCAAT 720
Db 670 cagctgttctactggtggcggaggttgaattacaagctggtgctctgtgttgcac 729
Qy 721 GTGACTGTATCCAAAGCAAGTGAAGCCATGCACTGCTTCACTGCTTTCGCTTACTCAA 780
Db 730 gtagctgaagcaagcaagtgatccacagagttgggtctctctctctctctctctctct 789
Qy 781 CTCCTGA 786
Db 790 cctctga 795

```

RESULT 4

```

US-09-911-904-131
; Sequence 131, Application US/09911904
; GENERAL INFORMATION:
; APPLICANT: Fart, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-911-904-131

```

Query Match 45.9%; Score 360.6; DB 5; Length 508;  
 Best Local Similarity 83.0%; Pred. No. 5e-87;  
 Matches 424; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

```

Qy 267 CCAGTTTGAAGCTTTGTGAAGGATATAATGTTAAACAAAGAGGAGACGACGAAAGAAA 326
Db 1 ccaatttgaagcctttctcaagagagataatgctaacaacgaaatgaagaaagaagaaaa 60
Qy 327 CAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCTCAAAATTCGGGCACATGTCTAAGTGA 386
Db 61 ca---ttgcaatgcaaaaaggtgatcagagatcctcgaattgagcccatgtcataagtga 117
Qy 387 GSCCAGCAGTAAACAAACATCTGCTTACAGTGGCTGAAAGAGGATACTACACCATGAG 446
Db 118 ggcctagttaaccacagcgtcctcgtcggcgcccaaaaggtactaccataag 177
Qy 447 CAACAACCTTGGTAAACCTTGGAAATGGAAACAGCTGACCGTTAAAGACAAAGGACTCTA 506
Db 178 cagcaacacctgtgagcctcgagaatggaaacagttggcgtgaaagacaagagactcta 237
Qy 507 TTATATCTATGTCACCAAGTCACTCTGTTTCCCAATCGGAAGCTTCGAGTCAAGTCCAT 566
Db 238 ttacgtctatgcccgaagtcaccttctcctcaatcggcgagcttcgagtcgaagctccgtt 297
Qy 567 TATAGCCAGCCTCTGCCTAAAGTCCCGGTAGATTCGAGAGAAATCTTACTCAGAGCTCC 626
Db 298 cgtcgccagcctcatcctcccatcctccagtggaacgagagagagcttactcgcgcgcg 357
Qy 627 AAATACCCACAGTTCGCGCAAACTTGGCGCAAACTTCCATTCATTCCTGGGAGGAGTATT 686
Db 358 gagctccgcgcgcgtcgtccaaaccttgccgaacagtcacactccttgaggagagatt 417
Qy 687 TGAATTCGAACAGAGTGTGCTGCTGTTTGTCAATGTGATGATCCAAAGCAAGTGAAGCA 746
Db 418 tgaattgatccaggtgcttcggtgctgctcaagctgactgatccaagccaagtgagcca 477
Qy 747 TGGCACTGGCTTCAGCTCCTTTGGCTTACTC 777
Db 478 cgggaccggctcagctcttttggcttactc 508

```

RESULT 5

```

US-09-875-453A-9
; Sequence 9, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurence, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Brulice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453A-9

```

Query Match 17.2%; Score 135; DB 5; Length 2395;  
 Best Local Similarity 83.6%; Pred. No. 2.1e-26;  
 Matches 153; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY	1	ATGATAGAACAATACAGCCAACTTCCCCACAGATCCGTGGCAACTGGACTTCACGACGAGC	60
Db	1939	atgatcgaaacatacaacaaactctcccgatctcggccactggactgcccatcagc	1998
QY	61	ATGAAGATTTTATATGATTTACTTACTGTCTTTCTTATCACCACAGATGATGGTGTCAGCA	120
Db	1999	atgaasaattttatgtatttactactgtttttcttataccccagatgattgggtcagca	2058
QY	121	CTTTTTCGTGTATCTTCATAGAAGTGTGGACAAGATAGAAGATGAAGAATCTCTTCAT	180
Db	2059	ctttttgcgtgtatcttcataagaagctggacaaggLaagatgaaccacaagcctttat	2118
QY	181	GAA	183
Db	2119	taa	2121

RESULT 6  
PCT-US02-10421-202  
Sequence 202, Application. PC/TUS0210421  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Wang, Tongtong  
APPLICANT: Wang, Siqing  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Gaiger, Alexander  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
OF AND DIAGNOSIS OF CANCER  
FILE REFERENCE: 210121.565PC  
CURRENT APPLICATION NUMBER: PCT/US02/10421  
CURRENT FILING DATE: 2002-03-28  
NUMBER OF SEQ ID NOS: 2959  
SEQ ID NO 202  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-10421-202

	Query Match	5.8%;	Score 45.6;	DB 1;	Length 569;
	Best Local Similarity	49.6%;	Prod. No. 0.012;		
	Matches 117;	Conservative	0; Mismatches 119;	Indels	0; Gaps
Qy	238	TCCTTACTGAACGTCTGAGGAGATTAAAGCCAGTGTGAGGCGTTTGTGAAGCATATAATG	297		
Db	165	ttcatattacagtggttggataaaaaattggatgaatgggttccggagagcagagta	224		
Qy	298	TTAAACAAAGAGGACGAGAAAGAAACACCTTTGAATGCCAAAAGCTGATCAGAT	357		
Db	225	ctcaaatcgtggacaccaatttgcagaaacagcgagaacttcaaaaagccaatcaggag	284		
Qy	358	CCTCAAAATTCGGGCACATCTCATAGCTGAGGCGCAGCAGTAAACAAACATCTGTGTACAG	417		
Db	285	cagtatgcagagggggaagatgcaggggggtgtcccccaggaagaagacatctggtctgcaa	344		
Qy	418	TGGGCTTGAAAAGGATACTACCATGAGCAACAACCTTGGTAACCCGTGGAANAATGG	473		
Db	345	cagaataaatttgaggtgaacacgaagaagaacaaacacadaaacaaccttggaattg	400		

RESULT 7  
US-10-112-699-202  
; Sequence 202, Application US/10112699  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Wang, Siqing  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Gaiger, Alexander  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; OF CANCER  
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER  
; FILE REFERENCE: 210121.565  
; CURRENT APPLICATION NUMBER: US/10/112.699  
; CURRENT FILING DATE: 2002-03-28

[illegible]

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RESULT      8
US-09-919-002-664
; Sequence 664, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919, 002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203.
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 664
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-664

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Query Match	5.6%	Score 44	DB 5	Length 2127	
Best Local Similarity	49.2%	Prod. No. 0.048			
Matches 116	Conservative	0	Mismatches 120	Indels 0	Gaps 0
QY	238	TCTTACTGA	CTGTCAGAGATTAAACCGAGTTTGAAGCTTTGTGAAGGATATATG	297	
Db	238	ttcatcattac	agtggttgggaataaaaaattggatgatgattgggttcaggagacagagta	297	
QY	298	TTAACAAAGAGGAGACG	AGAAAGAAACAGCTTTTGAATCCAAAAAGGTGATCAGAAAT	357	
Db	298	ctcaaatacgt	ggagaccatttgcagaaacgcgagaacttcaaaagccaatcaggag	357	
QY	358	CCTCAAAATTCGGC	CAGATGTCATAGTCAGGCCAGCAGCTAAACACACATCTCTGTTACAG	417	
Db	358	cagtatgcagag	gggaagatgaggggggtgtcccccaggaaagaaagacatcttgctgcgaa	417	
QY	418	TGGGCTGAAAAGGAT	ACTACACCATGAGCAACAACTTGGTAACTCCCTGGAANAATGG	473	
nb	418	cagaataat	tattgaactgaaacgcaaaagaaacaaacagaaacacactggaaatg	473	

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; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7000
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00141818
; NAME/KEY: unsure
; LOCATION: 24, 113
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-7000

Query Match 5.0%; Score 39.4; DB 5; Length 234;
Best Local Similarity 48.8%; Pred. No. 0.41;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps

QY 263 AAGCCAGTTTGAAGCGTTTGTGAAGGATATATGTTAAACAAGAGGAGGACGAGAAAG 322
Db 1 aaattgggaatgaatgggtcccnagagcagagtactcaaatcgtggacaccaatttgc 60
QY 323 AAAACAGCTTTGAAATGCAAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGTCATAA 382
Db 61 agaaacacgcagaacttcaaaaagccaatcaggacgagtgcagagggggaanatgagag 120
QY 383 GTAGGCCACGAGTAAACAACATCTGTTGTACAGTGGGCTGAAAAGAGATCTACACCA 442
Db 121 gggctgccccagaaagaacatctggctctgcacagaaaaatgttgagtgaaacga 180
QY 443 TGAGCAACAACCTTGGTAACCTCGAAAAATGG 473
Db 181 aaagaaacaacagaaaacacctggaaatgg 211

RESULT 10
US-09-540-210B-14649
; Sequence 14649, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Sellhamey, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.

```

us-08-982-272-6.rnpn

Thu May 30 05:46:20 2002

APPLICANT: Stuve, Laura L.  
APPLICANT: Mullaly, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE  
FILE REFERENCE: PD-1037 CIP  
CURRENT APPLICATION NUMBER: US/09/540,210B  
CURRENT FILING DATE: 2002-04-03  
PRIOR APPLICATION NUMBER: 08/972,899  
PRIOR FILING DATE: November 18, 1997  
PRIOR APPLICATION NUMBER: 08/395,244  
PRIOR FILING DATE: February 27, 1995  
PRIOR APPLICATION NUMBER: 08/722,922  
PRIOR FILING DATE: September 27, 1996  
PRIOR APPLICATION NUMBER: 60/005,526  
PRIOR FILING DATE: September 29, 1995  
PRIOR APPLICATION NUMBER: 08/824,029  
PRIOR FILING DATE: March 25, 1997  
PRIOR APPLICATION NUMBER: 60/014,010  
PRIOR FILING DATE: March 25, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/903,555  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/862,178  
PRIOR FILING DATE: May 22, 1997  
PRIOR APPLICATION NUMBER: 60/018,217  
PRIOR FILING DATE: May 23, 1996  
PRIOR APPLICATION NUMBER: 08/881,589  
PRIOR FILING DATE: June 24, 1997  
PRIOR APPLICATION NUMBER: 60/021,275  
PRIOR FILING DATE: June 25, 1996  
PRIOR APPLICATION NUMBER: 08/903,802  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/905,881  
PRIOR FILING DATE: August 1, 1997  
PRIOR APPLICATION NUMBER: 60/025,204  
PRIOR FILING DATE: August 1, 1996  
PRIOR APPLICATION NUMBER: 08/903,471  
PRIOR FILING DATE: July 30, 1997  
PRIOR APPLICATION NUMBER: 60/025,478  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/903,556  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/025,217  
PRIOR FILING DATE: August 22, 1996  
PRIOR APPLICATION NUMBER: 08/937,142  
PRIOR FILING DATE: September 23, 1997  
PRIOR APPLICATION NUMBER: 60/026,598  
PRIOR FILING DATE: September 24, 1996  
PRIOR APPLICATION NUMBER: 08/960,746  
PRIOR FILING DATE: October 29, 1997  
PRIOR APPLICATION NUMBER: 60/030,144  
PRIOR FILING DATE: October 30, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/755,524  
PRIOR FILING DATE: November 22, 1996  
PRIOR APPLICATION NUMBER: 60/007,495  
PRIOR FILING DATE: November 22, 1995  
PRIOR APPLICATION NUMBER: 09/021,031  
PRIOR FILING DATE: February 10, 1998  
PRIOR APPLICATION NUMBER: 60/039,325  
PRIOR FILING DATE: February 13, 1997  
PRIOR APPLICATION NUMBER: 09/035,172  
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431  
PRIOR FILING DATE: March 5, 1997  
PRIOR APPLICATION NUMBER: 09/041,894  
PRIOR FILING DATE: March 12, 1998  
PRIOR APPLICATION NUMBER: 60/040,199  
PRIOR FILING DATE: March 14, 1997  
PRIOR APPLICATION NUMBER: 09/050,817  
PRIOR FILING DATE: March 30, 1998  
PRIOR APPLICATION NUMBER: 60/043,792  
PRIOR FILING DATE: April 11, 1997  
PRIOR APPLICATION NUMBER: 09/074,999  
PRIOR FILING DATE: May 8, 1998  
PRIOR APPLICATION NUMBER: 60/048,431  
PRIOR FILING DATE: May 29, 1997  
PRIOR APPLICATION NUMBER: 09/107,592  
PRIOR FILING DATE: June 30, 1998  
PRIOR APPLICATION NUMBER: 60/052,751  
PRIOR FILING DATE: July 1, 1997  
PRIOR APPLICATION NUMBER: 09/094,079  
PRIOR FILING DATE: June 9, 1998  
PRIOR APPLICATION NUMBER: 60/049,975  
PRIOR FILING DATE: June 13, 1997  
NUMBER OF SEQ ID NOS: 35654  
SOFTWARE: PERL Program  
SEQ ID NO 14649  
LENGTH: 230  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc:feature  
OTHER INFORMATION: Incyte ID No: hu00678829  
US-09-540-210B-14649

Query Match 4.9%; Score 38.2; DB 5; Length 230;  
Best Local Similarity 50.8%; Pred No 0.85;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAGGATATAATG 297  
Db 32 ttcatattacagtgttggaataaaattggatgggttcgagagcagagta 91  
QY 298 TTAACAAGAGGAGGACGACGAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGAAT 357  
Db 92 ctcaaatcggtggacccaatttcgagaaacagcagcaggaacttcaaaagccaatcaggag 151  
QY 358 CCTCAAAATTGCGGCACATGTCATAGTGAGGCCAGCAGTAAACAAACATCTGTGTACA 416  
Db 152 cagtatgcagagggggaagatgagagggtgctgccccgagaaagacacatctggtctgca 210

RESULT 11  
US-10-027-632-35707  
Sequence 35707, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28

	Query Match	4.9%	Score 38.2;	DB 6;	Length 620;
	Best Local Similarity	51.5%;	Pred. No. 1.2;		
	Matches	88;	Conservative	0;	Mismatches 83; Indels 0; Gaps 0;
QY	57	GAGCATCAAGATTTTTATGATTTTACTACTGTGTTTTCTTTATCACCAGATGATGGGTC	116		
Db	190	gagattagtgattattattcactattggcagccttactttttcagacatttgaigcc	249		
QY	117	AGCACTTTTTCCTGTGTATCTTCATAGAAGGTTGGCAAGATAGAAAGTAAAGAAATCT	176		
Db	250	aatattaagtactttttcttgcttaagtcacagataaattgaagaacagaaatgatatca	309		

		Query Match	4.9%	Score 38.2;	DB 6;	Length 620;	
		Best Local Similarity	51.5%;	Pred. No. 1.2;			
		Matches	88;	Conservative	0;	Mismatches	83;
						Indels	0;
						Gaps	0;
QY	57	GAGCATCAAGATTTTATGATATTTACTTACTGTTTTTCTTTATCACCAGATGATGGGTC	116				
Db	190	gagattagtgattattattcactatttggcagcctactcttttcagacatttggatgcc	249				
QY	117	AGCACTTTTGCCTGTCATCTTCATAGAAGTTGGACAAAGATAGAAGATGAAGAAGAACTCT	176				
Db	250	aattaaagcactctttctattgctgaagcccaagaatttgaagaacagcaatgatacca	309				
QY	177	TCATGAAGATTTTGTATTCATGAAACGATACAGAGATGCACACAGAGAGA	227				
Db	310	tctgtagaattcttctatttaaatgaattggcactatgaacaaagataca	360				

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RESULT 14
US-10-027-632-206146
, Sequence 206146, Application US/10027632.
, GENERAL INFORMATION:
, APPLICANT: Wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
, TITLE OF INVENTION: Polymorphisms in the Human Genome
, FILE REFERENCE: 108827.129
, CURRENT APPLICATION NUMBER: US/10/027.632
, CURRENT FILING DATE: 2002-04-30
, PRIOR APPLICATION NUMBER: US 60/218,006
, PRIOR FILING DATE: 2000-07-12
, PRIOR APPLICATION NUMBER: US 60/198,676
, PRIOR FILING DATE: 2000-04-20
, PRIOR APPLICATION NUMBER: US 60/193,483
, PRIOR FILING DATE: 2000-03-29
, PRIOR APPLICATION NUMBER: US 60/185,218
, PRIOR FILING DATE: 2000-02-24

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:38 ; Search time 139.75 Seconds  
(without alignments)  
1381.524 Million cell updates/sec

Title: US-08-982-272-6  
Perfect score: 786  
Sequence: 1 ATGATAGAAACATACAGCA.....TTGGTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	763.6	97.2	786	1 US-08-446-922-3	Sequence 3, Appli
2	763.6	97.2	786	5 PCT-US93-10034-3	Sequence 3, Appli
3	763.6	97.2	840	1 US-07-940-605A-1	Sequence 1, Appli
4	763.6	97.2	840	1 US-08-184-422-7	Sequence 7, Appli
5	763.6	97.2	840	1 US-08-360-923A-1	Sequence 1, Appli
6	763.6	97.2	840	1 US-08-431-055-3	Sequence 3, Appli
7	763.6	97.2	840	2 US-08-690-096-1	Sequence 1, Appli
8	763.6	97.2	840	2 US-08-249-189-11	Sequence 11, Appli
9	763.6	97.2	840	2 US-08-484-624A-11	Sequence 11, Appli
10	763.6	97.2	840	2 US-08-477-733B-11	Sequence 11, Appli
11	763.6	97.2	840	3 US-08-763-995-1	Sequence 1, Appli
12	763.6	97.2	840	3 US-09-088-913A-11	Sequence 11, Appli
13	763.6	97.2	840	3 US-08-589-771B-7	Sequence 7, Appli
14	763.6	97.2	840	4 US-08-769-819-11	Sequence 11, Appli
15	763.6	97.2	840	4 US-08-770-974-11	Sequence 11, Appli
16	763.6	97.2	840	4 US-08-858-197-3	Sequence 3, Appli
17	638.2	81.2	1425	2 US-08-249-189-15	Sequence 15, Appli
18	638.2	81.2	1425	2 US-08-484-624A-15	Sequence 15, Appli
19	638.2	81.2	1425	2 US-08-477-733B-15	Sequence 15, Appli
20	638.2	81.2	1425	3 US-09-088-913A-15	Sequence 15, Appli
21	638.2	81.2	1425	4 US-08-769-819-15	Sequence 15, Appli
22	638.2	81.2	1425	4 US-08-770-974-15	Sequence 15, Appli
23	637.2	81.1	929	1 US-08-446-922-10	Sequence 10, Appli
24	637.2	81.1	929	2 US-08-249-189-20	Sequence 20, Appli
25	637.2	81.1	929	2 US-08-484-624A-20	Sequence 20, Appli
26	637.2	81.1	929	2 US-08-477-733B-20	Sequence 20, Appli
27	637.2	81.1	929	3 US-09-088-913A-20	Sequence 20, Appli

## ALIGNMENTS

## RESULT 1

US-08-446-922-3

: Sequence 3, Application US/08446922

: Patent No. 5716805

: GENERAL INFORMATION:

: APPLICANT: Spriggs, Melanie

: TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

: NUMBER OF SEQUENCES: 11

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Immunex Corporation

: STREET: 51 University Street

: CITY: Seattle

: STATE: WA

: COUNTRY: USA

: ZIP: 98101

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: Apple Macintosh

: OPERATING SYSTEM: Apple Operating System 7.1

: SOFTWARE: Microsoft Word for Apple, Version 5.1a

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/446,922

: FILING DATE:

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: USSN 08/107,353

: FILING DATE: 08-13-93

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Perkins, Patricia A

: REGISTRATION NUMBER: 34,693

: REFERENCE/DOCKET NUMBER: 1003-A

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (206)587-0430

: TELEFAX: (206)233-0644

: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 786 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA to mRNA

: HYPOTHETICAL: NO

: ANTI-SENSE: NO

: ORGANISM: Human

: STRAIN: CD40-L

: FEATURE:

Sequence 20, Appli  
Sequence 20, Appli  
Sequence 5, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
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Sequence 22, Appli

us-08-982-272-6.rni

Thu May 30 05:46:18 2002

NAME/KEY: CDS  
LOCATION: 1..783  
US-08-446-922-3

Query Match 97.2%; Score 763.6; DB 1; Length 786;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60  
DB 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60

QY 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120  
DB 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120

QY 121 CTTTTCTGCTGTATCTTCATAGAAGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 121 CTTTTCTGCTGTATCTTCATAGAAGTTGGACAGATAGAGATGAAGGAATCTTCAT 180

QY 181 GAAGATTTTGTATTCATGAAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 240  
DB 181 GAAGATTTTGTATTCATGAAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 240

QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 300  
DB 241 TTACTGAACTGTGAGGAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 300

QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCT 360  
DB 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCT 360

QY 361 CAATTTGGCGCACATGTCATAAAGTGAAGGAGAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 420  
DB 361 CAATTTGGCGCACATGTCATAAAGTGAAGGAGAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 420

QY 421 GCTGAAAGAGGATACATACCATGAGCAACACTTGTGTAACCTTGGAAATGGAAACAG 480  
DB 421 GCTGAAAGAGGATACATACCATGAGCAACACTTGTGTAACCTTGGAAATGGAAACAG 480

QY 481 CTGACCGTTTAAAGCAAGGACTCTTATTTATCTATGTCGCAAGTCACTTCTGTTCCTCAAT 540  
DB 481 CTGACCGTTTAAAGCAAGGACTCTTATTTATCTATGTCGCAAGTCACTTCTGTTCCTCAAT 540

QY 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTTCTGCTTAAAGTCCCGCGGTAGA 600  
DB 541 CGGGAAGCTTCAGTCAAGTCCATTTATAGCCAGCTTCTGCTTAAAGTCCCGCGGTAGA 600

QY 601 TTGAGAGATCTTACTCAGAGCTGCAATATCCACAGTTGCGCAACCTTGGGGCAA 660  
DB 601 TTGAGAGATCTTACTCAGAGCTGCAATATCCACAGTTGCGCAACCTTGGGGCAA 660

QY 661 CAATCATTACCTTGGGAGGATTTGTAATTCGAACAGGTCCTTGGTGTTCCTCAAT 720  
DB 661 CAATCATTACCTTGGGAGGATTTGTAATTCGAACAGGTCCTTGGTGTTCCTCAAT 720

QY 721 GTGACTGATCCAGCAAGTGAAGGATGAGCCATGGCTTCAAGTCCCTTTGGCTTACTCAA 780  
DB 721 GTGACTGATCCAGCAAGTGAAGGATGAGCCATGGCTTCAAGTCCCTTTGGCTTACTCAA 780

QY 781 CTCTGA 786  
DB 781 CTCTGA 786

RESULT 2  
PCT-US93-10034-3  
Sequence 3, Application PC/TUS9310034  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10034  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PCT-US93-10034-3

Query Match 97.2%; Score 763.6; DB 5; Length 786;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60  
DB 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTCGCACTGGACTTCCAGCGAGC 60

QY 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120  
DB 61 ATGCAAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATTGGGTACGA 120

QY 121 CTTTTCTGCTGTATCTTCATAGAAGTTGGCAAGATGAAGATGAAGGAATCTTCAT 180  
DB 121 CTTTTCTGCTGTATCTTCATAGAAGTTGGCAAGATGAAGATGAAGGAATCTTCAT 180

QY 181 GAAGATTTTGTATTCATGAAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 240  
DB 181 GAAGATTTTGTATTCATGAAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 240

QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 300  
DB 241 TTACTGAACTGTGAGGAGATTAAGCCAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 300

QY 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCT 360  
DB 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAAATCCT 360

QY 361 CAATTTGGCGCACATGTCATAAAGTGAAGGAGAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 420  
DB 361 CAATTTGGCGCACATGTCATAAAGTGAAGGAGAGTAAAGCCAGTTTGAAGGCTTTTGAAGGATTA 420

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Db 361 CAAATTCGGGCACATGTCTAAGTAGGCGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Qy 421 GCTGAAAGAGGATACACCATCAGCAACAACTTGGTAAACCCCTGGGAAATGGGAACAG 480
Db 421 GCTGAAAGAGGATACACCATCAGCAACAACTTGGTAAACCCCTGGGAAATGGGAACAG 480
Qy 481 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCTATGCTTATGCTTATGCTTCAAT 540
Db 481 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCTTATGCTTATGCTTCAAT 540
Qy 541 CGGGAAGCTTCGAGTCAGCTCAATTTATAGCCAGCCTCTGCCCTAAAGTCCCGGGTGA 600
Db 541 CGGGAAGCTTCGAGTCAGCTCAATTTATAGCCAGCCTCTGCCCTAAAGTCCCGGGTGA 600
Qy 601 TTCAGAGAACTTCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 660
Db 601 TTCAGAGAACTTCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 660
Qy 661 CAATCCATTCAGTTCGGGAGGAGTATTTGAATTCGAATTCGAATTCGAATTCGAATTCGAAT 720
Db 661 CAATCCATTCAGTTCGGGAGGAGTATTTGAATTCGAATTCGAATTCGAATTCGAATTCGAAT 720
Qy 721 GTGACTGATCCAAAGCAAGTTCAGCTGAGCCATGGCCTTTCAGCTTCTTGGCTTACTCAA 780
Db 721 GTGACTGATCCAAAGCAAGTTCAGCTGAGCCATGGCCTTTCAGCTTCTTGGCTTACTCAA 780
Qy 781 CTCTGA 786
Db 781 CTCTGA 786

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RESULT 3
US-07-940-605A-1
: Sequence 1, Application US/07940605A
: Patent No. 5540926
: GENERAL INFORMATION:
: APPLICANT: ARUFFO, ALEJANDRO
: APPLICANT: HOLLENBAUGH, DIANE
: APPLICANT: LEDBETTER, JEFFREY A.
: TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/940,605A
: FILING DATE: 04-SEP-1992
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 19,872
: REFERENCE/DOCKET NUMBER: 5624-184
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 840 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:

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; NAME/KEY: CDS
; LOCATION: 22...807
US-07-940-605A-1

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTCGCAACTGGACTTCCACCGAGC 60
Db 22 ATGATCGAAACATACAAACAACTTCCCGCAGATCCGTCGCAACTGGACTTCCCGCAGC 81
Qy 61 ATGAAGATTTTTATGATTTACTTTACTTTTCTTATATACCCAGATGATTTGGGTCAGCA 120
Db 82 ATGAATTTTTATGATTTACTTTACTTTTCTTATATACCCAGATGATTTGGGTCAGCA 141
Qy 121 CTTTTTCTGTGTATCTTTCATAGAGGTTGGACAGATAGAGATAGAAAGAAATCTTCAT 180
Db 142 CTTTTTCTGTGTATCTTTCATAGAGGTTGGACAGATAGAGATAGAAAGAAATCTTCAT 201
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 240
Db 202 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCTTATCC 261
Qy 241 TTACTGAACTGTGAGGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
Db 262 TTACTGAACTGTGAGGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 321
Qy 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 360
Db 322 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCT 381
Qy 361 CAAATTCGGGCACATGTCATAAGTGAAGCCAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 382 CAAATTCGGGCACATGTCATAAGTGAAGCCAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 441
Qy 421 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCCCTGGGAAATGGGAACAG 480
Db 442 GCTGAAAGAGGATACACACCATGAGCAACAACTTGGTAAACCCCTGGGAAATGGGAACAG 501
Qy 481 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGATGAT 540
Db 502 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGATGATGATGATGATGATGATGATGAT 561
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGGTGA 600
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTCTGCCCTAAAGTCCCGGGTGA 621
Qy 601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTTGGGGCAA 660
Db 622 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTTGGGGCAA 681
Qy 661 CAATCCATTCAGTTCGGGAGGAGTATTTGAATTCGAATTCGAATTCGAATTCGAATTCGAAT 720
Db 682 CAATCCATTCAGTTCGGGAGGAGTATTTGAATTCGAATTCGAATTCGAATTCGAATTCGAAT 741
Qy 721 GTGACTGATCCAAAGCAAGTTCAGCTGAGCCATGGCCTTTCAGCTTCTTGGCTTACTCAA 780
Db 742 GTGACTGATCCAAAGCAAGTTCAGCTGAGCCATGGCCTTTCAGCTTCTTGGCTTACTCAA 801
Qy 781 CTCTGA 786
Db 802 CTCTGA 807

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RESULT 4
US-08-184-422-7
: Sequence 7, Application US/08184422
: Patent No. 5565321
: GENERAL INFORMATION:
: APPLICANT: ARMITAGE, RICHARD
: APPLICANT: DAVISON, BARRY

```

APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSHAW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
TITLE OF INVENTION: IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,422  
FILING DATE:

PRIOR APPLICATION DATA: 08/009,258  
APPLICATION NUMBER: 01/22/93  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606

TELEFAX: 20638/0800  
7:  
INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
SPANNEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
OR-184-422-7

Query Match	97.2%	Score	763.6	DB 1	Length	840
Best Local Similarity	98.2%	Pred. No.	1.3e-213			
Matches	772	Conservative	0	Mismatches	14	Indels
1	ATGATGAACATACAGCCAAACCTTCCGCCAGATCCGTGGCAACTCGAATCTCCAGCGAGC	60				
46	ATGATCGAACAATACAAACAATCTTCCCGATCTCGCGCCACTGGAGTGCCCATCAGC	105				
61	ATGAAGATTTTTATGTATTTTACTTACTCTCTTTCTTATCACCAGATGATGGGTCAACA	120				
106	ATGAAATTTTTATGTATTTTACTTACTCTCTTTCTTATCACCAGATGATGGGTCAACA	165				
121	CTTTTTCGTGTGATCTCTTCATAGAAGTTGGCAAGATAGAGATGAAGGATCTTCAT	180				
166	CTTTTTCGTGTGATCTCTTCATAGAAGTTGGCAAGATAGAGATGAAGGATCTTCAT	225				
181	GAAGATTTTCTGATTCATGAAGCGATACAGAGATCAACACAGAGAGAAAGATCTTATCC	240				
226	GAAGATTTTCTGATTCATGAAGCGATACAGAGATCAACACAGAGAGAAAGATCTTATCC	285				
241	TTACTGAACCTGTGAGGAGATTTAAACCCAGTTTGAAGCTTTCTGTGAAGGATATAATGTGA	300				

RESULT 5  
US-08-360-923A-1  
Sequence 1, Application US/08360923A  
Patent No. 5674492  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MURPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX-CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360-923A  
FILING DATE: December 21, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424

```
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831
US-08-360-923A-1

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAGCAACCTTCCCGGAGTCCGTCGCAACTGGACCTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACCAACCAACTTCTCCCGGATCTCGGGCCACTGGACCTGCCATCAGC 105
Qy 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 120
Db 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 165
Qy 121 CTTTTGCTGTATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGAATCTTCAT 180
Db 166 CTTTTGCTGTATCTTCATAGAGGTTGGACAGATGAGAGTGAAGGAATCTTCAT 225
Qy 181 GAAGATTTTATTCATGAAACGATACAGATGCAACAGGAGGAAAGATCCTTATCC 240
Db 226 GAAGATTTTATTCATGAAACGATACAGATGCAACAGGAGGAAAGATCCTTATCC 285
Qy 241 TTACTGAAGTGTAGGAGATTAAAGCCAGTTTGAGGCTTTGCAAGGATATATGTTA 300
Db 286 TTACTGAAGTGTAGGAGATTAAAGCCAGTTTGAGGCTTTGCAAGGATATATGTTA 345
Qy 301 AACAAAGGAGGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
Db 346 AACAAAGGAGGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405
Qy 361 CAAATTCGGGCACATGTCATAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTCGGGCACATGTCATAGTGAAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
Qy 421 GCTGAAAAGGATACATACACATGAGCAACACTTGGTAAACCTGGGAAATGGGAAACAG 480
Db 466 GCTGAAAAGGATACATACACATGAGCAACACTTGGTAAACCTGGGAAATGGGAAACAG 525
Qy 481 CTGACCGTTAAAGAACAGGACTCTATTATATCTATGCCCCAGTCAACCTTCTGTTCCTCAAT 540
Db 526 CTGACCGTTAAAGAACAGGACTCTATTATATCTATGCCCCAGTCAACCTTCTGTTCCTCAAT 585
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 645
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAACCTTGGCGGCAA 660
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAACCTTGGCGGCAA 705

US-08-431-055-3
Sequence 3, Application US/08431055
Patent No. 5817516
GENERAL INFORMATION:
APPLICANT: KEHRY, MERILYN R
APPLICANT: CASTLE, BRIAN E
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND
DIFFERENTIATING B CELLS, AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 100 NEW YORK AVE. N.W. SUITE 600
CITY: WASHINGTON
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431.055
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,580
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 22..807
US-08-431-055-3

Query Match 97.2%; Score 763.6; DB 1; Length 840;
Best Local Similarity 98.2%; Pred. No. 1.3e-213;
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAAACATACAGCAACCTTCCCGGAGTCCGTCGCAACTGGACCTTCCAGCGAGC 60
Db 22 ATGATCGAAACATACCAACCAACTTCTCCCGGATCTCGGGCCACTGGACCTGCCATCAGC 81
Qy 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 120
Db 82 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGGTGACGA 141
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Thu May 30 05:46:18 2002

APPLICATION NUMBER: US/08/690,096  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/940,605  
FILING DATE: 04-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-184  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22..807  
US-08-690-096-1

Query Match 97.2%; Score 763.6; DB 2; Length 840;  
Best Local Similarity 98.2%; Pred. No 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 121 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 142 CTTTGTGCTGCTATCTTCATAGAGGTTGACAGATAGAGATGAAGGAATCTTCAT 201  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240  
DB 202 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 261  
QY 241 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTGTCAAGGATATATGTTA 300  
DB 262 TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGCTTGTCAAGGATATATGTTA 321  
QY 301 AACAAAG 360  
DB 322 AACAAAG 381  
QY 361 CAAATTCGGCGACATGTCTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 382 CAAATTCGGCGACATGTCTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441  
QY 421 GCTGAAAG 480  
DB 442 GCTGAAAG 501  
QY 481 CTGACCGTTTAAAGACAGAGACTTATATCTATGCCCCAAGTCACTTCTGTTCCAAAT 540  
DB 502 CTGACCGTTTAAAGACAGAGACTTATATCTATGCCCCAAGTCACTTCTGTTCCAAAT 561  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGCCTTAAAGTCCCGGTAGA 600  
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTTGCCTTAAAGTCCCGGTAGA 621  
QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTCGGGCAA 660  
DB 622 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCCAAACCTTCGGGCAA 681  
QY 661 CAATCCATCTACTTGGGAGGAGTATTTGAATTCGAACAGAGTCTTCGGTGTTCCTCAAT 720  
DB 682 CAATCCATCTACTTGGGAGGAGTATTTGAATTCGAACAGAGTCTTCGGTGTTCCTCAAT 741  
QY 721 GTGACTGATCCAAAGCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
DB 742 GTGACTGATCCAAAGCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 801  
QY 781 CTCGTA 786  
DB 802 CICTGA 807

RESULT 7  
US-08-690-096-1  
Sequence 1, Application US/08690096  
Patent No. 5945513  
GENERAL INFORMATION:  
APPLICANT: ARUFFO, ALEJANDRO  
APPLICANT: HOLLENBAUGH, DIANE  
APPLICANT: LEDBETTER, JEFFREY A.  
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

Db 622 TTCGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCAAACCTTCGGCGCAA 681  
Qy 661 CAATCCATTCTCTGGGAGGAGTATTGAATTCGAACAGGTCTTCGGTGTCTCAAT 720  
Db 682 CAATCCATTCTCTGGGAGGAGTATTGAATTCGAACAGGTCTTCGGTGTCTCAAT 741  
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 780  
Db 742 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 801  
Qy 781 CTCTGA 786  
Db 802 CTCTGA 807

RESULT 8

US-08-249-189-11  
; Sequence 11, Application US/08249189  
; Patent No. 5961974  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,189  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/805,723  
; FILING DATE: December 5, 1991  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870606  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46...831  
US-08-249-189-11

Query Match 97.2%; Score 763.6; DB 2; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATAGAAACATACAGCCAACTTCCGCCAGATCCGTGGCAACTGGAGATTCACAGCAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGCGCCACTGGAGTGGCCATCAGC 105  
Qy 61 ATGAAGATTTTATGTTACTTACTTCTTTCTTATCACCACAGATGATTGGGTGACGA 120  
Db 106 ATGAAATTTTATGTTACTTACTTCTTTCTTATCACCACAGATGATTGGGTGACGA 165  
Qy 121 CTTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 180  
Db 166 CTTTTTGTCTGTATCTTCATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285  
Qy 241 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA 345  
Qy 301 AACAAAGAGGACGACGAGAAAGAACAGCTTTGAATCAAAAGAGTATCAGATCTCT 360  
Db 346 AACAAAGAGGACGACGAGAAAGAACAGCTTTGAATCAAAAGAGTATCAGATCTCT 405  
Qy 361 CAAATTCGCGCACATGTCTATAAGTGAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 420  
Db 406 CAAATTCGCGCACATGTCTATAAGTGAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAAATGGGAAACAG 480  
Db 466 GCTGAAAAGAGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAAATGGGAAACAG 525  
Qy 481 CTGACCGTTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 645  
Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGATTCGCCCAAACTTGGCGGCAA 660  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGATTCGCCCAAACTTGGCGGCAA 705  
Qy 661 CAATCCATTCTCTGGGAGGAGTATTGAATTCGAACACAGGTCTTCGGTGTCTTGTCAAT 720  
Db 706 CAATCCATTCTCTGGGAGGAGTATTGAATTCGAACACAGGTCTTCGGTGTCTTGTCAAT 765  
Qy 721 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCCAAGCAAGTGGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 825  
Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 9  
US-08-484-624A-11  
; Sequence 11, Application US/08484624A  
; Patent No. 5962406

46	ATGATCGAAACATACAAACAACTCTCCCGGATCTGGGCCACTGGACCTGCCCATCAGC	105
QY		
61	ATGAAGATTTTATGTATTTACTTACTGTGTTTCTTATACACCCAGATGATGGGTGAGCA	120
QY		
106	ATGAAATTTTATGTATTTACTTACTGTGTTTCTTATACCCAGATGATGGGTGAGCA	165
Db		
121	CTTTTGTCTGTATCTTTCATAGAAGTTTGGACAAGATAGAAGATGAAGAATCTTCAT	180
QY		
166	CTTTTGTCTGTATCTTTCATAGAAGTTTGGACAAGATAGAAGATGAAGAATCTTCAT	225
Db		
181	GAAGATTTGTATTCATGAACCGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC	240
QY		
226	GAAGATTTGTATTCATGAACCGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC	285
Db		
241	TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
QY		
286	TTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
Db		
301	ACAAAGAGGAGACGAAGAAGAAACACAGTTTGAATCAAAAAGGTGATCAGAATCCT	360
QY		
346	ACAAAGAGGAGACGAAGAAGAAACACAGTTTGAATCAAAAAGGTGATCAGAATCCT	405
Db		
361	CAAAATTGGCGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGG	420
QY		
406	CAAAATTGGCGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGG	465
Db		
421	GCTGAAAAAGATACACCATGACGACAACACTTGTAACCTCGMAAATGGGAAACAG	480
QY		
466	GCTGAAAAAGATACACCATGACGACAACACTTGTAACCTCGMAAATGGGAAACAG	525
Db		
481	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCCTGTTCCAAT	540
QY		
526	CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCACTTCCTGTTCCAAT	585
Db		
541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGGTAGA	600
QY		
586	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCCCGGTAGA	645
Db		
601	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAAA	660
QY		
646	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTCGCGGCAAA	705
Db		
661	CAATCCATTACATTCGGAGGAGTATTGAAATTGCAACACAGATGCTTCGCGTTTGTTCAT	720
QY		
706	CAATCCATTACATTCGGAGGAGTATTGAAATTGCAACACAGTTCGCGTTTGTTCAT	765
Db		
721	GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAA	780
QY		
766	GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCAGTCTCTTGGCTTACTCAAA	825
Db		
781	CTCTGA 786	
QY		
826	CTCTGA 831	
Db		

RESULT 10  
US-08-477733B-11  
US-08-477733B-11, Application US/08477733B  
Sequence 11, Patent No. 5981724  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLLOW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET

GENERAL INFORMATION:  
APPLICANT: ARMSTRAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, MARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,624A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
SEQUENCE: 1-831

Query Match 97.2%; Score 763.6; DB 2; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
1 ATGATAGAAACATACAGCCAACTTCCTCCCCAGATCCGTGGCAACTGGACATTCAGCGAGC 60



CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Apple Macintosh  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,733B  
FILING DATE: June 07, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870506  
INFORMATION FOR SEQ ID NO.: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-477-733B-11

Query Match 97.2%; Score 763.6; DB 2; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 ATGATAGAAACATACAGCAACCTCCGCCAGATCGGTGGCAACTGGACTTCACGCGAGC 60  
DB 46 ATGATCGAAACATACAAACCAACTCTCCCGATCTGGCGCCACTGGAGTCCCATCAGC 105  
QY 61 ATGAAGATTTTATCTACTTACTTCTTCTTATCACCACAGATGATTGGTCCAGCA 120  
DB 106 ATGAAGATTTTATCTACTTACTTCTTCTTATCACCACAGATGATTGGTCCAGCA 165  
QY 121 CTTTTTGTGTATCTTTCATAGAGGTGGACAAGATAGAAAGATCTTCAT 180  
DB 166 CTTTTTGTGTATCTTTCATAGAGGTGGACAAGATAGAAAGATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAAAGATCTTATCC 240  
|||||

DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 285  
QY 241 TTACTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTTGAAGGATATATATGTTA 300  
DB 286 TTACTGAAGTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTTGAAGGATATATATGTTA 345  
QY 301 AACAAAGAGGACGACGAAGAAACAAACAGCTTTTGAATGCAAAAGGTGATCAGATCCCT 360  
DB 346 AACAAAGAGGACGACGAAGAAACAAACAGCTTTTGAATGCAAAAGGTGATCAGATCCCT 405  
QY 361 CAAATTCGCGCACATGTCTATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
DB 406 CAAATTCGCGCACATGTCTATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAGAGGATACCTACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 480  
DB 466 GCTGAAAGAGGATACCTACACCATGAGCAACAACCTTGGTAAACCTCGGAAATGGGAAACAG 525  
QY 481 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCAACCTTCTGTTCCAAT 540  
DB 526 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCAACCTTCTGTTCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGCTAGA 645  
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCAGTTCGCCCAAAACCTTTCGCGGCAA 660  
DB 646 TTCGAGAGAACTTACTCAGAGCTGCAATATACCCAGTTCGCCCAAAACCTTTCGCGGCAA 705  
QY 661 CAATCCATTCACTTGGGAGGAGTATTGTAATTCGAACACAGTTCGCTGCTGTTTGTCAAT 720  
DB 706 CAATCCATTCACTTGGGAGGAGTATTGTAATTCGAACACAGTTCGCTGCTGTTTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGAAGCCAGTGCCTGCTCAGCTGCTTTCGCTTACTCTACTCAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGAAGCCAGTGCCTGCTCAGCTGCTTTCGCTTACTCTACTCAA 825  
QY 781 CTCCTGA 786  
DB 826 CTCCTGA 831

RESULT 11  
US-08-763-995-1  
; Sequence 1, Application US/08763995  
; Patent No. 6017527  
; GENERAL INFORMATION:  
; APPLICANT: MARASKOVSKY, EUGENE  
; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Power Macintosh 7200/90  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/763,995  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/677,762  
; FILING DATE: 10 JUL 1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.

Thu May 30 05:46:18 2002

Db 706 CAATCCATTCACTTGGAGGAGTATTGAATTGCAACCAAGGCTTCGGTGTTCAT 765  
QY 721 GTGACTGATCCAGCAAGTGAAGCCATGCGCTTTCACGCTTCTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAGCAAGTGAAGCCATGCGCTTTCACGCTTCTGGCTTACTCAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 12

US-09-088-913A-11  
Sequence 11, Application US/09088913A  
Patent No. 6087329  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,913A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-763-995-1

Query Match 97.2%; Score 763.6; DB 3; Length 840;  
Best Local Similarity 98.2%; Pred..No.1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCCCGTGGCAACTGCGACTTCAGCGAGC 60  
Db 46 ATGATCGAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAGATTTTATGTTATTTACTTACTTCTTCTTATCACCCAGATGTTGGTTCAGCA 120  
Db 106 ATGAAATTTTATGTTATTTACTTACTTCTTCTTATCACCCAGATGTTGGTTCAGCA 165  
QY 121 CTTTGTCTGTATCTTCTATAGAGGTGGACAGATAGAGATGAAGATGAAGAAATCTTCAT 180  
Db 166 CTTTGTCTGTATCTTCTATAGAGGTGGACAGATAGAGATGAAGATGAAGAAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAGATACAGATGATGCAACAGAGAGAAATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAGATACAGATGATGCAACAGAGAGAAATCTTATCC 285  
QY 241 TTACTGAACGTGAGAGATTAAGACAGATTTGAAGCTTTGTGAAGATATAATGTTA 300  
Db 286 TTACTGAACGTGAGAGATTAAGACAGATTTGAAGCTTTGTGAAGATATAATGTTA 345  
QY 301 AACAAAG 360  
Db 346 AACAAAG 405  
QY 361 CAAATTCGGGCACATGCTATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 420  
Db 406 CAAATTCGGGCACATGCTATAGTAGGCGCCAGCAGTAAACACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAAGGATACACACATGAGCAACAACTTGGTAAACCTGGAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACACACATGAGCAACAACTTGGTAAACCTGGAATGGGAAACAG 525  
QY 481 CTGACCGTTTAAAGACAGAGACTCTATTATCTATGCCCCAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTTAAAGACAGAGACTCTATTATCTATGCCCCAGTCACTTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAATACCCAGTTCGCCAAACCTTCGGGGCAA 660  
Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAATACCCAGTTCGCCAAACCTTCGGGGCAA 705  
QY 661 CAATCCATTACATTGGGGAGGAGTATTGTAATTGCAACAGAGTCTGCTTCGGTGTTCAT 720

ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-982-913A-11

Query Match 97.2%; Score 763.6; DB 3; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAACATACACGCAACCTTCCCGCAGATCCGTGGCAACTGGCACTTCCAGCGAGC 60  
Db 46 ATGATGAACATACACCAAACTTCCCGCATCTCGGCCACTGGCACTCCCATCAGC 105

Qy 61 ATGAAGATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA 120  
Db 106 ATGAAGATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA 165

Qy 121 CTTTTCCTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTTCCTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225

Qy 181 GAAGATTTTGTATTCATGAACCATACAGATGCAACAGAGAGAGAAAGATCCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAACCATACAGATGCAACAGAGAGAGATCCTTATCC 285

Qy 241 TTACTGAACCTGTAGAGATTAAGCCAGCTTGAAGGCTTTGGAAGGATATAATGTTA 300  
Db 286 TTACTGAACCTGTAGAGATTAAGCCAGCTTGAAGGCTTTGGAAGGATATAATGTTA 345

Qy 301 AACAAAGAGAGAGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360  
Db 346 AACAAAGAGAGAGAGAAAGAAAGAAAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405

Qy 361 CAATTCGGGCACATGTCATAAGTGAAGGCGAGCAGTAAACAAACATCTGTGTTACAGTGG 420  
Db 406 CAATTCGGGCACATGTCATAAGTGAAGGCGAGCAGTAAACAAACATCTGTGTTACAGTGG 465

Qy 421 GCTGAAAAGGATACACTACACCATGAGCAACACTTGTGTAACCTGGAATGGGAACAG 480  
Db 466 GCTGAAAAGGATACACTACACCATGAGCAACACTTGTGTAACCTGGAATGGGAACAG 525

Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCAAGTCACTCTGTGTTCCAAT 540  
Db 526 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGCCAAGTCACTCTGTGTTCCAAT 585

Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGCGGTAGA 645

Qy 601 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCA 660  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGGCGGCA 705

Qy 661 CAATCCATTCAGTGGGAGGAGTATTGAATTGCAACAGAGTCTCGGTGTTGTTCAAT 720  
Db 706 CAATCCATTCAGTGGGAGGAGTATTGAATTGCAACAGAGTCTCGGTGTTGTTCAAT 765

Qy 721 GTGACTGATCCAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
Db 766 GTGACTGATCCAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 825

Qy 781 CTCGA 786  
Db 826 CTCGA 831

RESULT 13  
US-08-589-771B-7  
; Sequence 7, Application us/08589771B

Patent No. 6106832  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSHAW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING  
DEFECTIVE CD40L (as amended)  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589,771B  
FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JANIS C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-589-771B-7

Query Match 97.2%; Score 763.6; DB 3; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGATGAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGCACTTCCAGCGAGC 60  
Db 46 ATGATGAACATACAAACAACTTCTCCCGCATCTCGGCCACTGGCACTCCCATCAGC 105

Qy 61 ATGAAGATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA 120  
Db 106 ATGAAGATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATGGGTGACGA 165

Qy 121 CTTTTCCTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTTCCTGTGTATCTTCATAGAGGTTGGACAAGATAGAGATGAAGGAATCTTCAT 225

181	GAAGATTTTGTATTTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCC	240
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226	GAAGATTTTGTATTCATGAAAAAGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCC	285
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241	TTTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGGAAGGATATAATGTTTA	300
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286	TTTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGGAAGGATATAATGTTTA	345
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301	AACAAAGAGGAGACGAAGAAGAAAACACGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	360
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346	AACAAAGAGGAGACGAAGAAGAAAACACGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	405
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RESULT 14  
US-08-769-819-11  
Sequence 11, Application US/08/769819  
Patent No. 6264951  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLOW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
\* APPLICATION NUMBER: US/08/769,819  
FILING DATE: 19-DEC-1996  
CLASSIFICATION: 424

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/484,624
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/249,189
FILING DATE: May 24, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/969,703
FILING DATE: October 23, 1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/805,723
FILING DATE: December 5, 1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/783,707
FILING DATE: October 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2802-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46..831

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Query Match	97.2%	Score 763.6;	DB 4;	Length 840;
Best Local Similarity	98.2%;	Pred. No. 1.3e-213;		
Matches	772;	Conservative	0;	Mismatches 14;
			Indels	Gaps
QY	1	ATGATAGAAACATACAGCCAACTTC	00000	CAGATCCGGTGGCAACTGACCTTCACGGCAGG 60
DB	45	ATGATCGAAACATACAACCAACTCT	00000	CCCGATCTGCGGCCACTGGACTGCCCATCAGC 105
QY	61	ATGAAGATTTTATGCTATTCTTACT	TTTTT	TATCAGCCAGATGATTTGGGTACAGA 120
DB	106	ATGAAAAATTTTATGCTATTCTTACT	TTTTT	TATCAGCCAGATGATTTGGGTACAGA 165
QY	121	CTTTTTGCTGTGTCCTTCATAGAAG	TTTGG	CAACATAGAGATGAAGGAATCTTCAT 180
DB	166	CTTTTTGCTGTGTCCTTCATAGAAG	TTTGG	CAACATAGAGATGAAGGAATCTTCAT 225
QY	181	GAAGATTTTGATTCATGAAACGAT	ACAGAC	ATGCAACAGGAGAAAGATCCTTATCC 240
DB	226	GAAGATTTTGATTCATGAAACGAT	ACAGAC	ATGCAACAGGAGAAAGATCCTTATCC 285
QY	241	TTACTGAACTGTGAGGAGATTAAAG	CCAGT	TTGAAGCGTTTGTGAAGCATATATGTTA 300
DB	286	TTACTGAACTGTGAGGAGATTAAAG	CCAGT	TTGAAGCGTTTGTGAAGCATATATGTTA 345
QY	301	AACAAAGAGGACGAGAAAGAAACAG	CTTTT	TGAATGCAAAAAGGTGATCAGAAATCCT 360
DB	346	AACAAAGAGGAGACGAGAAAGAAAC	AGCTTT	TGAATGCAAAAAGGTGATCAGAAATCCT 405
QY	361	CAAAATGGGSCACATGTCATAAGT	GTGAG	CGCCAGCAGTAAACACATCTGTTGTACAGTGG 420
DB	406	CAAAATGGGSCACATGTCATAAGT	GTGAG	CGCCAGCAGTAAACACATCTGTTGTACAGTGG 455
QY	421	GCTGAAAAAGGATACATACCATGAC	CAACAA	CTTGTTAAACCCTGGAAAAATGGGAACAG 480

Db 466 GCTGAAAAAGGATACTACACCATGAGCAACAACCTGGTAACCCCTGGAAAAATGGGAACAG 525  
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGGCAAGTCACCTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGGCAAGTCACCTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 645  
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCAA 660  
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCAA 705  
Qy 661 CAATCCATTCTCTGGGAGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAAT 720  
Db 706 CAATCCATTCTCTGGGAGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTTCAGCTGCTTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCACTGGCTTTCAGCTGCTTTGGCTTACTCAAA 825  
Qy 781 CTCCTGA 786  
Db 826 CTCCTGA 831

RESULT 15  
US-08-770-974-11  
Sequence 11, Application US/08770974  
Patent No. 6290972  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08770, 974  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-770-974-11

Query Match 97.2%; Score 763.6; DB 4; Length 840;  
Best Local Similarity 98.2%; Pred. No. 1.3e-213;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCCCAACCTTCCCCCAGATCCGTGGCAACTGGACTTCCACGGAGC 60  
Db 46 ATGATCGAAACATACACCAACCTTCTCCCGATCTGGCGCCACTGGACTGCCCATCAGC 105  
Qy 61 ATGAAGATTTTATGTTTACTTACTTACTTCTTATCACCACAGATGATGGGTGACGA 120  
Db 106 ATGAAGATTTTATGTTTACTTACTTACTTCTTATCACCACAGATGATGGGTGACGA 165  
Qy 121 CTTTTGCTGTGTAATCTTATAGAAAGTTGGACAAAGATAGAAAGTGAAGGAATCTTCAT 180  
Db 166 CTTTTGCTGTGTAATCTTATAGAAAGTTGGACAAAGATAGAAAGTGAAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAACAGATACAGATGCAACACAGAGAGAAAGATCCCTATCC 240  
Db 226 GAAGATTTTGTATTCATGAACAGATACAGATGCAACACAGAGAGAAAGTCCCTATCC 285  
Qy 241 TTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTA 345  
Qy 301 AACAAAGAGGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 360  
Db 346 AACAAAGAGGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 405  
Qy 361 CAAATTGGCGCACATGTCATAGTCAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 420  
Db 406 CAAATTGGCGCACATGTCATAGTCAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAAGGATACCTACACCATGAGCAACAACCTTTGGTAAACCTGGAAATGGGAAACAG 480  
Db 466 CTTGAAAAAGGATACCTACACCATGAGCAACAACCTTTGGTAAACCTGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGGCAAGTCACCTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGGCAAGTCACCTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 645  
Qy 601 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCAA 660  
Db 646 TTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCAA 705  
Qy 661 CAATCCATTCTCTGGGAGGAGTATTGAATTGCAACAGGTGCTTCGGTGTGTTGTCAAT 720

Thu May 30 05:46:18 2002

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Db 706 CAATCCATTCACTTGGGAGGAGTATTGCAATTGCAACGAGTGCTTCGGTCTTGTCAAT 765
QY 721 GTCACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTTCAGGTCTCTTTGGCTTACTCAAA 780
Db 766 GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTTCAGGTCTCTTTGGCTTACTCAAA 825
QY 781 CTCTGA 786
Db 826 CTCTGA 831

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Search completed: May 30, 2002, 02:51:45  
 Job time: 11609 sec

Description

Thu May 30 05:46:21 2002

JOURNAL Patent: US 5817516-A 3 06-OCT-1998;		Location/Qualifiers		1. .840		/organism="unknown"		214 t	
FEATURES		source		263 a		182 c		181 g	
BASE COUNT		263 a		182 c		181 g		214 t	
ORIGIN									
Query Match		95.9%; Score 754;		DB 6;		Length 840;			
Best Local Similarity		97.5%;		Pred. No. 1.3e-188;					
Matches 766;		Conservative 0;		Mismatches 20;		Indels 0;		Gaps 0;	
QY	1	ATCATAGAACATACAGCAACCTTCCGCCAGATCCGTGGCAACTGGACTTCCAGCGAGC	60						
DB	1	ATGATGAAACATACACCAACCTTCTCCCGATCTGGCGCACTGGACTGCCATCAGC	60						
QY	61	ATGAAGATTTTATGATTTACTTCTTCTTATCACCAGATGATGGTTCAGCA	120						
DB	61	ATGAAATTTTATGATTTACTTCTTCTTATCACCAGATGATGGTTCAGCA	120						
QY	121	CTTTTCTGCTGTATCTTATGAAAGTGGACAAGATGAGATGAAAGAAATCTTCAT	180						
DB	121	CTTTTCTGCTGTATCTTATGAAAGTGGACAAGATGAGATGAAAGAAATCTTCAT	180						
QY	181	GAAGATTTTCTATGATGAAAGATGAGATGAGATGAGATGAGATGAGATGAGAT	240						
DB	181	GAAGATTTTCTATGATGAAAGATGAGATGAGATGAGATGAGATGAGATGAGAT	240						
QY	241	TTACTGAATCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	300						
DB	241	TTACTGAATCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	300						
QY	301	AACAAAG	360						
DB	301	AACAAAG	360						
QY	361	CAAAATGGCGCACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	420						
DB	361	CAAAATGGCGCACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	420						
QY	421	GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480						
DB	421	GCTGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	480						
QY	481	CTGACCGTTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT	540						
DB	481	CTGACCGTTTAAAGACAGAGACTTATATATATATATATATATATATATATATAT	540						
QY	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTCCCTTAAAGTCCCGGTAGA	600						
DB	541	CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTTCCCTTAAAGTCCCGGTAGA	600						
QY	601	TTGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAGCTTGGGGCAA	660						
DB	601	TTGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGCCAAGCTTGGGGCAA	660						
QY	661	CAATCCATTCACCTGGGAGAGATTTGAATTCGACAGAGTCTTCCGTGTTTGTCAAT	720						
DB	661	CAATCCATTCACCTGGGAGAGATTTGAATTCGACAGAGTCTTCCGTGTTTGTCAAT	720						
QY	721	GTGACTGATCCAGCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	780						
DB	721	GTGACTGATCCAGCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	780						
QY	781	CTCTGA 786							
DB	781	CTCTGA 786							
RESULT 2		AR044779		840 bp		DNA		linear	
LOCUS		AR044779		Sequence 3 from patent US 5817516.					
DEFINITION		Sequence 3 from patent US 5817516.							
ACCESSION		AR044779							
VERSION		AR044779.1		GI:5966244					
KEYWORDS									
SOURCE		Unknown.							
ORGANISM		Unknown.							
REFERENCE		1 (bases 1 to 840)							
AUTHORS		Kehry, M. and Castle, B.							
TITLE		Methods for proliferating and differentiating B cells with high density membrane CD40 ligand							
LOCUS		AR076926		840 bp		DNA		linear	
DEFINITION		Sequence 11 from patent US 5961974.							
LOCUS		AR076926		840 bp		DNA		linear	
DEFINITION		Sequence 11 from patent US 5961974.							



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ACCESSION AR076926
VERSION AR076926.1 GI:10003672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 840)
Unclassified.
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition
comprising the same and hybridomas producing the same
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..840
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCACCTTCCCCACAGATCGGTGGCAACTGGACTTCCACGGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAGATTTTATCTATTACTTACTTCTTCTTATCACCACAAATGATTGGATCTGTG 120
DB 106 ATGAAATTTTATCTATTACTTACTTCTTCTTATCACCACAGATGATTGGGTACGA 165
QY 121 CTTTTCGTGTATCTTTCATAGAGGTGGACAAAGATAGAGATGAAAGGAATCTTCAAT 180
DB 166 CTTTTCGTGTATCTTTCATAGAGGTGGACAAAGATAGAGATGAAAGGAATCTTCAAT 225
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGACGAAGAAACAGCTTTTGAATGCAAAAGAGGTGATCAGAAATCCT 360
DB 346 AACAAAGAGGAGACGAAGAAACAGCTTTTGAATGCAAAAGAGGTGATCAGAAATCCT 405
QY 361 CAAATTCGGGCACATGTCTAAGTGGCCACAGTAAACACATCTGTGTACAGTGG 420
DB 406 CAAATTCGGGCACATGTCTAAGTGGCCACAGTAAACACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 480
DB 466 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCACAGTCACTCTCTGTCCCAAT 540
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCACAGTCACTCTCTGTCCCAAT 585
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645

QY 1 ATGATAGAAACATACAGCCACCTTCCCCACAGATCGGTGGCAACTGGACTTCCACGGAGC 60
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAGATTTTATCTATTACTTACTTCTTCTTATCACCACAAATGATTGGATCTGTG 120
DB 106 ATGAAATTTTATCTATTACTTACTTCTTCTTATCACCACAGATGATTGGGTACGA 165
QY 121 CTTTTCGTGTATCTTTCATAGAGGTGGACAAAGATAGAGATGAAAGGAATCTTCAAT 180
DB 166 CTTTTCGTGTATCTTTCATAGAGGTGGACAAAGATAGAGATGAAAGGAATCTTCAAT 225
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAGGAGACGAAGAAACAGCTTTTGAATGCAAAAGAGGTGATCAGAAATCCT 360
DB 346 AACAAAGAGGAGACGAAGAAACAGCTTTTGAATGCAAAAGAGGTGATCAGAAATCCT 405
QY 361 CAAATTCGGGCACATGTCTAAGTGGCCACAGTAAACACATCTGTGTACAGTGG 420
DB 406 CAAATTCGGGCACATGTCTAAGTGGCCACAGTAAACACATCTGTGTACAGTGG 465
QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 480
DB 466 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAAACCTTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCACAGTCACTCTCTGTCCCAAT 540
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCACAGTCACTCTCTGTCCCAAT 585
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645

QY 601 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCA 660
DB 646 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCCAACCTTGGCGGCA 705
QY 661 CAATCCATTCACTTGGGAGGATTTGAATTCGAACACAGTTCGCTCGGTGTTTCTCAAT 720
DB 706 CAATCCATTCACTTGGGAGGATTTGAATTCGAACACAGTTCGCTCGGTGTTTCTCAAT 765
QY 721 GTGACTGATCCCAAGCAAGTGAGCCATGGCACTGGCTTCACTGCTCTTTGGCTTACTCAA 780
DB 766 GTGACTGATCCCAAGCAAGTGAGCCATGGCACTGGCTTCACTGCTCTTTGGCTTACTCAA 825
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QY	601	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGC GGSCAA	660
Db	646	TTGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTGC GGSCAA	705
QY	661	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTGTTGCAAT	720
Db	706	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGTCCTTCGGTGTGTTGCAAT	765
QY	721	GTGACTGATCCAGCCAAAGTGAGCCATGCGACTTTCACGTCTTTCGGCTTACTCAAA	780
Db	766	GTGACTGATCCAGCCAAAGTGAGCCATGCGACTTTCACGTCTTTCGGCTTACTCAAA	825
QY	781	CTCTGA 786	
Db	826	CTCTGA 831	
RESULT	5		
LOCUS	AR085419	840 bp DNA linear	PAT 01-SEP-2000
DEFINITION	Sequence 11 from patent US 5981724.		
ACCESSION	AR085419		
VERSION	AR085419.1	GI:10012188	
KEYWORDS	unknown.		
SOURCE	unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 840)		
AUTHORS	Armitage, R.J., Fanslow, W.C., Spriggs, M.K., Srinivasan, S., Gibson, M.G., Morris, A.E. and McGrew, J.T.		
TITLE	DNA encoding CD40 ligand, a cytokine that binds CD40		
JOURNAL	Patent: US 5981724-A 11 09-NOV-1999;		
FEATURES	Location/Qualifiers		
Source	1...840		
BASE COUNT	266 a 185 c 175 g 214 t		
ORIGIN			
Query Match	95.9%;	Score 754;	DB 6; Length 840;
Best Local Similarity	97.5%;	Pred. No. 1.3e-188;	
Matches	766; Conservative	0; Mismatches 20; Indels	0; Gaps
QY	1	ATCATGAAACATACAGCCAAACCTTCCCGAGATCCGTCGCACTGGACTTCCAGCGAGC	60
Db	46	ATGTCGAAACATACACCAAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC	105
QY	61	ATGAAGATTTTATGTAATTTACTTACTGTTTTCTTATACCCAAATGATTTGATCTGTG	120
Db	106	ATGAAATTTTATGTAATTTACTTACTGTTTTCTTATCACCCAGATGATTGGTCAGCA	165
QY	121	CTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGAATCTTCAT	180
Db	166	CTTTTCTGTGTATCTTCATAGAGGTTGGACAAGATGAGATGAAAGGAATCTTCAT	225
QY	181	GAAGATTTTGTATTCATGAAGACATACAGAGATGCAACACAGAGAAAAGATCTTATCC	240
Db	226	GAAGATTTTGTATTCATGAAGACATACAGAGATGCAACACAGAGAAAAGATCTTATCC	285
QY	241	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA	300
Db	286	TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA	345
QY	301	RACAAAGAGGACGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT	360
Db	346	RACAAAGAGGACGAAGAAAGAAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT	405
QY	361	CAAAATTTGGGCACATGTCATAGTGCAGCCAGCAGTAAAAACATCTGTGTTCAGTGG	420
Db	406	CAAAATTTGGGCACATGTCATAGTGCAGCCAGCAGTAAAAACATCTGTGTTCAGTGG	465
QY	421	GCTGAAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAATGGGAAACAG	480

Db	466	GCTGAAAAAGGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAATAATGGGAAACAG	525
QY	481	CTGACCGTTAAAGACAGACGACTCTATTATATCTATGCCCCAAAGTCACCTCTCTGTTCCAAAT	540
Db	526	CTGACCGTTAAAGACAGACGACTCTATTATATCTATGCCCCAAAGTCACCTCTCTGTTCCAAAT	585
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGGCTTGCTTAAAGTCCCGGCTAGA	600
Db	586	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCAGGCTTGCTTAAAGTCCCGGCTAGA	645
QY	601	TTGAGAGATCTTACTTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTTCGGGCAA	660
Db	646	TTGAGAGATCTTACTTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTTCGGGCAA	705
QY	661	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGCTTCGCTGTTGTTCAAT	720
Db	706	CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGGCTTCGCTGTTGTTCAAT	765
QY	721	GTGACTGATCCAGCCAAAGTCAGCATGGCTTTCACGTCCTTTTGGCTTACTCAA	780
Db	766	GTGACTGATCCAGCCAAAGTCAGCATGGCTTTCACGTCCTTTTGGCTTACTCAA	825
QY	781	CTCTGA 786	
Db	826	CTCTGA 831	
RESULT	6		
LOCUS	AR103375	840 bp DNA linear	PAT 14-FEB-2001
DEFINITION	Sequence	11 from patent US 6087329.	
ACCESSION	AR103375		
VERSION	AR103375.1	GI:12814963	
KEYWORDS	unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 840)		
AUTHORS	Armstrong, R.J., Fanslow, W.C. and Spriggs, M.K.		
TITLE	CD40 ligand polypeptide		
JOURNAL	Patent: US 6087329-A 11 11-JUL-2000;		
FEATURES	Location/Qualifiers		
source	1..840		
BASE COUNT	266 a 185 c 175 g 214 t		
ORIGIN	/organism="unknown"		
Query Match	95.9%; Score 754; DB 6; Length 840;		
Best Local Similarity	97.5%; Pred. No. 1.3e-188;		
Matches	766; Conservative 0; Mismatches 20; Indels 0; Gaps 0		
QY	1	ATGATGAACATACAGCCAACTTCCCCAGATCCGTGCGCAACTGACCTCCAGCGAGC	60
Db	46	ATGATGAACATACAGCCAACTTCCCCAGATCCGTGCGCAACTGACCTCCAGCGAGC	105
QY	61	ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCACAAATGATTTGATCTGTG	120
Db	106	ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCACAAATGATTTGATCTGTG	165
QY	121	CTTTTCTGCTGTATCTTCATAGAGTTGGCAAGATAGCAAGATGAAGGAATCTTCAT	180
Db	166	CTTTTCTGCTGTATCTTCATAGAGTTGGCAAGATAGCAAGATGAAGGAATCTTCAT	225
QY	181	GAAATTTTGTATTTTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATTC	240
Db	226	GAAATTTTGTATTTTCATGAAACCATACAGATGCAACAGAGAAAGATCTTATTC	285
QY	241	TTACTGAACTGTAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
Db	286	TTACTGAACTGTAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGAGACGAGAAAGAAAACAGCTTGAATGCAAAAAGGATGATCAGAAATCCT	360

|||||  
Db 346 AACAAAGAGGACGAAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 405  
Qy 361 CAAATTTGGGACATGTCATAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
Db 406 CAAATTTGGGACATGTCATAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645  
Qy 601 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCCAAACCTTTCGCGGCAA 660  
Db 646 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCCAAACCTTTCGCGGCAA 705  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCGGTGTTTGTCAAT 720  
Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCGGTGTTTGTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCAAGTTCCTTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCAAGTTCCTTTGGCTTACTCAAA 825  
Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 7  
LOCUS ARI06246 840 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 7 from patent US 6106832.  
ACCESSION ARI06246  
VERSION ARI06246.1 GI:12820776  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.  
TITLE Treatment of individuals exhibiting defective CD40L  
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-188;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60  
Db 46 ATGATCGAAACATACAGCAACCTTCTCCCGATCTGGCGCCAGTGGACTGCCATCAGC 105  
Qy 61 ATGAGATTTTATGTAATTTACTTACTGTGTTTCTTATACCCAAATGATTGGATCTGTG 120  
Db 106 ATGAAAATTTTATGTAATTTACTTACTGTGTTTCTTATACCCAGATGATTGGGTGAGCA 165  
Qy 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAAATCTTCAT 180  
Db 166 CTTTTTGTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAAATCTTCAT 225

Qy 181 GAAGATTTTGTATTTCATGAAAACGATACAGAGATCAACACAGAGAGAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTTCATGAAAACGATACAGAGATCAACACAGAGAGAAGATCTTATCC 285  
Qy 241 TTACTGAAGTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTA 300  
Db 286 TTACTGAAGTGTGAGGAGATTAAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTA 345  
Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 360  
Db 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCT 405  
Qy 361 CAAATTTGGGACATGTCATAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
Db 406 CAAATTTGGGACATGTCATAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACCTACACCATGAGCAACAACTTGGTAAACCTCGGAAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAAGGACTCTATTATCTATGCGCCAAAGTCACTTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645  
Qy 601 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCCAAACCTTTCGCGGCAA 660  
Db 646 TTCGAGAGAACTCTTACTCAGAGCTCAAAATACCCACAGTTCGCGCCAAACCTTTCGCGGCAA 705  
Qy 661 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCGGTGTTTGTCAAT 720  
Db 706 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTTCGCGGTGTTTGTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCAAGTTCCTTTGGCTTACTCAAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGCCTTCAAGTTCCTTTGGCTTACTCAAA 825  
Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 8  
LOCUS ARI69232 840 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 11 from patent US 6290972.  
ACCESSION ARI69232  
VERSION ARI69232.1 GI:17907047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.  
TITLE Method of augmenting a vaccine response by administering CD40 ligand  
JOURNAL Patent: US 6290972-A 11 18-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 95.9%; Score 754; DB 6; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-188;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCAACCTTCCCGCAGATCCGTGGCAACTGGACTTCCAGCGAGC 60



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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 840)
AUTHORS     Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.
TITLE       Soluble and its use in B cell stimulation
JOURNAL     Patent: US 5540926-A 1 30-JUL-1996;
FEATURES    Location/Qualifiers
            source
            1..840
            /organism="unknown"
BASE COUNT  263 a 182 c 181 g 214 t
ORIGIN

Query Match      95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
Db 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
QY 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 81
Db 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 81
QY 61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATTTGGATCTGTG 120
Db 61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATTTGGATCTGTG 120
QY 82 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGCA 141
Db 82 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGCA 141
QY 121 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
Db 121 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
QY 142 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 201
Db 142 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 240
Db 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 240
QY 202 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 261
Db 202 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 261
QY 241 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 241 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
QY 262 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321
Db 262 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 321
QY 301 AACAAAGAGGACGACGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360
Db 301 AACAAAGAGGACGACGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360
QY 322 AACAAAGAGGACGACGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 381
Db 322 AACAAAGAGGACGACGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 381
QY 361 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 361 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
QY 382 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 441
Db 382 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 441
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 480
Db 421 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 480
QY 442 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 501
Db 442 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 501
QY 481 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTCCCAAT 540
Db 481 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTCCCAAT 540
QY 502 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTCCCAAT 561
Db 502 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTCCCAAT 561
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
QY 562 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 621
Db 562 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 621
QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 660
Db 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 660
QY 622 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 681
Db 622 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 681
QY 661 CAATCCATTCACTTGGAGGAGTATTGAAATGCAACAGGTCGCTTCGGTGTGTTCAT 720
Db 661 CAATCCATTCACTTGGAGGAGTATTGAAATGCAACAGGTCGCTTCGGTGTGTTCAT 720
QY 682 CAATCCATTCACTTGGAGGAGTATTGAAATGCAACAGGTCGCTTCGGTGTGTTCAT 741
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QY 721 GTGACTGTATCCAAAGCAAGTGGCCATGGCTTCCAGCTTCCTTTGGCTTACTCAAA 780
Db 721 GTGACTGTATCCAAAGCAAGTGGCCATGGCTTCCAGCTTCCTTTGGCTTACTCAAA 780
QY 742 GTGACTGTATCCAAAGCAAGTGGCCATGGCTTCCAGCTTCCTTTGGCTTACTCAAA 801
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QY 781 CTCTGA 786
Db 802 CTCTGA 807
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RESULT 11
I27345 LOCUS I27345 840 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5565321.
ACCESSION I27345
VERSION I27345.1 GI:1818121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 840)
AUTHORS Spriggs,M.K., Armitage,R.J. and Fanslow,W.C. III.
TITLE Detection of mutations in a CD40 ligand gene
JOURNAL Patent: US 5565321-A 7-15-OCT-1996;
FEATURES Location/Qualifiers
            1..840
            /organism="unknown"
BASE COUNT  266 a 185 c 175 g 214 t
ORIGIN

Query Match      95.9%; Score 754; DB 6; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCAACTGGACTTCCAGCGAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATTTGGATCTGTG 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCAGATGATTTGGTCAGCA 165
QY 121 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 180
Db 166 CTTTTGCTGTCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATGAAACAGTACAGAGATGCAACACAGGAGAAAGATCTTATCC 285
QY 241 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
Db 286 TTACTGAAGTGTAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 345
QY 301 AACAAAGAGGACGACGAAAGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 360
Db 346 AACAAAGAGGACGACGAAAGAAACAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 405
QY 361 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 406 CAAATTTGGCGCACATCTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 480
Db 466 GCTGAAAGAGGATCTACACCATGAGCAACACTTGGTAACCCCTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAT 540
Db 526 CTGACCGTTAAAGACAGAGGACTTATTATATCTATGCCCAAGTCACCTTCTGTTCCAAT 585
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 660
Db 646 TTCGAGAGAACTTCTACTCAGAGCTGCAATACCCAGAGTTCGCCCAACCTTCCGGGCAA 705
QY 661 CAATCCATTCACTTGGAGGAGTATTGAAATGCAACAGGTCGCTTCGGTGTGTTCAT 720
Db 661 CAATCCATTCACTTGGAGGAGTATTGAAATGCAACAGGTCGCTTCGGTGTGTTCAT 720
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Db 706 CAATCCATTCACTTGGGAGGAGTAATTTGAATTCGAACCAAGTCTTGGCTGTTTGTCAAT 765  
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Db 766 GTCACTGATCCAGCAAGTGAAGCCATGCACTGGCTTCACGCTCTTTGGCTTACTCAAA 825  
QY 781 CTCCTGA 786  
Db 826 CTCCTGA 831  
  
RESULT 12  
167828  
LOCUS 167828 840 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 1 from patent US 5674492.  
ACCESSION 167828.1 GI:2829950  
VERSION 167828.1  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.  
TITLE Method of preventing or treating disease characterized by neoplastic cells expressing CD40  
JOURNAL Patent: US 5674492-A 1 07-OCT-1997;  
FEATURES  
Location/Qualifiers  
1..840  
/organism="unknown"  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN  
  
Query Match 95.9%; Score: 754; DB 6; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-188;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
QY 1 ATGATGAACATACAGCCAACTTCCCGCATCTCGGCCACTGGACATCCAGCGAGC 60  
Db 46 ATGATGAACATACAGCCAACTTCCCGCATCTCGGCCACTGGACATCCAGCGAGC 105  
QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCACAAATGATTTGGATCTGTG 120  
Db 106 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCACAAATGATTTGGATCTGTG 165  
QY 121 CTTTGTGCTGTATCTTCTATAGAGGTGGACAAGATAGAGATGAAGAAATCTTTCAT 180  
Db 166 CTTTGTGCTGTATCTTCTATAGAGGTGGACAAGATAGAGATGAAGAAATCTTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAACCATACAGATGCAACAGAGAGAGAGAGATCCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAACCATACAGATGCAACAGAGAGAGAGATCCTTATCC 285  
QY 241 TTACTGAACCTGTAGGAGATTAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACCTGTAGGAGATTAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAG 360  
Db 346 AACAAAG 405  
QY 361 CAATTTGGGCGACATGTCATAGTGAGGCCAGCAGTAAACACATCTGTCTTACAGTGG 420  
Db 406 CAATTTGGGCGACATGTCATAGTGAGGCCAGCAGTAAACACATCTGTCTTACAGTGG 465  
QY 421 GCTGAAAAGGATACACCATGAGCAACAACTTGTGTAACCCCTGGAAAATGGGAACAG 480  
Db 466 GCTGAAAAGGATACACCATGAGCAACAACTTGTGTAACCCCTGGAAAATGGGAACAG 525  
QY 481 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAGTCACCTTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAGTCACCTTCTGTTCCTCAAT 585

QY 541 CGGAAGCTTCGAGTCAAGCTCCATTTATATCCAGAGCTTCGCTTAAAGTCCCGGCTAGA 600  
Db 586 CGGAAGCTTCGAGTCAAGCTCCATTTATATCCAGAGCTTCGCTTAAAGTCCCGGCTAGA 645  
QY 601 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGGGCAA 660  
Db 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGGGGCAA 705  
QY 661 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTGGCTTGTCTCAAT 720  
Db 706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTGGCTTGTCTCAAT 765  
QY 721 GTGACTGATCAAGCCAACTGAGCCATGCGCACTGGCTTTCAGCTCTTGTGCTTACTCAAA 780  
Db 766 GTGACTGATCAAGCCAACTGAGCCATGCGCACTGGCTTTCAGCTCTTGTGCTTACTCAAA 825  
QY 781 CTCCTGA 786  
Db 826 CTCCTGA 831  
  
RESULT 13  
AX090039  
LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 1 from Patent WO0116180.  
ACCESSION AX090039  
VERSION AX090039.1 GI:13444004  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 879)  
AUTHORS Ahuja, S.U. and Bonewald, L.U.  
TITLE CD40 agonist compositions and methods of use  
JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;  
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)  
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Best Local Similarity 97.5%; Pred. No. 1.3e-188;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
  
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Db 22 ATGATGAACATACAGCCAACTTCCCGCATCTCGGCCACTGGACATCCAGCGAGC 81  
QY 61 ATGAAGATTTTATGTTTACTTACTTCTTCTTATCACCACAAATGATTTGGATCTGTG 120  
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QY 121 CTTTGTGCTGTATCTTCTATAGAGGTGGACAAGATAGAGATGAAGAAATCTTTCAT 180  
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QY 241 TTACTGAACCTGTAGGAGATTAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA 300  
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Db 322 AACAAAG 381

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Db 802 CTCTGA 807
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ACCESSION Z15017 S49392
VERSION Z15017.1 GI:38483
KEYWORDS glycoprotein 39.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Hollenbaugh,D., Grosmaire,L.S., Kullas,C.D., Chalupny,N.J.,
Braesch-Andersen,S., Noelle,R.J., Stamenkovic,I., Ledbetter,J.A.
and Aruffo,A.
TITLE The human T cell antigen gp39, a member of the TNF gene family, is
a ligand for the CD40 receptor: expression of a soluble form of
gp39 with B cell co-stimulatory activity
JOURNAL EMBO J. 11 (12), 4313-4321 (1992)
MEDLINE 93049181
AUTHORS Hollenbaugh,D.L.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
REFERENCE 3 (bases 1 to 879)
AUTHORS Hollenbaugh,D.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
PRI, Seattle, WA, 98121
COMMENT The original submission [1] reported 934bp.
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BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN
Query Match 95.9%; Score 754; DB 9; Length 879;
Best Local Similarity 97.5%; Pred. No. 1.3e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGATAGAAACATACAGCCAACTTCCCCACAGATCGGTGGCAACTGGACTTCCAGCGAGC 60
Db 22 ATGATCGAAACATACAAACCAACTTCTCCCGCATGCGGGCCACTGGACTGCCATCAGC 81
QY 61 ATGAAGATTTTATGTATTTACTTACTGTGTTCCTTATCACCACAAATGATTGGATCTGTG 120
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QY 121 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATAGAAAGGAATCTTCAT 180
Db 142 CTTTTCGTGTGTATCTTCATAGAGGTTGGACAGATAGAGATAGAAAGGAATCTTCAT 201
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240
Db 202 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 261
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGATATAATGTTA 300
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QY 301 ACAAGAGGAGACGAAAGAAACAGCTTTGAAATCGAAAGGTCTATCAGATCTCT 360
Db 322 AACAAAGAGGAGACGAAAGAAACAGCTTTGAAATCGAAAGGTCTATCAGATCTCT 381
QY 361 CAAATTCGGGCACATCTCATAGTCAGGCCAGCAGTAAACACACATCTGTGTACAGTGG 420
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QY 421 GCTGAAAAGGATACACTACACATGAGCAACAACTTGGTAACCTCGGAAAATGGGAAACAG 480
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QY 601 TTCGAGAGAACTTACTCAGAGTCAATATACCCACAGTTCGCGCAAACTTTCGCGGCAA 660
Db 622 TTCGAGAGAACTTACTCAGAGTCAATATACCCACAGTTCGCGCAAACTTTCGCGGCAA 681
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QY 781 CTCTGA 786
Db 802 CTCTGA 807
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Search completed: May 30, 2002, 02:49:14  
Job time: 22033 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:13 ; Search time 5112.58 Seconds  
(without alignments)  
2075.001 Million cell updates/sec

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Perfect score: 786  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	277.2	35.3	398	9	AW486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.pk007
C 4	50.2	6.4	1027	12	AZ166561 SP-0088_B
C 5	48.8	6.2	997	12	AL060767 Drosophil
C 6	48.4	6.2	1043	12	AL103735 Drosophil
7	47.2	6.0	396	10	BF820152 MR1-RT002
8	47.2	6.0	486	9	AV714252 AV714252
9	47.2	6.0	578	9	AV724813 AV724813
10	47.2	6.0	583	10	BI713130 ie02f03.y
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12	47.2	6.0	797	9	AL534423 AL534423
13	47.2	6.0	845	10	BF715238 602676117
14	47.2	6.0	845	10	BI601432 603249012
15	47.2	6.0	861	10	BF573761 602077072
16	47.2	6.0	873	10	BG616023 602643466
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26	46	5.9	636	10	BG771854
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38	45.6	5.8	515	10	BE895474
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## ALIGNMENTS

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LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001  
DEFINITION BF599437  
ACCESSION BF599437  
VERSION BF599437.1 GI:11695919  
KEYWORDS EST.  
SOURCE COW.  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.  
1 (bases 1 to 492)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

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 Library made from pooled tissue from marrow, alveolar  
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 Db GCTGAAAGAGATACATACACCATGAGC 492

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 DEFINITION 75217 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION AW486605  
 VERSION AW486605.1 GI:7056711  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 398)  
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,  
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,  
 Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and,  
 Keefe, J.W.  
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 JOURNAL Genome Res. 11 (4), 626-630 (2001)  
 MEDLINE 21180013  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
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 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCCAGTCACGACG  
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 Library made from pooled tissue from lymph node, ovary,  
 fat, hypothalamus, and pituitary."  
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Query Match 35.3%; Score 277.2; DB 9; Length 398;  
 Best Local Similarity 87.6%; Pred. No. 1.5e-52;  
 Matches 303; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
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 QY 121 CTTTTCTGCTGATCTTCATAGAGTTGGCAAGATAGAGATGAAAGGAATCTTCAT 180  
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 Db AACAAAGAGGAGACGAGAAAGAAACACAGCTTTGAAATGCAAAAG 398

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 ACCESSION AI982044  
 VERSION AI982044.1 GI:5885072  
 KEYWORDS EST.  
 SOURCE Chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 638)  
 Tirunagaru, V.G., Sofer, L., Cui, J. and Burnside, J.  
 TITLE An expressed sequence tag database of T-cell-enriched activated  
 chicken splenocytes: sequence analysis of 5251 clones  
 JOURNAL Genomics 66 (2), 144-151 (2000)  
 MEDLINE 20318616

Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu  
Plate: 88 row: F column: 3  
Seq primer: T7  
Class: BAC ends  
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      BASE COUNT
      ORIGIN

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967	AAGAAAAAAGAGGAGGAAAGATCAAAAAAATAATATATGTTTATAGTGATGGGAAAAAAA	908		
· 261	TAAAACCCAGTTTGAAGGCTTTGTGAAGGATATAAATGTTTAAACAAGAGAGACGAGAA	320		
907	AAAAGATTAGGATATAAAAAATAAAGAAATATAGAAATAAAGAAAAAGAAAAAATGAA	848		
· 321	AGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAATCCCTCAAATTCGGCGACATGTCAT	380		
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RESULT      5
CNS005TE/c
LOCUS
DEFINITION
BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION  AL060767.1
VERSION     AL060767.1
KEYWORDS    GI:4943573
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
             Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 997)
AUTHORS     Direct Submission
TITLE       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL     BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT     - Web : www.genoscope.cns.fr
             Determination of this BAC-end sequence was carried out as part of a
             collaboration with the Berkeley Drosophila Genome Project (BDGP).
             The BDGP is constructing a physical map of the Drosophila
             melanogaster genome using these BACs. For further information
             please see http://www.fruitfly.org The BDGP Drosophila
             melanogaster BAC library was prepared by Kazutoyo Osoegawa and
             Aaron Mammoser in Pieter de Jong's laboratory in the Department of

```



```

Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
  source
    1..486
      Location/Qualifiers
        .organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="DCBADF07"
        /clone_lib="PCB"
        /cell_type="dendritic cells"
        /dev_stage="mature"
        /lab_host="BM25.8"
        /note="Vector: pTriplex2; Site_1: sflIA; Site_2: sflIB"
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      ORIGIN

Query Match      6.0%; Score 47.2; DB 9; Length 486;
Best Local Similarity 50.0%; Pred. No. 1.4;
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATATG 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 TTCATACATTACAGTGTAGTGGAAATAAAATTTGTGATGAATGGTTCGCGAGAGCAAAATTA 198
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 TTAAACAAGAGGAGAGCGAAGAAAGAAACAGCTTTGAAATGCAGAAAGGTGTATCAGAAAT 357
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 CTCAAATACGTGGACACCAATTTTCAGAAACAGCGAGAACTTCAAAAAGCCATCATGAG 258
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 CCTCAAAATTCGGGCACATGTCATTAAGTGTAGGCCAGCAGTAAACAACATCTGTGTTACAG 417
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 CAGTATGCAGAGGGGAAGATGAGAGGGCTGCCCCAGGAAGAAGACATCTGATCTGCAA 318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 TGGCTCAAAAAGGATACTACACCATGAGCAACACTTGGTAACCCCTGGAAAAATGG 473
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 CAGAAAAATGTTGAAGTGAACCAAGAAAGAAACAGAAACACCTGGAATGG 374
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RESULT 9
AV724813 AV724813 HTB Homo sapiens cDNA clone HTBAKC04 5', mRNA sequence. EST 16-OCT-2000
LOCUS
DEFINITION
ACCESSION AV724813
VERSION AV724813.1 GI:10829575
KEYWORDS EST.
SOURCE human.
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1. (bases 1 to 578)
  AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
    Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu,
    S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
    Chen, J., Chen, Z. and Han, Z.
  TITLE Homo sapiens cDNA HTB clones
  JOURNAL Unpublished (2000)
  COMMENT
    Contact: Zequang Han
    Chinese National Human Genome Center at Shanghai
    351 Guo Shoujing Road, Zhangjiang Hi-tech Park, Pudong, Shanghai
    201203, P. R. China
    Tel: 86-21-50801919(ex.45)
    Fax: 86-21-50801922
    Email: hanzq@chgc.sh.cn
    This clone is available at CHGC in Shanghai.
    Location/Qualifiers
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        /db_xref="taxon:9606"
        /clone="HTBAKC04"
        /clone_lib="HTB"
        /tissue_type="Hypothalamus"
        /dev_stage="Adult"
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/note="Vector: pbluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 206 a 98 c 148 g 126 t

ORIGIN

Query Match 6.0%; Score 47.2; DB 9; Length 578;  
Best Local Similarity 50.0%; Pred. NO. 1.4;  
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGACGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATG 297  
DB 28 TTATACATATACAGTGGTGGAAATAAAATTCGGATGAATGGTTCGGAGAGACAGTA 87  
QY 298 TTAACAAAGAT 357  
DB 88 CTCAATACGTGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCCAATCAGGAG 147  
QY 358 CCTCAATTCGGCCACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 417  
DB 148 CAGTATGATCTGCTGCAA 207  
QY 418 TGGGCTCAAAAAGAGTACTACACCATGAGCAACAACTTGGTAACTTGAAGTGAAGTGAAG 473  
DB 208 CAGAAAATGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 263

RESULT 10  
BI713130 583 bp mRNA linear EST 19-SEP-2001  
LOCUS ie02f03.y1 HR85 islet Homo sapiens cDNA 5' similar to IR:O95899  
DEFINITION O95899 UNKNOWN ; mRNA sequence.  
ACCESSION BI713130  
VERSION BI713130  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 583)  
Melton, D., Brown, J., Kenly, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Seearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blinston, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, V., Williams, T., Jackson, Y. and Bowers, Y.  
Endocrine Pancreas Consortium  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Other ESTs: ie02f03.x1  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@bioh.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 471.  
Location/Qualifiers  
1. .583  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/tissue\_type="Purified pancreatic islet"  
/lab\_host="PH108"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1: NotI; Site\_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5'

XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

BASE COUNT 206 a 101 c 149 g 127 t

ORIGIN

Query Match 6.0%; Score 47.2; DB 10; Length 583;  
Best Local Similarity 50.0%; Pred. NO. 1.4;  
Matches 118; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 238 TCCTTACTGACGTGAGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATG 297  
DB 104 TTATACATATACAGTGGTGGAAATAAAATTCGGATGAATGGTTCGGAGAGACAGTA 163  
QY 298 TTAACAAAGAT 357  
DB 164 CTCAATACGTGACACCAATTTGCAGAAACAGCGAGAACTTCAAAAAGCCCAATCAGGAG 223  
QY 358 CCTCAATTCGGCCACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 417  
DB 224 CAGTATGATCTGCTGCAA 283  
QY 418 TGGGCTCAAAAAGAGTACTACACCATGAGCAACAACTTGGTAACTTGAAGTGAAGTGAAG 473  
DB 284 CAGAAAATGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 339

## RESULT 11

BI791160 586 bp mRNA linear EST 12-JAN-2001  
LOCUS 602251255F1 NIH\_MGC\_81 Homo sapiens cDNA clone IMAGE:4338636 5',  
DEFINITION mRNA sequence.  
ACCESSION BI791160  
VERSION BI791160.1  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 586)  
NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1214 row: n column: 13  
High quality sequence stop: 582.  
Location/Qualifiers

## FEATURES

## source

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/note="Organ: muscle (skeletal); Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCCATTTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained







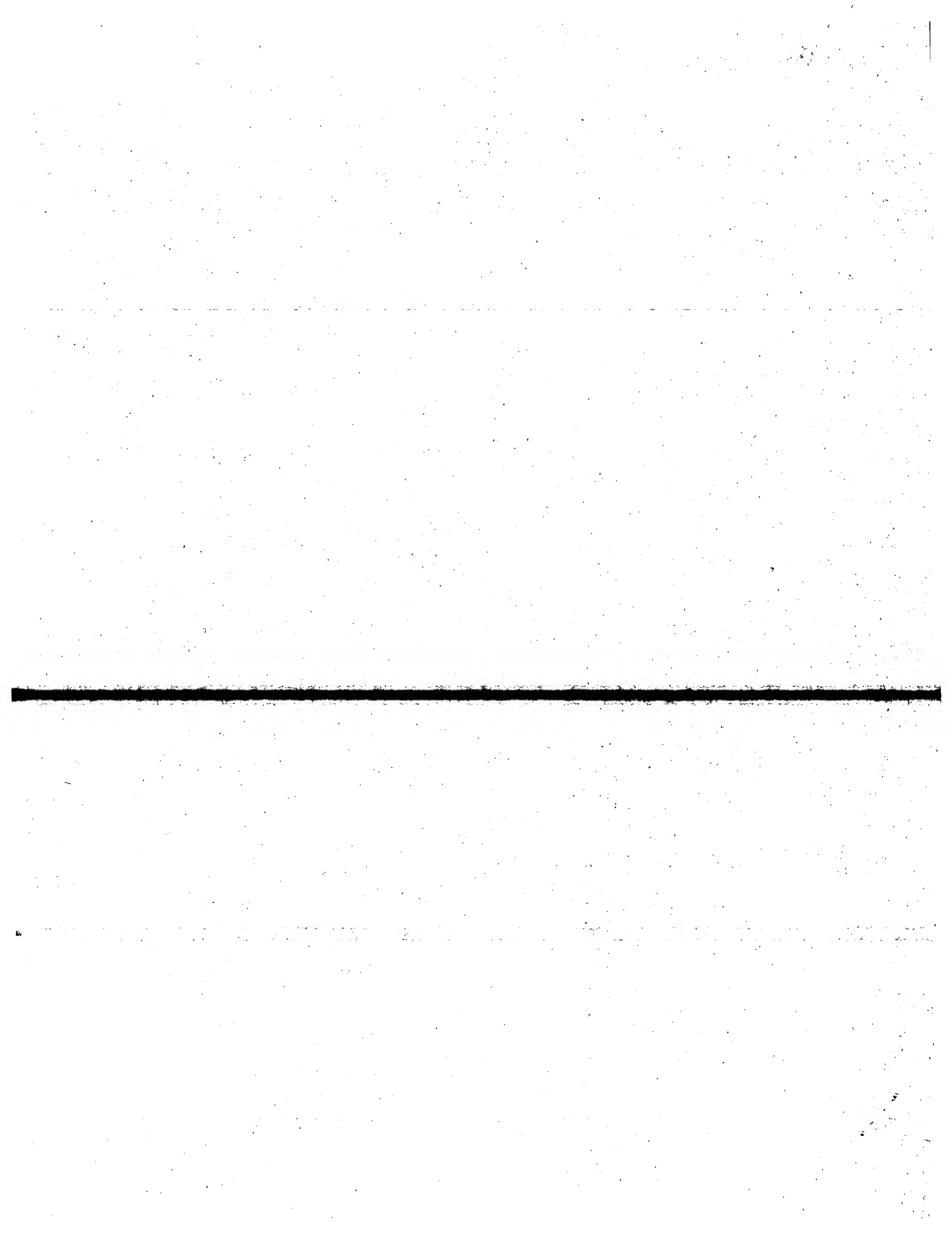


full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT	ORIGIN	subcategories (radio mics, cty):	
308 a	169 c	220 g	163 t
			1 others

[illegible]

Search completed: May 30, 2002, 01:00:16  
Job time: 22226 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:31 ; Search time 680.87 Seconds

(without alignments)

182.015 Million cell updates/sec

Title: US-08-982-272-7

Perfect score: 786

Sequence: 1 ATGATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.\*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.\*
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- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.\*
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- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.\*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.\*
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- 23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	100.0	786	19	AAV39003
2	776.4	98.8	786	19	AAV39002
3	763.6	97.2	786	15	AAV39000
4	754	95.9	786	15	AAQ63959
5	754	95.9	786	19	AAV38997
6	754	95.9	786	19	AAV12852
7	754	95.9	840	14	AAQ41506
8	754	95.9	840	15	AAQ67123
9	754	95.9	840	16	AAQ05763
1	786	100.0	786	19	AAV39003
2	776.4	98.8	786	19	AAV39002
3	763.6	97.2	786	15	AAV39000
4	754	95.9	786	15	AAQ63959
5	754	95.9	786	19	AAV38997
6	754	95.9	786	19	AAV12852
7	754	95.9	840	14	AAQ41506
8	754	95.9	840	15	AAQ67123
9	754	95.9	840	16	AAQ05763

10	754	95.9	840	18	AAV933782	CDNA of CD40L, a n
11	754	95.9	840	19	AAV61063	Human CD40 ligand
12	754	95.9	840	20	AAV27525	Human CD40-L codin
13	754	95.9	879	22	AAV55539	Nucleotide sequenc
14	754	95.9	1816	21	AAV51745	Human CD40 ligand
15	754	95.9	1816	23	AAV86571	DNA encoding novel
16	752.4	95.7	840	15	AAV57984	Genomic sequence o
17	751	95.5	840	18	AAV58132	Human CD40L mutain
18	749.2	95.3	840	16	AAV94091	Human CD40-L cDNA
19	694.8	88.4	783	19	AAV42184	Exemplary nucleoti
20	648.2	82.5	1552	22	AAV25525	Nucleotide sequenc
21	642.8	81.8	865	22	AAV82933	HIV-1 gp120 V3 loo
22	642.8	81.8	906	22	AAV82932	HIV-1 gp120 V3 loo
23	642.8	81.8	2209	22	AAV82929	HIV-1 gp120-human
24	642.8	81.8	2252	22	AAV82928	HIV-1 gp120-human
25	638.2	81.2	1425	14	AAQ41516	Human CD40-L/FC fu
26	638.2	81.2	1425	20	AAV27534	Human CD40-L/FC fu
27	637.2	81.1	929	18	AAV58123	CDNA encoding years
28	637.2	81.1	929	20	AAV27537	Human trimeric CD4
29	635.6	80.9	864	19	AAV39004	CD40 ligand gene u
30	598.8	76.2	885	21	AAV25540	Feline CD154 cDNA
31	598.8	76.2	885	21	AAV25541	Feline CD154 cDNA
32	595.8	75.8	780	21	AAV55542	Feline CD154 cDNA
33	595.8	75.8	780	21	AAV55543	Feline CD154 cDNA
34	594	75.6	783	15	AAQ63960	Feline CD154 cDNA
35	594	75.6	783	19	AAV12853	Mouse CD40-L type
36	594	75.6	783	20	AAV27524	Mouse CD40-L codin
37	592.4	75.4	783	19	AAV38998	CD40 ligand gene u
38	592.4	75.4	818	19	AAV61062	Murine CD40 ligand
39	589.8	75.0	782	14	AAQ41507	Murine CD40-L DNA
40	576.4	73.3	1878	21	AAV25534	Canine CD154 cDNA
41	576.4	73.3	1878	21	AAV25535	Canine CD154 cDNA
42	573.4	73.0	780	21	AAV25536	Canine CD154 cDNA
43	573.4	73.0	780	21	AAV25537	Canine CD154 cDNA
44	570	72.5	783	19	AAV39001	Exemplary CD40 lig
45	560.4	71.3	783	19	AAV38999	Exemplary CD40 lig

# ALIGNMENTS

RESULT 1

AAV39003

ID AAV39003 standard; DNA; 786 BP.

AC AAV39003;

DT 23-SEP-1998 (first entry)

Exemplary CD40 ligand gene used in the course of the invention.

CD40 ligand; alteration: immunoreactivity; human cell;

accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

PN WO9826061-A2.

PD 18-JUN-1998.

PF 08-DEC-1997; 97WO-US22740.

PR 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

PA (REGC ) UNIV CALIFORNIA.

PI Cantwell M, Kipps TJ, Sharma S;

DR WPI; 1998-348521/30.

XX

PT Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis.  
XX Disclosure: Page 107; 167pp; English.

The present sequence represents an exemplary CD40 ligand gene, comprising nucleotides encoding the extracellular domains (Domains III and IV) of the human CD40 ligand gene (AAV389998) operatively linked to nucleotides encoding the cytoplasmic domain (Domain I) and transmembrane domain (Domain II) of the murine CD40 ligand gene (AAV38997). The sequence is used to exemplify the method of the invention. The specification describes a method for altering the immunoreactivity of human cells which comprises introducing a gene encoding an accessory molecule ligand (AML) into the cells so that the AML is expressed on the surface of the cells. Vectors containing the AML genes can be used in gene therapy for treating neoplasia or autoimmune disorders such as rheumatoid arthritis. They can also be used for vaccination to produce immunity against a virus cell, bacteria, protein, fungus or neoplasia.

Sequence 786 BP: 250 A; 166 C; 170 G; 200 T; 0 other;

Query Match	100.0%;	Score 786;	DB 19;	Length 786;
Best Local Similarity	100.0%;	Pred. No. 4.3e-216;		
Matches 786;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps

Qy	1	ATGATAGAAACATACAGCCACACTTCCCCAGATCCGTTGGCACTGACACTGACACTTCCAGCCAGC	60
Db	1	atgatagaacaacacagccaacctccccagatccgctggcaacttggacttccagcagc	60
Qy	61	ATGAAGATTTTATGTATTTACTTACTGTGTTTCCCTTATCACCCAAATGATTGGATCTGTG	120
Db	61	atgaagattttatgtatttaacttactgttttcccttatccaccaaatgattggatctgtg	120
Qy	121	CTTTTTCCTGTGTATCTTCATCAAGGTTGGACAGATAGAGATGAAGAACTTCTCAT	180
Db	121	ctttttctgtgtatcttcataagaagtttggacacagatagaagatgaaaggaaacttctcat	180
Qy	181	GAAGATTTTGTATTTCATGAAACGATTACAGAGATGCACACAGGAGAAGATTCCTTATCC	240
Db	181	gaagattttgtatttcatagaacagatcacagatgcaacacacaggagaagatccttatccc	240
Qy	241	TTACTGTAACTGTGAGGAGATTAAAGCCAGTTTGAGGCTTTGTCAAGGATATAATGTTA	300
Db	241	tactgtactgtgaggagattaagaccagtttgaaggctttgtgaaggatataatgttta	300
Qy	301	AACAAAGAGGAGACGAAGAAGAAAACAGCTTTGAAATCGAAAAGGTGATCAGAACTCT	360
Db	301	aacaaagagagacgaagaagaaaacagctttgaaatgcaaaaggatgcagaatcct	360
Qy	361	CAAAATTGGGCACATGTCATTAAGTGAGGCCAGCAGTTAAACACACTCTGTGTTACAGTGG	420
Db	361	caaatggcgacatgtcataagtgaggccagcagtaaacacaactctgtgtacagctgg	420
Qy	421	GCTGAAAAGGATACTACACCATGAGCAACAACCTTGTTAACCTCGAAAATGGGAAACAG	480
Db	421	gctgaaaagagatactacaccatgagcaacaacttggtaacctggaaaatgggaacag	480
Qy	481	CTGACCGTTTAAAGACAAGACTCTATTATCTATGTCGCCAAGTCACCTTCCTGTTCCCAAT	540
Db	481	ctgacgcttaaaagacaaggactctaatactatgcccacagcacccttctgttccaat	540
Qy	541	CGGGAAGCTTCGAGTCAAGCTTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGA	600
Db	541	cgggaagcttcgagtcgaagctccattatagcagcgcctctgctaaagtccccccggtaga	600
Qy	601	TTGAGAGAAATCTTACTCAGAGCTTGCAAAATACCCACAGTTCCGCCAAAACCTTCGGGCAA	660
Db	601	ttcgagaagaattctactcagagctgcgaaatcccacacagttcccgccaaaaccttgcgggcaa	660
Qy	661	CAATCCATTCACCTTGGGAGGAGTATTTGAATGTCAACCAAGTGCTTTCGGTGTGTTGTCAT	720

Db	661	caatccattcacttggaggagatttgattgaattgcaaccagggtgcttcgggtgtttgccaat	720
Qy	721	GTGACTGATCCACGCAAGTGAGCCATGGCAGTGGCTTCACTGCTTGGCTTACTCAA	780
Db	721	gtgactgatccaggccaagtggacgatggcactggcttcacgtccctttggcttactcaaa	780
Qy	781	CTCTGA 786	
Db	781	ctctga 786	

## RESULT

AAV39002  
ID AAV39002 standard: DNA: 786 BP.

XX  
 20  
 22220002:

XX: 23-SEP-1998 (first entry)

normalative CD40 ligand gene used in the course of the invention.

XX  
KW CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW rheumatoid arthritis; vaccine; chimera; ss.  
KW

XX

OS chimeric - Homo sapiens.

PN W09826061-A2.

18-JUN-1998

XX  
DE 09-DEC-1997:

**XX**

PR 09.-DEC-1996; 96US-0032145.

PA (REGC ) UNIV CALIFORNIA.

XX Cantwell M. Kipps T.J. sharma S;

XX  
1000-248531/20

XX  
PT  
PT  
PT

XX  
ps Disclosure: Page 106: 167pp; English.

XX The present sequence represents an exemplary CD40 ligand gene,  
CC comprising nucleotides encoding the extracellular domains (Domains III  
CC and IV) and transmembrane domain (Domain II) of human CD40 ligand gene  
CC (AAV38998) operatively linked to nucleotides encoding the cytoplasmic  
CC domain (Domain I) of the murine CD40 ligand gene (AAV38997). The sequence  
CC is used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells which  
CC comprises introducing a gene encoding an accessory molecule ligand (AML)  
CC into the cells so that the AML is expressed on the surface of the cells.  
CC Vectors containing the AML genes can be used in gene therapy for  
CC treating neoplasia or autoimmune disorders such as rheumatoid arthritis.  
CC They can also be used for vaccination to produce immunity against a virus  
CC or cell bacteria, protein, fungus or neoplasia.

XX  
sequence 786 BP: 250 A: 166 C: 171 G: 199 T: 0 other;  
SO

Query Match.	98.8%	Score	776.4	DB	19	Length	786
Best Local Similarity	99.2%	pred. No.	2.5e-213				
Best Local Conservative	99.2%	Mismatches	0	Indels	0	Gaps	0

Qy 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCCTGGCAACTGGACTTCCAGCGAGC 60



QY 481 CTGACCGTTAAAGACAAGGACTATTATATCTATGTCAGTCCCAAGTCACTCTGTTCCTCAAT 540  
 Db 481 ctgacccgttaaaagacaaaggactctattatctatgctcagtcacactctctgttcccaat 540  
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
 Db 541 cgggaagcttcgagtcgaagctccatttatagccagctctgctttaaagtcctcccggtaga 600  
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCAGCTTCGGCCAAACCTTCGGGGCAA 660  
 Db 601 ttccgagagaattactcagagctgcaaataccacccagcttcgcgcaaaccttgcgggcaa 660  
 QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATGCAACCAAGTGTCTCGTGTGTCTCAAT 720  
 Db 661 caatccattctctgggagagatttgaaatgcaaccagctgtctcggtgtgtctcaat 720  
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCCAGTGCAGCTGCTTCAGCTCTTGGCTTACTCAAA 780  
 Db 721 gtgactgatcccaagcaagtgagccatggcactggcttcagctccttggcttactcaaa 780  
 QY 781 CTCTGA 786  
 Db 781 ctcctga 786

RESULT 4

AAQ63959 standard; cDNA to mRNA; 786 BP.  
 AC AAQ63959;  
 DT 11-JAN-1995 (first entry)  
 XX Human CD40-L type II transmembrane protein coding sequence.  
 DE Leucine zipper; trimerisation; trimeric CD40-L; fusion protein;  
 KW hetero-oligomer; homo-oligomer; type II transmembrane protein;  
 KW soluble CD40-L; tumour necrosis factor family; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT 1..786  
 FT CDS /\*tag= a  
 FT /product= human\_CD40-L  
 FT /note= "nucleotides 148-783 code for the  
 FT extracellular region (amino acids 50-261)."

W09410308-A.  
 XX 11-MAY-1994.  
 XX 20-OCT-1993; 93WO-US10034.  
 XX 23-OCT-1992; 92US-0969703.  
 XX 13-AUG-1993; 93US-0107353.  
 XX (IMMUNEX ) IMMUNEX CORP.  
 XX Spriggs MK, Srinivasan S;  
 XX WPI; 1994-167465/20.  
 XX P-PSDB; AAR53969.  
 XX Prepn. of soluble oligomeric mammalian proteins - using host  
 XX cells to express a fusion protein comprising a leucine zipper  
 XX domain and a heterologous mammalian protein  
 XX Example 1; Page 22-23; 35pp; English.  
 XX A DNA fragment encoding the extracellular (soluble) region of human  
 XX CD40-L was ligated to a synthetic oligonucleotide sequence coding  
 XX for a leader peptide, a 33 amino acid leucine zipper sequence

CC (AAR53969) and the Flag (RTM) linker sequence. Cells expressing the  
 CC fusion construct are grown to accumulate oligomeric, soluble CD40-L  
 CC in the supernatant. The leucine zipper sequence spontaneously  
 CC trimerises in solution and fusion proteins comprising  
 CC the sequence fused to a heterologous mammalian protein also form  
 CC oligomers.  
 XX  
 XX Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;  
 Query Match 95.98; Score 754; DB 15; Length 786;  
 Best Local Similarity 97.5%; Pred. No. 7e-207;  
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTCGCACTGGACTTCCACCGAGC 60  
 Db 1 atgataaatacacaacaaactctcccgatctgcgcactggactgcccacatcgc 60  
 QY 61 ATGAAGATTTTATGTTACTTACTTCTTCTTATCACCCTTATGTTGGATCTGTG 120  
 Db 61 atgaaatatttatgtatttacttactgtttcttcttaccacagatgattgggtcagca 120  
 QY 121 CTTTGTGCTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180  
 Db 121 ctttgtgctgtatctcttcataagaggttggaagatagaagatgaaagaattctcat 180  
 QY 181 GAAGATTTTATTCATGAAACGATACAGAGATGCAACAGGAGAGATCTTATCC 240  
 Db 181 gaagatttttattcatgaaacgatacagagatgcaacacacaggaagatccttatcc 240  
 QY 241 TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTCAAGATATATGTTA 300  
 Db 241 ttactgaactgtgagagattaaaagccagtttgaagctttgtgaagatataatgta 300  
 QY 301 AACAAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 360  
 Db 301 aaaaagaggagacgaagaaagaaacagcttgaatgcaaaaaaggatcagaatcct 360  
 QY 361 CAAATTCGCGCACATGTCTAATAGTGAAGCCAGCAGCTAAACCAACATCTGTGTACAGTGG 420  
 Db 361 caaatgcgacatgtcataagtgagccagcagtaaaacaacatctgtgtacagtgg 420  
 QY 421 GCTGAAAGAGGATACACCATGAGCAACACTTTGGTAACCTTGAAATGCGAAACAG 480  
 Db 421 gctgaaaaggatatactacacatgagcaaacacttggtaaccttgaaaatgggaacag 480  
 QY 481 CTGACCGTTAAAGACAAGGACTATTATATCTATGTCAGTCCCAAGTCACTCTGTTCCTCAAT 540  
 Db 481 ctgacccgttaaaagacaaaggactctattatctatgctcagtcacactctgttccaat 540  
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTTCGGCCAAACCTTCGGGGCAA 600  
 Db 541 cgggaagcttcgagtcgaagctccatttatagccagctctgctttaaagtcctcccggtaga 600  
 QY 601 TTCGAGAGAACTTACTCAGAGCTGCAATACCCAGCTTCGGCCAAACCTTCGGGGCAA 660  
 Db 601 ttccgagagaattactcagagctgcaaataccacccagcttcgcgcaaaccttgcgggcaa 660  
 QY 661 CAATCCATTCTCTGGGAGGAGTATTGAATGCAACCAAGTGTCTCGTGTGTCTCAAT 720  
 Db 661 caatccattctctgggagagatttgaaatgcaaccagctgtctcggtgtgtctcaat 720  
 QY 721 GTGACTGATCCCAAGCAAGTGAAGCCAGTGCAGCTGCTTCAGCTCTTGGCTTACTCAAA 780  
 Db 721 gtgactgatcccaagcaagtgagccatggcactggcttcagctccttggcttactcaaa 780  
 QY 781 CTCTGA 786  
 Db 781 ctcctga 786

RESULT 5  
 AAV38997

AAV38997 standard; DNA; 786 BP.  
AAV38997;  
23-SEP-1998 (first entry)  
CD40 ligand gene used in the course of the invention.  
CD40 ligand; alteration: immunoreactivity; human cell;  
accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
autoimmune disorder; rheumatoid arthritis; vaccine; ss.  
Mus sp.  
W09826061-A2.  
18-JUN-1998.  
08-DEC-1997; 97WO-US22740.  
01-DEC-1997; 97US-0982272.  
PR DEC-1996; 96US-0032145.  
(REGC ) UNIV CALIFORNIA.  
Cantwell M, Kipps TJ, Sharma S;  
WPI; 1998-348521/30.  
Vectors containing accessory molecule ligand genes - used for  
altering immunoreactivity of cells, particularly for treatment of  
neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
Disclosure; Page 104; 167pp; English.  
The present sequence represents the CD40 ligand gene. The sequence is  
used to exemplify the method of the invention. The specification  
describes a method for altering the immunoreactivity of human cells  
which comprises introducing a gene encoding an accessory molecule  
ligand (AML) into the cells so that the AML is expressed on the surface  
of the cells. Vectors containing the AML genes can be used in gene  
therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
arthritis. They can also be used for vaccination to produce immunity  
against a virus cell, bacteria, protein, fungus or neoplasia.  
Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;  
Query Match 95.9%; Score 754; DB 19; Length 786;  
Best Local Similarity 97.5%; Pred. No. 7e-207;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 ATGATAGAAACATACAGCCACCTCCCGAGATCCGTGGCACTGGACCTCCACGAGC 60  
DB 1 atgacgaacatacaacacactctcccgatctg9gcacactggactgccatcagc 60  
QY 61 ATGAGATTTTATGTATTACTTACTTCTTCTTATCACCACCAATGATTGGATCTGTG 120  
DB 61 atgaaattttatgtatttacttacttcttcttcttaccacccagatgattgggtcagca 120  
QY 121 CTTTTTGTGTGATCTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 121 ctttttgtgtattcttcataaggttggacaagatagaagatgaagaaatcttcat 180  
QY 181 GAAGATTTTGTATTCATGAACAGATACAGAGATGCACACAGGAGAAAGATTCCTTATCC 240  
DB 181 gaagattttgtattcatgaacagatagacagatgcaacacagggagaaatccctatcc 240  
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 300  
DB 241 ttactgaactgtgaggagatgaagccagtttgaagcgtttgtgaagataataatgta 300  
QY 301 AACAAAGAGGAGAGCAAGAAAGAAACACAGCTTTGAAATGCAAAAGAGGTGATCAGATCCT 360

DB 301 aacaaaggaggagagcaagaagaaagactttgaaatgcaaaaggatcagatcct 360  
QY 361 CAATTTGGCGCACATGTCATAAGTGGAGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 420  
DB 361 caaattgcggcacatgtcataagtggccagcagtaaaacaacatctgtgttacagtgg 420  
QY 421 GCTGAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTCGAAATGGAAACAG 480  
DB 421 gctgaaaaggatatacaccatgagcaacacttggtaaccctggaaaatggaaacag 480  
QY 481 CTGACCGTTAAAGAACAGGACTCTATTATATCTATGTCGCCAAGTCAACCTTCTGTTCAT 540  
DB 481 ctgaccgttaaaagacaagactctattatctatctatgcccgaagtcacottctgttccaat 540  
QY 541 CGGGAAGCTTCAGTCAAGCTCCATTATAGCCAGCCTGCTTAAGTCCCGCGGTAGA 600  
DB 541 cgggaagcttcagtcaggctccatttatagccagcctctgcttaagtcctcccggtaga 600  
QY 601 TTCGAGAGAATCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTTGCCGGCAA 660  
DB 601 ttcgagagaattcttactcagagctcaaataccacagttccgcacaaaccttgcgggcaa 660  
QY 661 CAATCCATTCACTTGGGAGGAGTATTGAATTCGAACCAAGCTGCTTCGCTGTGTTCAT 720  
DB 661 caatccattcacttgggaggagtatttgaattgcaaccagtgcttcggtgttgcatt 720  
QY 721 GTGACTGATCCCAAGCAAGTGGAGCTGATGCTTCACTGCTTCCCTTGGCTTACTCAA 780  
DB 721 gtgactgatcccaagcgaagtggccatggcactggcttcacgtcccttggcttactcaa 780  
QY 781 CTCCTGA 786  
DB 781 cctctga 786  
RESULT 6  
AAV12852  
ID AAV12852 standard; cDNA to mRNA; 786 BP.  
XX AC AAV12852;  
DT 13-MAY-1998 (first entry)  
XX DE CD40 ligand coding sequence.  
XX KW Leucine zipper; fusion protein production; soluble oligomeric protein;  
XX KW heterologous mammalian type II transmembrane protein; activated T cell;  
XX KW heterologous mammalian type I transmembrane protein; antibody production;  
XX KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.  
OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..786  
XX FT /\*tag= a  
XX PN US5716805-A.  
XX PD 10-FEB-1998.  
XX PF 18-MAY-1995; 95US-0446922.  
XX PR 18-MAY-1995; 95US-0446922.  
XX PR 25-OCT-1991; 91US-0783707.  
XX PR 05-DEC-1991; 91US-0805723.  
XX PR 23-OCT-1992; 92US-0969703.  
XX PR 13-AUG-1993; 93US-0107353.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Spriggs MK, Sriniwasan S;  
XX

WPI; 1998-144799/13.

P-PSDB; AAW41178.

Soluble oligomeric fusion proteins - comprising leucine zipper fused to extracellular region of transmembrane protein

Example 1: column 19-20: 21pp: English.

This sequence is the coding sequence for the human CD40 ligand (CD40-L). The encoded protein can be used in a fusion protein produced using the method of the invention. The method is for preparing soluble oligomeric protein by culturing a host cell transfected with a vector for a fusion protein. The soluble oligomeric proteins comprise a leucine zipper fused to the N terminus of the extracellular region of a heterologous mammalian type II transmembrane protein or to the C terminus of the extracellular region of a heterologous mammalian type I transmembrane protein, where the leucine zipper is a peptide comprising at least part of AA41171 or AA41172, optionally with conservative amino acid substitutions, provided that the peptide trimersises in solution. A soluble fusion protein comprising the leucine zipper of AA41171 linked to the extracellular region of CD40-L (a type II transmembrane protein) that is found on activated T cells and acts as a ligand for the B-cell antigen CD40) stimulates B-cell proliferation and antibody production in a similar manner to membrane-bound CD40-L. A soluble fusion protein comprising the leucine zipper of AA41172 linked to the extracellular region of CD27-L (a type II transmembrane protein that binds to the lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein comprising the extracellular region of CD27 and a human IgG1 Fc region) to EBV-transformed B cells expressing CD27-L.

Sequence 786 BP: 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 95.9%; Score 754; DB 19; Length 786;  
Best Local Similarity 97.5%; Pred. No. 7e-207;  
Matches 766; Conservative 0; Mismatches 20; Indels

1	ATGATGAACAATACAGCCAACTCTCCCCGATCCGGTGGCAACTGGACTTCCAGCGAGC	60
Qy		
1	atgatgaacaatacagccaaactctcccgatccgggtggcaactggacttccagcgagc	60
Db		
1	atgtcgaacaatcacaccaaactctcccgatctgoggccactggactgcccatacgc	60
Qy		
61	ATGAAGATTTTATGTATTACTTACTGTCTTCCCTTATCACCCAATGATTGGATCTGTG	120
Qy		
61	atgaaatTTTTATGTATTACTTACTGTCTTCCCTTATCACCCAATGATTGGATCTGTG	120
Db		
121	CTTTTGTCTGTATCTTCATAGAAAGTTGGCAGAGATAGAGATGAAGAATCTTCAT	180
Qy		
121	cttttgtctgtatcttcatagaagttggacaagatagaagatgaagaagatcttcat	180
Db		
181	GAAGATTTCTATTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	240
Qy		
181	gaagattttgatactcatgaaaaacgatacagagatgacaacagagagaagatccattacc	240
Db		
241	TTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA	300
Qy		
241	ttactgaactgtgaggagattaaagccagtttgaaggctttgtgaaggatataatgta	300
Db		
301	AACAAGACGAGCAGGAGAAGAACAACAGCTTTTGAATGCAAAAAGGTGATCAGAACTCT	360
Qy		
301	aacaagagagagacgagaagaagaacacagctttgaaatgcataaagggtgatcagaatcct	360
Db		
361	CAAAATTCGGGCATGTCATAAGTGAGGCCGACGAGTAAACAACATCTCTGTTCAGTGG	420
Qy		
361	caaatTCGGGCATGTCATAAGTGAGGCCGACGAGTAAACAACATCTCTGTTCAGTGG	420
Db		
421	GCTGAAAAGGATACTACACCATGAGCAACAACCTTGATAACCTCGGAAAATGGGAACAG	480
Qy		
421	gctgaaaaggatactacacccatgagcaacaaccttggtaacctggaaaaatgggaacag	480
Db		
481	CTGACCGGTTAAAGACAAAGGACTCTATTATATCTATGTCGCCCAAGTCACTCTGTCCCAAT	540
Qy		
481	ctgaccgTTAAAGACAAAGGACTCTATTATCTATGTCGCCCAAGTCACTCTGTCCCAAT	540
Db		

Qy	541	CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCAGAGCTCTGCTAAAGTCCCGCGTAGA	600
Db	541	cggaaagcttcgagtcgaagctccattatagcaagcctctgctaaagtcctcccgcgtaga	600
Qy	601	TTGGAGAGAATCTTACTTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAGCTTCGGGGCAA	660
Db	601	ttcgagagaattcttactcagagctgcaaataccacagttccgccaaacctgcggggcaa	660
Qy	661	CAATCCATTCACTTGGGAGGAGTATTTGAAATTGCACCAGGTCGCTTCGGTGTTGTGTCAT	720
Db	661	caatccattcaactgggagagattttgaattgcaaccagggtcttcggtgtttgccaat	720
Qy	721	GTGACTGATCAAGCCAAAGTAGCCATGGCACTGGGTTACGTCCTCTTGGCTTACTCAAA	780
Db	721	gtgactgatccaaagcaagtgagccatggcaatgcttcacgtcccttggcttaactcaaa	780
Qy	781	CTCTGA	786
Db	781	cictga	786

## 7 RESULT

RESOL  
AAQ41506  
ID AAQ41506 standard: DNA: 840 BP.

AA  
AC  
AAO41506;XX  
DT 12-AUG-1993 (first entry)

CD40-L. DNA

Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;  
transmembrane; region; intracellular; soluble; activity; B cell;  
proliferation; induction; antibody; secretion; IgE; agonist;  
antagonist; binding assay; ss.

XX  
OS Homo sapiens.

XX	Key	Location/Qualifiers
FH	CDS	46..831
FT		/*tag= a

XX PN WO9308207-A.

XX  
PD  
29-APR-1993

XX  
23-000-1992:  
92WO-US08990

XX  
BB: 25-OCT-1991. 91US-0783707

PR 05-DEC-1991; 91US-0805/23

PA (IMMV) IMMUNEX CORP.

PI Armitage RJ, Fanslow WC, Spriggs MK,

DR WPI; 1993-152417/18.

XXXX

PT treating allergies, lupus, rheumatoid arthritis,  
PT graft-versus-host disease and insulin-dependent diabetes mellitus

PS Claim 1; Fig 2; 80pp; English.

This sequence encodes a human CD40-L polypeptide which binds to CD40. CD40-L is a type II membrane polypeptide which has an extracellular region at its C-terminus, a transmembrane region and an intracellular region at its N-terminus. A soluble form of CD40-L lacks the transmembrane domain. CD40-L activity is mediated by binding with CD40 and induces B cell proliferation and induction of antibody secretion, including IgE. Membrane bound CD40-L acts as a CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L can be used in a binding assay to detect cells expressing CD40.









PN US5817516-A.  
 XX 06-OCT-1998.  
 PD 28-APR-1995; 95US-0431055.  
 XX 28-APR-1995; 95US-0431055.  
 PR 28-APR-1994; 94US-0234580.  
 XX (BOEHR) BOEHRINGER INGELHEIM PHARM INC.  
 PA Castle B, Kehry M;  
 PI WPI; 1998-556393/47.  
 XX P-PSDB; AAW71751.  
 DR Increased proliferation of B cells in culture - by incubating them  
 XX in the presence of membrane-bound CD40 ligand  
 PT Example 1; Fig 1; 37pp; English.  
 XX  
 PS The present sequence encodes human CD40 ligand which is used in the  
 CC method of the invention. The method has been developed for proliferating  
 CC B cells to increase their number at least 100-fold. The method  
 CC comprises: (a) providing high density, membrane bound CD40 ligand; and  
 CC (b) culturing one or more B cells in the presence of this ligand. The  
 CC culture results in a proliferation in the number of B cells of at least  
 CC 100 fold. Also described is a method as above where the B cells are  
 CC induced to differentiate into antibody-producing cells in the presence  
 CC of one or more cytokines. The method can be used for stimulating B-cell  
 CC proliferation in vitro or in vivo, e.g. for treating conditions in which  
 CC B-cell proliferation and activation is suppressed. Eight rounds of  
 CC division over six days can be achieved, corresponding to a 256-fold  
 CC increase in cell numbers, which is a vast increase compared to previous,  
 CC culturing methods.  
 XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;  
 SQ

Query Match 95.98; Score 754; DB 19; Length 840;  
 Best Local Similarity 97.58; Pred No. 7-2e-207;  
 Matches 766; Conservative 0; Mismatches - 20; Indels 0; Gaps 0;

1 ATGATAGAAACATACAGCCACCTTCCCGCAGATCCCTGGCACTGCTCCAGCCAGC 60.  
 22 atgatgaacatacaacacaaactctccgcgactctgcccactgactgcccactcgc 81  
 61 ATGAGATTTTATGCTATTTACTTCTTCTTCTTATCACCACCAATGATTGATCTGTG 120  
 82 atgaataattttatgattttacttactgttttttttttttttttttttttttttttt 141  
 121 CTTTTTGTGTGTATCTTCATAGAGGTGGACAGATAGAGATAGAGAAATCTTCAT 180  
 142 ctttttgtgtgtatcttcataagaaggttgacaagatagaagatagaagaaatcttc 201  
 181 GAAGATTTGTATTATGAACAGATACAGATGCAACAGAGAGAAAGATCTTATCC 240  
 202 gaagattttgtattcatgaacacgatacagagatgacacacagagagaaagatcttc 261  
 241 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATAATGTTA 300  
 262 ttactgaactgtgagagagattaaagccagtttgagcgtttgtgaagataataatgta 321  
 301 AACAAAG 360  
 322 aacaag 381  
 361 CAATTCGGCAGATCTCATAGTGGCCAGCAGTAAACAACTCTGTGTACAGTGG 420  
 382 caatttcgacatgctcagagtgagggccagcagcaaacacatctgtgtacagtg 441  
 421 GCTGAAAGAGGATACCTACACCATGAGCAACAACTTGGTAACTCGAAATGGGAAACAG 480

Db 442 gctgaaaaagga tactacaccatgagcaacaacttgtaaacctcctggagaaacag 501  
 QY 481 CTGACCGTTAAAGACAAAGACTCTATTATATCTATGCGCAAGTACCTCTGTTCCAAAT 540  
 Db 502 ctgaccgtttaaaagacaaagagactctattatctatgccaagtcacctctgttccaat 561  
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATTATAGCCAGCTCTGCTTAAGTCCCGGTAGA 600  
 Db 562 cgggaagcttcgagtcgaagctccatttagccagcctctgctaaagtcctcccggtaga 621  
 QY 601 TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCAAGTTCGCCAAACCTTCGCGGCA 660  
 Db 622 ttgagagaatcttactcagagctgcaaataccacacagttccgccaaaccttgcgggcaa 681  
 QY 661 CAATCCATTCACTTGGGAGGAGTATTGTAATTCACACAGGTGCTCGGTTGTTGCAAT 720  
 Db 682 caatccattcacttggggaggtatttgaaattgcaaccaggtgcttcggtgtttgcaat 741  
 QY 721 GTGACTGATCCCAAGCAAGTGGAGCTGAGCATGGCTGCTTACGCTCTTGGCTTACTCAA 780  
 Db 742 gtgactgatcccaagtgagccatggcactggcttcacgtccttggcttactcaaa 801  
 QY 781 CTCTGA 786  
 Db 802 ctctga 807  
 RESULT 12  
 AAZ27525  
 ID AAZ27525 standard; cDNA; 840 BP.  
 XX AC AAZ27525;  
 XX DT 13-DEC-1999 (first entry)  
 XX DE Human CD40-L coding sequence.  
 XX KW CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;  
 XX KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;  
 XX KW peripheral blood B cell; proliferation inhibitor; ss.  
 XX OS Homo sapiens.  
 XX PN US5961974-A.  
 XX PD 05-OCT-1999.  
 XX PF 24-MAY-1994; 94US-0249189.  
 XX PR 25-OCT-1991; 91US-0783707.  
 XX PR 05-DEC-1991; 91US-0805723.  
 XX PR 23-OCT-1992; 92US-0969703.  
 XX PA (IMMV ) IMMUNEX CORP.  
 XX PI Spriggs MK, Fanslow WC, Armitage RJ;  
 XX WP1; 1999-579604/49.  
 XX P-PSDB; AAV39938.  
 XX PT Anti-human CD40-Ligand monoclonal antibodies -  
 XX PS Disclosure; Fig 2; 59pp; English.  
 XX This sequence encodes the human CD40 receptor ligand (CD40-L). The  
 CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted  
 CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma  
 CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40  
 CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce  
 CC proliferation of peripheral blood B cells.  
 XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;  
 SQ

KW	osteoporosis; osteonecrosis; inflammatory arthritis; estrogen loss;
KW	ovariectomy; historectomy; lupus nephritis; Takayasu's arteritis;
KW	Wegener's granulomatosis; nephritis; myositis; scleroderma;
KW	thrombocytopenia; asthma; lung disease; cancer; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FD	Location/Qualifiers
FT	CDS
FT	22...807
FT	/tag= a
FT	/product= "gp39"
XX	
XX	WO200116180-A2.
PN	
PD	08-MAR-2001.
XX	
XX	24-AUG-2000; 2000WO-US23276.
PF	
XX	
PR	27-AUG-1999; 99US-0151250.
XX	
PA	(TEXA ) UNIV TEXAS SYSTEM.
XX	
PI	Ahuja SS, Bonewald LF;
XX	
WP	WPI; 2001-169007/17.
DR	P-PSDB; AAB67612.
DR	
XX	
PT	CD40 agonist containing composition, used to reduce bone cell death or
PT	apoptosis associated with osteoporosis, osteonecrosis and inflammatory
PT	arthritis
XX	
PS	Disclosure; Page 113; 118pp; English.
XX	
CC	The present sequence encodes a gp39 protein. It is a CD40 ligand.
CC	CD40 ligands are used for reducing osteoblast cell death or apoptosis,
CC	and for treating or preventing bone loss in animals, preferably humans
CC	at risk of, or undergoing, bone loss. The bone loss is associated with
CC	osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal
CC	estrogen loss, estrogen loss due to ovariectomy, total historectomy,
CC	lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,
CC	anti-glomerular basement membrane nephritis, myositis, scleroderma,
CC	idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive
CC	lung disease, nephrotic/nephritic syndrome, or cancer. They may also be
CC	used to treat or prevent bone loss in a subject undergoing, or schedul
CC	for, an organ or bone marrow transplant.
XX	
SO	Sequence 879 BP: 274 A; 193 C; 190 G; 222 T; 0 other;

Qy	1	ATGATAGAAACATACACGCCAACCTTCCCCCAGATCCGTGCAACTGGACTTCAGCGAGC	60
Db	22	atgatogaaacatacaaccaaaactctcccccgatctgcggccactggactggccatcagc	81
Qy	61	ATGAAGATTTTATGTATTTACTTTACTTCTGTTTTCTTATCACCCAAATGATTGGATCTGTG	120
Db	82	atgaaaattttatgtatttacttactgtttctctatcaccagatgattgggtcagca	141
Qy	121	CTTTTTCGTGTGATCTTCATGAAGGTTGCGACAAGATAGAAGTGAAGGAATCTTTCAT	180
Db	142	ctttttgtctgttatcttcataagaaggctggacaagataagaagatgaagggaattcttc	201
Qy	181	GAAGATTTGTATTTCATGAAGACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	240
Db	202	gaagatttggattcatgaaaacgatacagagatgcaaacacaggaaagatcccttatcc	261
Qy	241	TTACTGAACGTGTGAGGAGATTAAAGCCACGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
Db	262	ttactgaactgtgaggagattaaagccagtttgaaggcctttgtgaaggagataaatgta	321

RESULT	13
AAF55539	
ID	AAF55539 standard; DNA; 879 BP.
XX	
XX	
AC	
AAF55539;	
XX	
XX	
DT	29-MAY-2001 (first entry)
XX	
XX	
DE	Nucleotide sequence of human gp39 protein, a CD40 ligand.
XX	
XX	
KW	gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

RESULT 14	AAA51745	AAA51745 standard; CDNA; 1816 BP.
XX	AC	
XX	DT	
XX	XX	
XX	DE	
XX	XX	
XX	KW	CD40 ligand; CD40; T cell; T cell receptor; rearrangement; maturation;
XX	KW	cell death inhibition; stress-induced; immunosuppressive; anti-thyroid
XX	KW	anti-inflammatory; anti-diabetic; anti-rheumatic; anti-anaemic;
XX	KW	opthalmological; anti-psoriatic; nephrotrophic; hepatotropic; virucide;
XX	KW	dermatological; cytostatic; ss.
XX	OS	Homo sapiens.
XX	XX	
XX	PH	Location/Qualifiers
XX	FT	40..825
XX	FT	/*tag= a
XX	FT	/product= Human_CD40_ligand
XX	XX	WO200039283-A1.
XX	XX	
XX	PD	06-JUL-2000.
XX	XX	
XX	PF	22-DEC-1999; 99WO-US30930.
XX	XX	
XX	PR	29-DEC-1998; 98US-0114106.
XX	XX	
XX	PA	(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX	PI	Newell MK, Wagner D, Newell B;
XX	XX	
XX	DR	WPI; 2000-452387/39.

Query Match	95.9%	Score 754	DB 21	Length 181b	
Best Local Similarity	97.5%	pred. No. 1e-206;			
Matches 766	Conservative	0	Mismatches 20	Indels 0	Gaps 0
QY	1	ATGATAGAAACATACAGCCACCTTC	CCCCAGATCCGTGGCACTGGACTTCCAGCGAGC	60	
Db	40	atgatcaaaacatacaaaccaactctcccgatctcggccactggactgcccatcagc	99		
QY	61	ATGAAGATTTTATGTATTTACTTACTGT	TTTCCTTATCACCCAAATGATTGGATCTGTG	120	
Db	100	atgaaattttatgtattacttactgtttttctatcccccagatgctgggccagca	159		
QY	121	CTTTTTCGTGTATCTTCATAGAAGTGTGGCAAGATAGAAAGATGAAGGAATCTTCAT	180		
Db	160	cttttgcgtgtatcttcatagaagttggacaagatagaagatgaaaggaattctcat	219		
QY	181	GAAGATTTTGTATTTCATGAACGATACAGAGATC	CAACACAGGAGAAAGATTCCTTATCC	240	
Db	220	gaagattttgtatcatgaaacgatacagatgcacacacagggagaaagatccttatcc	279		
QY	241	TTACTGAACCTGTGAGGAGATTAAAAGCCAGTTTGAAGCGTTTGTGAAGGATTAATGTTA	300		
Db	280	ttactgaactgtgaggagattaaaggcagtttgaaggtttgtgaaggatataatgtta	339		
QY	301	AACAAGAGGAGACGAGAAAGAAACACCTTTGAATGCAAAAAGTGATCAGAAATCCT	360		
Db	340	aacaagaggagacgagaaagaaacacgttttgaatgcataaagggtgatcagaatcct	399		
QY	361	CAAAATTGCGGCACATCTCATTAAGTGAAGCGCAGAGTAAACAAACATCTGTGTTTACAGTGG	420		
Db	400	caaatTgcggcacatgtcataagtggccagcagTaaacaacatctgtttcacagtg	459		
QY	421	GCTGAAAAAGGATTACTACACCATGAGCAACACTTGGTACCTCGAAAATGGAAACAG	480		
Db	460	gctgaaaaaggaTactacacatgagcaacaacttggtaaccttggaatggaaaatggaaaacag	519		
QY	481	CTGACCGTTAAAAAGACAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCCAAT	540		
Db	520	ctgacctttaaagacaaggactctattaTactatgtcccaagtcacctctgttccaat	579		
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCGCTCTGCCTTAAAGTCCCCCGGTAGA	600		
Db	580	cgggaagcttcgagtcgaagctccatttatagccagcctctgcctaaagtcgcccggtaga	639		
QY	601	TTGAGAGAAATCTTACTTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTGCGGGCAA	660		

Db	100	atgaaaaattttatgtattacttactgttttttcttatccccagatgatcgggccagca	139
Qy	121	CTTTTTCGCTGCTATCTTCATGAAGGTTGGCAAGATAGAAGATGAAGGAATCTTCAT	180
Db	160	cttttttcgtcgtaacctctcatagaagttggacaagatagaagatgaaggaattctcat	219
Qy	181	GAAGATTTTGTATTTCATGAACGATACAGAGATCCACACAGGAGAAGATCTTATCCC	240
Db	220	gaagattttgtattcatgaaacgatacagatgcaacacagggagaagataacctatcc	279
Qy	241	TTTCTGAACCTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA	300
Db	280	ttactgaactctgagagagattaaaggcagtttgaaggtttgtgaaggatataatgtta	339
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Db	340	acaagaagagagacgagaagaagaaacagctttgaaatgcaaaaaagttgatcagaatcct	399
Qy	361	CAAAATTCGCGCACATCTCATTAAGTGAGGCGCAGCTAAACAAACATCTGTGTTACAGTGG	420
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Qy	481	CTGACCGCTTAAAAGACAAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCCAAT	540
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Db	580	cgggaagcttcgagtcgaagctccatttatagccagcctctgcctaaagtcctcccggtaga	639
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Db 700 caatccattcacttgggagggatttgaattgaattgaacacagtgcttcggtttgttcaat 759  
Qy 721 GTGACTGATCCCAAGCCAAAGTCAGGCATGGCACTGGCTTCAAGTCTCTTTGGCTTACTCAA 780  
Db 760 gtgactgatccaagccaagttagccatggcactggcttcaagctccttggcttactcaaa 819  
Qy 781 CTCCTGA 786  
Db 820 cctctga 825

RESULT 15  
AAS86571  
ID AAS86571 standard; cDNA; 1816 BP.  
XX AC  
XX AC  
XX AAS86571;  
DT 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #2375.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.  
OS Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX P-PSDB; ABG22384.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity  
XX Claim 1; SEQ ID No 2375; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. AAS64197-AAS94564 represent novel human  
XX diagnostic coding sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1816 BP; 520 A; 461 C; 343 G; 492 T; 0 other;  
Query Match 95.9%; Score 754; DB 23; Length 1816;  
Best Local Similarity 97.5%; Pred. No. 1e-206;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
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Db 40 atgacgaacatacaacaaacttctccogactctgogccactggactgcccacga 99  
Qy 61 ATGAAGATTTTATCTATTACTTCTTCTTATCACCCTTATCAGATCTGGATCTGTG 120  
Db 100 atgaaaattttatgtatttacttactgttttcttaccacccagatgattgggtcagca 159  
Qy 121 CTTTGTGTGTATCTTATAGAAAGGTGGCAAGATAGAAAGATCAAGAGATCTTTCAT 180  
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Qy 181 GAAGATTTTGTATTTCATGAAACGATACAGATGCAACACAGAGAAAGATCTTATCC 240  
Db 220 gaagattttgtattcatgaaaacgatacagagatgcaacacagagagaatcttattcc 279  
Qy 241 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGCATATATGTTA 300  
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Qy 301 AACAAAGAGGACGACGAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 360  
Db 340 aacaaagaggagacgaagaagaaacagctttgaaatgcaaaaaggatcagaatcct 399  
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Qy 421 GCTGAAAAGGATGACTACACCATGAGCAACACTTGGTAACCTCGAAATGGGAACAG 480  
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Qy 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAT 540  
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Db 700 caatccattcacttgggagggatttgaattgaattgaacacagtgcttcggtttgttcaat 759  
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Qy 781 CTCCTGA 786  
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Search completed: May 30, 2002, 03:03:39  
Job time: 11268 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:23:08 ; Search time 8356.06 Seconds  
(without alignments)  
2035.054 Million cell updates/sec

Title: US-08-982-272-7  
Perfect score: 786  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	776.4	98.8	786	13	US-08-982-272-6	Sequence 6, Appli
3	763.6	97.2	786	13	US-08-982-272-4	Sequence 4, Appli
4	754	95.9	786	5	US-08-107-353-3	Sequence 3, Appli
5	754	95.9	786	13	US-08-982-272-1	Sequence 1, Appli
6	754	95.9	840	1	PCT-US94-00786-7	Sequence 7, Appli
7	754	95.9	840	1	PCT-US94-14767-1	Sequence 1, Appli
8	754	95.9	840	1	PCT-US97-11956-1	Sequence 1, Appli
9	754	95.9	840	3	US-07-805-723-10	Sequence 10, Appli
10	754	95.9	840	3	US-07-969-703A-11	Sequence 11, Appli
11	754	95.9	840	3	US-07-969-703B-11	Sequence 11, Appli
12	754	95.9	840	4	US-08-009-238-7	Sequence 7, Appli
13	754	95.9	840	5	US-08-172-664-1	Sequence 1, Appli
14	754	95.9	840	6	US-08-215-862-1	Sequence 1, Appli
15	754	95.9	840	6	US-08-234-580-3	Sequence 3, Appli
16	754	95.9	840	7	US-08-396-230-1	Sequence 1, Appli
17	754	95.9	840	8	US-08-477-733A-11	Sequence 11, Appli
18	754	95.9	840	8	US-08-484-634-11	Sequence 11, Appli
19	754	95.9	840	9	US-08-589-771-7	Sequence 7, Appli
20	754	95.9	840	10	US-08-677-762-1	Sequence 1, Appli
21	754	95.9	840	11	US-08-770-981-11	Sequence 11, Appli
22	754	95.9	840	14	US-09-088-913-11	Sequence 11, Appli
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24	754	95.9	840	17	US-09-322-021A-11	Sequence 11, Appli
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27	754	95.9	840	17	US-09-387-935-1	Sequence 1, Appli
28	754	95.9	840	17	US-09-388-079-1	Sequence 1, Appli
29	754	95.9	840	17	US-09-388-079A-1	Sequence 1, Appli
30	754	95.9	840	17	US-09-392-618-11	Sequence 11, Appli
31	754	95.9	840	17	US-09-399-106-11	Sequence 11, Appli

[illegible]

## RESULTS

US-08-982-272-1  
: sequence 7 Application US/08982272

GENERAL INFORMATION: Thomas J. Kipps, Applicant.

APPLICANT: Sharima, Sanjati  
APPLICANT: Cantwell, Mark

;  
TITLE OF INVENTION:  
CONTAINING ACCESSORY  
-NOVEL EXPRESSION VECTORS

**TITLE OF INVENTION: MOLECULE LIGAND GENES AND**

TITLE OF INVENTION: MODULATION AND TREATMENT OF

TITLE OF INVENTION: TELECOMMUNICATED  
NUMBER OF SEQUENCES: 44

;; CORRESPONDENCE ADDRESS:  
ADDRESSEE: I von f. I von

ADDRESSEE: LYON & LYON  
COMPET: 633 West Fifth Street

STREET: 633 West Fifth Street  
STREET: Suite 4700

CITY: Los Angeles

COUNTRY: U.S.A.

; COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb storage

COMPUTER: IBM COMPACT  
OPERATING SYSTEM: IBM P.C. DOS 5.0

```

; SOFTWARE: FASTseq VERSION 2.0
;
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/982,272

**CLASSIFICATION:**

APPLICATION NUMBER: 60/132145

FILING DATE: 12/9/96  
ATTORNEY / AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REFERENCE/DOCKET NUMBER: 231/003

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEFAX: 67-2510

; INFORMATION FOR SEQ ID NO: 7:

LENGTH: 786 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLGY: linear

Query Match 100.0%; Score 786; DB 13;

BEST LOCAL SIMILARITY 100.00, 100.00, 100.00

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982.272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid

Query Match 98.8%; Score 776.4; DB 13; Length 786;
Best Local Similarity 99.28; Pred. No. 1.2e-197;
Matches 780; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCGCCAGATCCGTCGCAACTGGACCTCCAGCGAGC 60
DB 1 ATGATAGAAACATACAGCAACCTTCCCGCCAGATCCGTCGCAACTGGACCTCCAGCGAGC 60
QY 61 ATGAGATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 120
DB 61 ATGAGATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 120
QY 121 CTTTTCGTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
DB 121 CTTTTCGTGTATCTTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGGAAAGATCCCTTATCC 240
DB 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACAGAGGAAAGATCCCTTATCC 240
QY 241 TTACTGAAGTGTAGGAGATTAAGAGCCAGTTGAGGCTTTGCAAGGATATATGTTA 300
DB 241 TTACTGAAGTGTAGGAGATTAAGAGCCAGTTGAGGCTTTGCAAGGATATATGTTA 300
QY 301 AACAAAGAGGAGACCAACAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGAACTCT 360
DB 301 AACAAAGAGGAGACCAACAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGAACTCT 360
QY 361 CAAATTCGGCCACATGTCATAGTGAGGCGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
DB 361 CAAATTCGGCCACATGTCATAGTGAGGCGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420
QY 421 GCTGAAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGGAAACAG 480
DB 421 GCTGAAAAAGGATACATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGGAAACAG 480

US-08-982-272-6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982.272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-982-272-7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982.272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid

US-08-982-272-4
Sequence 4, Application US/08982272
GENERAL INFORMATION:
APPLICANT: Kipps, Thomas J.
APPLICANT: Sharma, Sanjai
APPLICANT: Cantwell, Mark
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
TITLE OF INVENTION: CONTAINING ACCESSORY
TITLE OF INVENTION: MOLECULE LIGAND GENES AND
TITLE OF INVENTION: THEIR USE FOR IMMUNO-
TITLE OF INVENTION: MODULATION AND TREATMENT OF
TITLE OF INVENTION: MALIGNANCIES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: 1.44 Mb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982.272
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/132145
FILING DATE: 12/9/96
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 231/003
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
```

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-982-272-4

Query Match 97.2%; Score 763.6; DB 13; Length 786;  
Best Local Similarity 98.2%; Pred. No. 3.3e-194;  
Matches 772; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCCAACTTCCCCAGATCGGTGGCACTGGACTCCACGAGC 60  
DB 1 ATGATGAACATACAGCCAACTTCCCCAGATCGGTGGCACTGGACTCCACGAGC 60

QY 61 ATCAAGATTTTATGATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 61 ATCAAGATTTTATGATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120

QY 121 CTCTTTGCTGTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 121 CTCTTTGCTGTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180

QY 181 GAAGATTTTGTATTCATGAAGGATACAGATGCAACAGGAGAGAGATCCTTATCC 240  
DB 181 GAAGATTTTGTATTCATGAAGGATACAGATGCAACAGGAGAGAGATCCTTATCC 240

QY 241 TTACTGAACATCTGAGGAGATTAAGCCAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 241 TTACTGAACATCTGAGGAGATTAAGCCAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300

QY 301 AACAAAGAGGAG 360  
DB 301 AACAAAGAGGAG 360

QY 361 CAATTCGCGCACATGTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 361 CAATTCGCGCACATGTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

QY 421 GCTGAAAAAGGATACATACAGGAGCAACACTTGGTAAACCTTGGAAATGGAAACAG 480  
DB 421 GCTGAAAAAGGATACATACAGGAGCAACACTTGGTAAACCTTGGAAATGGAAACAG 480

QY 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATCCCAAGTCACTTCTCTTCCAAT 540  
DB 481 CTGACCGTTAAAGACAGAGGACTTATATATCTATCCCAAGTCACTTCTCTTCCAAT 540

QY 541 CGGAAGCTTCGAGTCAAGCTTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGGTTAGA 600  
DB 541 CGGAAGCTTCGAGTCAAGCTTCCATTTATAGCCAGCCTCTGCCTTAAAGTCCCGGTTAGA 600

QY 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATATCCACAGTTCGCGCAACCTTGGGGCAA 660  
DB 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATATCCACAGTTCGCGCAACCTTGGGGCAA 660

QY 661 CAATCCATCTACTTGGGAGGAGTATTCATTAATGCAACAGTGCTTCGGTGTGTGTCAT 720  
DB 661 CAATCCATCTACTTGGGAGGAGTATTCATTAATGCAACAGTGCTTCGGTGTGTGTCAT 720

QY 721 GTGACTGATCAAGCAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
DB 721 GTGACTGATCAAGCAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780

QY 781 CTCTGA 786  
DB 781 CTCTGA 786

RESULT 4  
US-08-107-353-3  
Sequence 3, Application US/08107353  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107,353  
FILING DATE: 19930813  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-107-353-3

Query Match 95.9%; Score 754; DB 5; Length 786;  
Best Local Similarity 97.5%; Pred. No. 1.2e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAACATACAGCCAACTTCCCCAGATCGGTGGCACTGGACTCCACGAGC 60  
DB 1 ATGATGAACATACAGCCAACTTCCCCAGATCGGTGGCACTGGACTCCACGAGC 60

QY 61 ATCAAGATTTTATGATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 61 ATCAAGATTTTATGATTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120

QY 121 CTCTTTGCTGTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 121 CTCTTTGCTGTGTATCTTCTATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180

QY 181 GAAGATTTTGTATTCATGAAGGATACAGATGCAACAGGAGAGAGATCCTTATCC 240  
DB 181 GAAGATTTTGTATTCATGAAGGATACAGATGCAACAGGAGAGAGATCCTTATCC 240

QY 241 TTACTGAACATCTGAGGAGATTAAGCCAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 241 TTACTGAACATCTGAGGAGATTAAGCCAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300

QY 301 AACAAAGAGGAG 360  
DB 301 AACAAAGAGGAG 360

QY 361 CAATTCGCGCACATGTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
DB 361 CAATTCGCGCACATGTATAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

```

Db 361 CAAATGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAAACATCTGTCTTACAGTGG 420
Qy 421 GCTGAAAAGGATACACTACACCATGAGCAACAACTTGTAAACCTGGGAAATGGGAAACAG 480
Db 421 GCTGAAAAGGATACACTACACCATGAGCAACAACTTGTAAACCTGGGAAATGGGAAACAG 480
Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGATGCGGCAAGTCCACCTTCTGTTCCAA 540
Db 481 CTGACCGTTAAAGACAGAGGACTCTATTATATCTATGATGCGGCAAGTCCACCTTCTGTTCCAA 540
Qy 541 CCGGAAGCTTCGAGTCAGCTCCATTTATAGCCAGCCTCTCCCTAAAGTCCCGCGGTAGA 600
Db 541 CCGGAAGCTTCGAGTCAGCTCCATTTATAGCCAGCCTCTCCCTAAAGTCCCGCGGTAGA 600
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCA 660
Db 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGGGGCA 660
Qy 661 CAATCCCAATCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTTGTCAAT 720
Db 661 CAATCCCAATCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTTGTCAAT 720
Qy 721 GTGACTGATCAAGCAAGTCCAGCATGCGCTTCAAGTCCCTTTGGCTTACTCAAA 780
Db 721 GTGACTGATCAAGCAAGTCCAGCATGCGCTTCAAGTCCCTTTGGCTTACTCAAA 780
Qy 781 CTCCTGA 786
Db 781 CTCCTGA 786

```

RESULT 5

```

US-08-982-272-1
; Sequence 1, Application US/08982272
; GENERAL INFORMATION:
; APPLICANT: Kipps, Thomas J.
; APPLICANT: Sharma, Sanjai
; APPLICANT: Cantwell, Mark
; TITLE OF INVENTION: NOVEL EXPRESSION VECTORS
; TITLE OF INVENTION: CONTAINING ACCESSORY
; TITLE OF INVENTION: MOLECULE LIGAND GENES AND
; TITLE OF INVENTION: THEIR USE FOR IMMUNO-
; TITLE OF INVENTION: MODULATION AND TREATMENT OF
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette,
; MEDIUM TYPE: 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/132145
; FILING DATE: 12/9/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 231/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

```

```

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-982-272-1

Query Match 95.9%; Score 754; DB 13; Length 786;
Best Local Similarity 97.5%; Pred. No. 1.2e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0:

Qy 1 ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTCGCAACTGGACTTCCACGCGAG 60
Db 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCCATCAGC 60
Qy 61 ATGAAGATTTTATGTTATTTACTTACTCTTTTCTCTTATCACCCTAAATGATTGGATCTGT 120
Db 61 ATGAAATTTTATGTTATTTACTTACTCTTTTCTCTTATCACCCTAGATGATTGGTGCAGCA 120
Qy 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACACAGATAGAGATGAAGAAATCTTCAT 180
Db 121 CTTTTTGTGTATCTTTCATAGAGGTTGGACACAGATAGAGATGAAGAAATCTTCAT 180
Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCC 240
Db 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAGAAAGATCCTTATCC 240
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGTGAAGGATATAATGTTA 300
Db 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGTGAAGGATATAATGTTA 300
Qy 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
Db 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
Qy 361 CAATTTGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Db 361 CAATTTGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 420
Qy 421 GCTGAAAAGGATACACTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 480
Db 421 GCTGAAAAGGATACACTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 480
Qy 481 CTGACCGTTAAAGACAGAGGACTCTATTATCTATGCGGCAAGTCCACCTTCTGTTCCAA 540
Db 481 CTGACCGTTAAAGACAGAGGACTCTATTATCTATGCGGCAAGTCCACCTTCTGTTCCAA 540
Qy 541 CCGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTCGCTAAAGTCCCGCGGTAGA 600
Db 541 CCGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTCGCTAAAGTCCCGCGGTAGA 600
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCA 660
Db 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAACTTGGCGGCA 660
Qy 661 CAATCCCAATCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTTGTCAAT 720
Db 661 CAATCCCAATCACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTCTTTGTCAAT 720
Qy 721 GTGACTGATCAAGCAAGTCCAGCATGCGCTTCAAGTCCCTTTGGCTTACTCAAA 780
Db 721 GTGACTGATCAAGCAAGTCCAGCATGCGCTTCAAGTCCCTTTGGCTTACTCAAA 780
Qy 781 CTCCTGA 786
Db 781 CTCCTGA 786

```

RESULT 6  
PCT-US94-00786-7

Sequence 7, Application PC/TUS9400786

GENERAL INFORMATION:  
 APPLICANT: ARMITAGE, RICHARD  
 APPLICANT: DAVISON, BARRY  
 APPLICANT: FANSLAW, WILLIAM  
 APPLICANT: RENSCHAW, BLAIR  
 APPLICANT: SPRIGGS, MELANIE  
 APPLICANT: WIDMER, MICHAEL  
 TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
 TITLE OF INVENTION: IN A CD40 LIGAND GENE  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: IMMUNEX CORPORATION  
 STREET: 51 UNIVERSITY STREET  
 CITY: SEATTLE  
 STATE: WASHINGTON  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.1  
 SOFTWARE: MS Word for Apple 5.1, Version a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/00786  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/009,258  
 FILING DATE: 01/22/93  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PERKINS, PATRICIA ANNE  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2810-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 2065870430  
 TELEFAX: 2065870606  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 840 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 IMMEDIATE SOURCE:  
 CLONE: CD40-L  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 46..831  
 PCT-US94-00786-7

Query Match 95.9%; Score 754; DB 1; Length 840;  
 Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	1	ATGATGAAACATACAGCAACCTTCCCGGAGTCCGTCGCAACTGGACATTCACCGCAGC	60
DB	46	ATGATGAAACATACAGCAACCTTCCCGGAGTCCGTCGCAACTGGACATTCACCGCAGC	105
QY	61	ATGAGATTTTATGTTATTTACTTACTGTTTCCCTTATCACCACCAATGATTGGATCTGTG	120
DB	106	ATGAAATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATTGGATCTGTG	165
QY	121	CTTTTGGTGTGTTATTTCTATGAGAGTGGACAGATAGAGTGAAGGAATCTTCAT	180
DB	166	CTTTTGGTGTGTTATTTCTATGAGAGTGGACAGATAGAGTGAAGGAATCTTCAT	225
QY	181	GAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGGAAAGATCTTATCC	240

DB	226	GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGAGGAAAGATCTTATCC	285
QY	241	TTACTGAAGTGTGAGGAGTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA	300
DB	286	TTACTGAAGTGTGAGGAGTAAAGCCAGTTTGAAGGCTTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGAGAGGAAAGAAACAGCTTTTGAATGCAAAAGAGTGTATCAGATCTCT	360
DB	346	AACAAAGAGGAGAGGAAAGAAACAGCTTTTGAATGCAAAAGAGTGTATCAGATCTCT	405
QY	361	CAAAATCCGGCACATGTCATAAGTGAGGCGCAGCAGTAAACACATCTGTGTTACAGTGG	420
DB	406	CAAAATCCGGCACATGTCATAAGTGAGGCGCAGCAGTAAACACATCTGTGTTACAGTGG	465
QY	421	GCTCAAAAGGATACATACACATGAGCAACAACTTGGTAACCTTGGAAAAATGGAAACAG	480
DB	466	GCTCAAAAGGATACATACACATGAGCAACAACTTGGTAACCTTGGAAAAATGGAAACAG	525
QY	481	CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT	540
DB	526	CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCAAGTCACCTTCTGTTCCTCAAT	585
QY	541	CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCCTTAAAGTCCCGGCTAGA	600
DB	586	CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCCTTAAAGTCCCGGCTAGA	645
QY	601	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA	660
DB	646	TTGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGCGGCAA	705
QY	661	CAATCCATTCCTTGGGAGGAGTATTTCAATGCAACAGAGTGTCTGCGTGTGTTCCTCAAT	720
DB	706	CAATCCATTCCTTGGGAGGAGTATTTCAATGCAACAGAGTGTCTGCGTGTGTTCCTCAAT	765
QY	721	GTGACTGATCCAAAGCAAGTGGAGCATGGCAGTGGCTTACGCTTCTTGGCTTACTCAA	780
DB	766	GTGACTGATCCAAAGCAAGTGGAGCATGGCAGTGGCTTACGCTTCTTGGCTTACTCAA	825
QY	781	CTCTGA 786	
DB	826	CTCTGA 831	

RESULT 7  
 PCT-US94-14767-1  
 ; Sequence 1, Application PC/TUS9414767  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: LONGO, DAN L.  
 ; APPLICANT: MURPHY, WILLIAM  
 ; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
 ; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
 ; TITLE OF INVENTION: EXPRESSING CD40  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Macintosh  
 ; OPERATING SYSTEM: Apple Macintosh System 7.1  
 ; SOFTWARE: Microsoft Word for Macintosh, Version 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/14767  
 ; FILING DATE: December 21, 1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:

```
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
NAME/KEY: CDS
LOCATION: 46...831
PCT-US94-14767-1

Query Match 95.9%; Score 754; DB 1; Length 840;
Best Local Similarity 97.5%; Pred. No. 1.3e-191;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTCCCGAGATCGGTGGCAACTGACATTCAGCGGAGC 60
DB 46 ATGATGAAACATACACCAACTTCTCCCGATCTCGGCGCACTGGCACTCCCATCAGC 105
QY 61 ATGAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 120
DB 106 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCACCAATGATGGATCTGTG 165
QY 121 CTTTTCGTGTATCTATAGAAAGGTGGCAAGATAGAAATGAAAGAAATCTTCAT 180
DB 166 CTTTTCGTGTATCTATAGAAAGGTGGCAAGATAGAAATGAAAGAAATCTTCAT 225
QY 181 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAAAGATCTTATCC 240
DB 226 GAAGATTTTGTATTCATGAAACCATACAGAGATGCAACAGAGAAAGATCTTATCC 285
QY 241 TTACTGAACTGTAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300
DB 286 TTACTGAACTGTAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345
QY 301 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 360
DB 346 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACTCT 405
QY 361 CAATTTGGGACATGTCATTAAGTGAAGGCGCAGAGTAAACAAACATCTGTGTACAGTGG 420
DB 406 CAATTTGGGACATGTCATTAAGTGAAGGCGCAGAGTAAACAAACATCTGTGTACAGTGG 465
QY 421 GCTGAAAGAGATACTACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAAACAG 480
DB 466 GCTGAAAGAGATACTACACCATGAGCAACACTTGTGTAACCTGGAAATGGGAAACAG 525
QY 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAA 540
DB 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTCTGTGTCCAA 585
QY 541 CGGGAAGCTTCGATCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600
DB 586 CGGGAAGCTTCGATCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645

PCT-US97-11956-1
Sequence 1, Application PC/TUS9711956
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Macintosh 7200/90
OPERATING SYSTEM: Apple Operating System 7.6
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11956
FILING DATE: 09-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/677,762
FILING DATE: 10-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/763,995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2845-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD40-L
FEATURE:
NAME/KEY: CDS
LOCATION: 46...831
PCT-US97-11956-1

Query Match. 95.9%; Score 754; DB 1; Length 840;
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Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCCACATCGGTGGCAACTGGACTTCCACGGAGC 60  
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGGGCCACTGGACTGCCATCAGC 105  
QY 61 ATGAGATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 106 ATGAAATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 165  
QY 121 CTTTTCGTGTTATCTTCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 166 CTTTTCGTGTTATCTTCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACCTGTGAGGAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCT 360  
DB 346 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCT 405  
QY 361 CAAATTCGCGCATCTCATAGTGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
DB 406 CAAATTCGCGCATCTCATAGTGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAAGAGGATACACCATGAGCAACACTTGGTAACCCCTGGAAAATGGAAACAG 480  
DB 466 GCTGAAAAGAGGATACACCATGAGCAACACTTGGTAACCCCTGGAAAATGGAAACAG 525  
QY 481 CTGACCGTTAAAGAGAGAGACTCTATTATATATATATATATATATATATATATATAT 540  
DB 526 CTGACCGTTAAAGAGAGAGACTCTATTATATATATATATATATATATATATATATAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGATCTTACTAGAGTGCATATACCCAGCTTCGCCAAACCTTGGGGGCAA 660  
DB 646 TTCGAGAGATCTTACTAGAGTGCATATACCCAGCTTCGCCAAACCTTGGGGGCAA 705  
QY 661 CAATCCATTCACCTTGGGAGGATTTTGAATTCGAACAGGCTCTCGGTGTTGTTCAT 720  
DB 706 CAATCCATTCACCTTGGGAGGATTTTGAATTCGAACAGGCTCTCGGTGTTGTTCAT 765  
QY 721 GTGACTGATCCAAAGCCAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 780  
DB 766 GTGACTGATCCAAAGCCAGTGGCCATGGCACTGGCTTCACGTCCTTGGCTTACTCAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

RESULT 9  
US-07-805-723-10  
; Sequence 10, Application US/07805723  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE

STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/805,723  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSTER, JEFFREY B.  
REGISTRATION NUMBER: 32585  
REFERENCE/DOCKET NUMBER: 2802  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
US-07-805-723-10

Query Match 95.9%; Score 754; DB 3; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCAACCTTCCCCACATCGGTGGCAACTGGACTTCCACGGAGC 60  
DB 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGGGCCACTGGACTGCCATCAGC 105  
QY 61 ATGAGATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 120  
DB 106 ATGAAATTTTATGTTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 165  
QY 121 CTTTTCGTGTTATCTTCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
DB 166 CTTTTCGTGTTATCTTCATAGAGTTGGACAGATAGAGATGAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACCTGTGAGGAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACCTGTGAGGAGTTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCT 360  
DB 346 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATCCAAAAGGTGATCAGATCCT 405  
QY 361 CAAATTCGCGCATCTCATAGTGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
DB 406 CAAATTCGCGCATCTCATAGTGGCCAGCAGTAAACCAACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAAGAGGATACACCATGAGCAACACTTGGTAACCCCTGGAAAATGGAAACAG 480  
DB 466 GCTGAAAAGAGGATACACCATGAGCAACACTTGGTAACCCCTGGAAAATGGAAACAG 525  
QY 481 CTGACCGTTAAAGAGAGAGACTCTATTATATATATATATATATATATATATATATAT 540



Db 526 CTGACCGTTAAAGACAGAGCTCTATTATATCTATGCCCCAAGTCACCTTCTGTCTCCAAAT 585  
 QY 541 CGGGAGCTTCAGTCAAGCTCCATTATATAGCAGCCTCTGCTTAAGTCCCGCGGTAGA 600  
 Db 586 CGGGAGCTTCAGTCAAGCTCCATTATATAGCAGCCTCTGCTTAAGTCCCGCGGTAGA 645  
 QY 601 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGAACTCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTGGCGGCAA 705  
 QY 661 CAATCCATTCACCTGGGAGGAGTATTGAATTCGACACAGGTGCTTCGGTGTGTTGTCAT 720  
 Db 706 CAATCCATTCACCTGGGAGGAGTATTGAATTCGACACAGGTGCTTCGGTGTGTTGTCAT 765  
 QY 721 GTGACTGATCCCAAGCAAGTGGAGCTGACCTGCTTCACGCTCTTTCGGCTTACTCAAA 780  
 Db 766 GTGACTGATCCCAAGCAAGTGGAGCTGACCTGCTTCACGCTCTTTCGGCTTACTCAAA 825  
 QY 781 CTCTGA 786  
 Db 826 CTCTGA 831

RESULT 10

US-07-969-703A-11  
 ; Sequence 11, Application US/07969703A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; TITLE OF INVENTION: NOVEL CYTOKINE  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/969,703A  
 ; FILING DATE: 19921023  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2802-B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 2065870430  
 ; TELEFAX: 2065870606  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 840 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; IMMEDIATE SOURCE:  
 ; CLONE: CD40-L  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 46..831  
 ; US-07-969-703A-11

Query Match 95.9%; Score 754; DB 3; Length 840;  
 Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
 Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 ATGATAGAAACATACAGCCAACTTCCCGCAGATCGTGGCAACTGGACTTCCAGCGAGC 60  
 Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTCGGCCACTGACTGCCCATCAGC 105  
 QY 61 ATGAGAGATTTTATGTATTACTTACTTCTTATCCTTATCACCAGATGATTGATCTGTG 120  
 Db 106 ATGAAATTTTATGTATTACTTACTTCTTATCCTTATCACCAGATGATTGATCTGTG 165  
 QY 121 CTTTTCCTGCTGTATCTTCATAGAGTTGGCAAGATGAAGATGAAAGGAATCTTTCAT 180  
 Db 166 CTTTTCCTGCTGTATCTTCATAGAGTTGGCAAGATGAAGATGAAAGGAATCTTTCAT 225  
 QY 181 GAAGATTTTGTATTATGAAAGAGTACAGATGACACAGAGGAAAGATCTCTTATCC 240  
 Db 226 GAAGATTTTGTATTATGAAAGAGTACAGATGACACAGAGGAAAGATCTCTTATCC 285  
 QY 241 TTACTGAACCTGACGAGATTTAAAGCCAGTTTGAAGGCTTTGTAAGGATATAATGTTA 300  
 Db 286 TTACTGAACCTGACGAGATTTAAAGCCAGTTTGAAGGCTTTGTAAGGATATAATGTTA 345  
 QY 301 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAGCTGATCAGATCTCT 360  
 Db 346 AACAAAGAGGACGAGAAAGAAACAGCTTTGAAATGCAAAAGCTGATCAGATCTCT 405  
 QY 361 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACACATCTGTGTACAGTGG 420  
 Db 406 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACACATCTGTGTACAGTGG 465  
 QY 421 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTGGAANAATGGGAACAG 480  
 Db 466 GCTGAAAAAGGATCTACACCATGAGCAACACTTGGTAACCTGGAANAATGGGAACAG 525  
 QY 481 CTGACCGTTTAAAGACAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTCTTCCAAT 540  
 Db 526 CTGACCGTTTAAAGACAGAGCTCTATTATATCTATGCCCCAAGTCACTTCTCTTCCAAT 585  
 QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA 600  
 Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCTCTGCTTAAAGTCCCGCGTAGA 645  
 QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTGGCGGCAA 660  
 Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCCGCCAAACCTTGGCGGCAA 705  
 QY 661 CAATCCATTCACCTGGGAGGAGTATTGAATTCGACACAGGTGCTTCGGTGTGTTGTCAT 720  
 Db 706 CAATCCATTCACCTGGGAGGAGTATTGAATTCGACACAGGTGCTTCGGTGTGTTGTCAT 765  
 QY 721 GTGACTGATCCCAAGCAAGTGGAGCTGACCTGCTTCACGCTCTTTCGGCTTACTCAAA 780  
 Db 766 GTGACTGATCCCAAGCAAGTGGAGCTGACCTGCTTCACGCTCTTTCGGCTTACTCAAA 825  
 QY 781 CTCTGA 786  
 Db 826 CTCTGA 831

RESULT 11

US-07-969-703B-11  
 ; Sequence 11, Application US/07969703B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; TITLE OF INVENTION: NOVEL CYTOKINE  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION

STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/969,703B  
FILING DATE: 19921023  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-B  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-07-969-703B-11

Query Match 95.98; Score 754; DB 3; Length 840;  
Best Local Similarity 97.58; Pred. No. 1.3e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCCAACTTCCCGCAGATCCGTCGCAACTGACCTCCAGCCAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCCCGCATCTGCGGCACCTGGCACTGCCCATCAGC 105  
Qy 61 ATGAGATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACCAATGATGGATCTGTG 165  
Qy 121 CTTTTCGTGTATCTTCATAGAGGTTGGACAAGATGAGAGATGAAAGAAATCTTCAT 180  
Db 166 CTTTTCGTGTATCTTCATAGAGGTTGGACAAGATGAGAGATGAAAGAAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAAACACATACAGATGCAACACAGAGAAAGATCTTATTC 240  
Db 226 GAAGATTTTGTATTCATGAAACACATACAGATGCAACACAGAGAAAGATCTTATTC 285  
Qy 241 TTACTGAACTGTGAGAGATTAAGACCACTTTGAAGCTTTGTAAGGATATATGTTA 300  
Db 286 TTACTGAACTGTGAGAGATTAAGACCACTTTGAAGCTTTGTAAGGATATATGTTA 345  
Qy 301 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGATGATCAGAAATCCT 360  
Db 346 AACAAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGATGATCAGAAATCCT 405  
Qy 361 CAAATTCGGCCACATGTCTAATAGTGAGGCCAGCACTAAACACATCTGTGTACAGTGG 420  
Db 406 CAAATTCGGCCACATGTCTAATAGTGAGGCCAGCACTAAACACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAAGGATACACTACACCATGAGCAACAACTTGGTAACCTCGAAATGGGAAACAG 480

Db 466 GCTGAAAAGGATACACTACACCATGAGCAAACTTGGTAACCTCGAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 540  
Db 526 CTGACCGTTAAAGACAGAGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTCCAAT 585  
Qy 541 CGGAAGCTTCGAGTCAGCTCCATTTATATGAGCCAGCTCTCCCTAAAGTCCCCGGGTAGA 600  
Db 586 CGGAAGCTTCGAGTCAGCTCCATTTATATGAGCCAGCTCTCCCTAAAGTCCCCGGGTAGA 645  
Qy 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCAAAACCTTTGCGGGCAA 660  
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCAAAACCTTTGCGGGCAA 705  
Qy 661 CAATCCATTCACTTGGGAGAGTATTTGAATTCGAACACAGTGTCTCGGTGTTTGTCAAT 720  
Db 706 CAATCCATTCACTTGGGAGAGTATTTGAATTCGAACACAGTGTCTCGGTGTTTGTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTCAGCCATGAGCCATGCGCTTACAGTCTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTCAGCCATGAGCCATGCGCTTACAGTCTTGGCTTACTCAA 825  
Qy 781 CTTCTGA 786  
Db 826 CTTCTGA 831  
RESULT 12.  
US-08-009-258-7  
Sequence 7, Application US/08009258  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
TITLE OF INVENTION: IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/009,258  
FILING DATE: 19930122  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-009-258-7

Query Match 95.9%; Score 754; DB 4; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCGCCAGATCGGTGGCAACTGGACTTCAGCGAGC 60  
DB 46 ATGATCGAAACATACAACTTCTCCCGCATCTGGCGCCACTGGACTGCCATCAGC 105  
QY 61 ATGACAGATTTTATGTATTTACTTACTTGTTCCTTATCACCACAAATGATGATCTGTG 120  
DB 106 ATGAAATTTTATGTATTTACTTACTTGTTCCTTATCACCACAAATGATGATCTGTG 165  
QY 121 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAAGATGAAGATGAAAGGAATCTTCAT 180  
DB 166 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAAGATGAAGATGAAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGGAGCAGAAAGAAACACAGCTTTGAAATCAAAAGGTGATCAGATCTCT 360  
DB 346 AACAAAGAGGAGCAGAAAGAAACACAGCTTTGAAATCAAAAGGTGATCAGATCTCT 405  
QY 361 CAAATTCGGCCACATGTCTAATAGTAGGAGCCAGCAGTAAACAAACATCTGTGTACAGTG 420  
DB 406 CAAATTCGGCCACATGTCTAATAGTAGGAGCCAGCAGTAAACAAACATCTGTGTACAGTG 465  
QY 421 GCTGAAAAGGATACCTACACCATGACCAACACTTGGTAAACCTTGGAAATGGGAAACAG 480  
DB 466 GCTGAAAAGGATACCTACACCATGACCAACACTTGGTAAACCTTGGAAATGGGAAACAG 525  
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTCCTCAAT 540  
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATCTATGCCCAAGTCACTTCTGTTCCTCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCGCCCAAACTTCGCGGCAAA 660  
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCGCCCAAACTTCGCGGCAAA 705  
QY 661 CAATCCATTTCACCTTGGGAGGAGTATTGAAATGCAACACAGGTCCTTCGGTGTGTTGTCAT 720  
DB 706 CAATCCATTTCACCTTGGGAGGAGTATTGAAATGCAACACAGGTCCTTCGGTGTGTTGTCAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGAAGGATGAGGCTTCAGGCTTCAGGCTTCCTTGGCTTACTCAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGAAGGATGAGGCTTCAGGCTTCAGGCTTCCTTGGCTTACTCAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

RESULT 13  
US-08-172-664-1  
; Sequence 1, Application US/08172664  
; GENERAL INFORMATION:

APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANLOW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MORPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-172-664-1

Query Match 95.9%; Score 754; DB 5; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-191;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCGCCAGATCGGTGGCAACTGGACTTCAGCGAGC 60  
DB 46 ATGATCGAAACATACAACTTCTCCCGCATCTGGCGCCACTGGACTGCCATCAGC 105  
QY 61 ATGACAGATTTTATGTATTTACTTACTTGTTCCTTATCACCACAAATGATGATCTGTG 120  
DB 106 ATGAAATTTTATGTATTTACTTACTTGTTCCTTATCACCACAAATGATGATCTGTG 165  
QY 121 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAAGATGAAGATGAAAGGAATCTTCAT 180  
DB 166 CTTTTCCTGTCTGTCTTCTCATAGAGGTTGGACAAGATGAAGATGAAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285  
QY 241 TTACTGAACTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACTGTGAGGAGATTAAGACCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345



Db 826 CTCTGA 831

RESULT 15

US-08-234-580-3

Sequence 3. Application US/08234580

GENERAL INFORMATION:

APPLICANT: KEHRY, MERILYN R

APPLICANT: CASTLE, BRIAN E

TITLE OF INVENTION: METHODS FOR PROLIFERATING AND

TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX

STREET: 100 NEW YORK AVE. N.W. SUITE 600

CITY: WASHINGTON

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234.580

FILING DATE: 28-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MILLMAN, ROBERT A

REGISTRATION NUMBER: 36,217

REFERENCE/DOCKET NUMBER: 1011.1030000/RAM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 840 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 22..807

US-08-234-580-3

Query Match 95.9%; Score 754; DB 6; Length 840;

Best Local Similarity 97.5%; Pred. NO. 1.3e-191;

Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAACATACAGCAACCTCCGCCAGATCCGTCGGCACTGGACCTCCAGCGAGC 60

Db 22 ATGATCGAAACATACAAACAACTTCTCCCGATCTGGCGGCACTGGACCTCCATCAGC 81

QY 61 ATGAGAGATTTTATGTATTTACTTACTGTTCCTTATCACCCAAATGATGGATCTGTG 120

Db 82 ATGAAATTTTATGTATTTACTTACTGTTCCTTATCACCCAGATGATGGGTCAGCA 141

QY 121 CTTTTCGTCTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180

Db 142 CTTTTCGTCTGTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 201

QY 181 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGGAGAAAGATCTTCATCC 240

Db 202 GAAGATTTTGTATTCATGAAACAGATACAGATGCAACACAGGAGAAAGATCTTCATCC 261

QY 241 TTACTGAACGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300

Db 262 TTACTGAACGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 321

QY 301 AACAAAGAGGACGAGAAAGAAACACAGCTTTGAAATGCAAAAGGATCAGAAATCCT 360

Search completed: May 30, 2002, 05:23:15

Job time: 18674 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:40:03 ; Search time 627.19 Seconds  
(without alignments)  
1315.293 Million cell updates/sec

Title: US-08-982-272-7  
Perfect score: 786  
Sequence: 1 ATGATAGAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
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2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	754	95.9	1816	5	US-09-053-375B-226
2	754	95.9	1816	5	US-09-442-384B-457
3	594	75.6	1250	5	US-09-053-375B-821
4	360.6	45.9	508	5	US-09-911-904-131
5	125.4	16.0	2395	5	US-09-875-453A-9
6	45.6	5.8	569	1	PCT-US02-10421-202
7	45.6	5.8	569	6	US-10-112-699-202
8	44	5.6	2127	5	US-09-919-002-664
9	39.4	5.0	234	5	US-09-540-210B-7000
10	38.2	4.9	230	5	US-09-540-210B-14649
11	38.2	4.9	775	6	US-10-123-155-120
12	38	4.8	663	6	US-10-027-632-206146
13	38	4.8	663	6	US-10-027-632-206147
14	36.8	4.7	438	5	US-09-539-331D-26090
c 15	36.4	4.6	1751	6	US-10-105-299-1996
c 16	36.4	4.6	1751	6	US-10-106-698-239
c 17	35.8	4.6	418	5	US-09-789-189-1323
c 18	35.8	4.6	621	6	US-10-027-632-83794
c 19	35.8	4.6	621	6	US-10-027-632-83795
c 20	35.8	4.6	10351	5	US-09-442-384B-628
c 21	35.6	4.5	803	6	US-10-105-299-824
c 22	35.4	4.5	766	6	US-10-027-632-27253
c 23	35.2	4.5	646	5	US-09-919-002-11996
c 24	35	4.5	620	6	US-10-027-632-35707
c 25	35	4.5	620	6	US-10-027-632-62305
c 26	35	4.5	620	6	US-10-027-632-297617

c 27	35	4.5	1635	6	US-10-027-632-251270
c 28	34.8	4.4	817	6	US-10-027-632-172014
c 29	34.8	4.4	26496	6	US-10-105-299-12937
c 30	34.6	4.4	350	5	US-09-721-544-15838
c 31	34.6	4.4	576	5	US-09-721-544-732
c 32	34.6	4.4	606	6	US-10-027-632-84272
c 33	34.6	4.4	606	6	US-10-027-632-296495
c 34	34.6	4.4	624	6	US-10-027-632-208277
c 35	34.6	4.4	663	6	US-10-027-632-230025
c 36	34.6	4.4	1225	6	US-10-027-632-208276
c 37	34.4	4.4	502	5	US-09-789-189-648
c 38	34.4	4.4	586	6	US-10-027-632-317028
c 39	34.4	4.4	586	6	US-10-027-632-317029
c 40	34.4	4.4	1640	6	US-10-106-698-499
c 41	34.4	4.4	1665	5	US-09-919-002-8655
c 42	34.2	4.4	637	6	US-10-027-632-5638
c 43	34.2	4.4	638	6	US-10-027-632-45221
c 44	34.2	4.4	638	6	US-10-027-632-45222
c 45	34.2	4.4	646	6	US-10-027-632-210375

ALIGNMENTS

RESULT 1  
US-09-053-375B-226  
; Sequence 226, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-226

Query Match 95.9%; Score 754; DB 5; Length 1816;  
Best Local Similarity 97.5%; Pred. NO. 1.1e-188;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy	1	ATGATAGAACATACAGCCAACCTTCCCCCAGATCGGTGGCACTGGACTTCAGGAGC	60
Db	40	atgatgaacacatacaacaaacttctcccgatctgcggccactggactgcccacgc	99
Qy	61	ATCAAGATTTTATGTATTTACTTACTTCTTCTTATCACCACCAATGATTGGATCTG	120
Db	100	atgaataattttatgtatttacttcttcttcttaccacagatgattgggtcagca	159
Qy	121	CTTTTGTCTGTATCTTCTCATAGAGTTGGACAAGATAGAAGTGAAGAGTCTTCAT	180
Db	160	cttttgcgtgtatcttcatagaaggttggacaagatagaagaggaatcttcat	219
Qy	181	GAAGATTTTGTATTCATGAAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC	240
Db	220	gaagatttgcgtgtatcttcatagaaggttggacaagatagaagaggaatcttcat	279
Qy	241	TTACTGAAGTGTGAGAGATTAAGCCAGTTTGAAGGCTTTGTCAAGATATATATGTA	300
Db	280	ttactgaagctgagagatataaagccagtttgaagcgttctgtgaagataataatgta	339
Qy	301	AACAAGAGGACCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
Db	340	aacaagagagagacgaagaaagaaacagcttggaaatgcaaaagggatcagaatcct	399
Qy	361	CAAAATGGCGCACATGTCTAATAGTGAGGCCAGCAGTAAACACATCTCTGTACAGTGG	420

```

Db 400 caaattgcgcacatgtcataagtgagccagcagtaaaacacatctgtgttacagtgg 459
QY 421 GCTGAAAGAGGATACACCATGAGCAACACTTGGTAACCTGGGAAATGGGAAACAG 480
Db 460 gctgaaagaggatactacacacagcagcagcagcagcagcagcagcagcagcagcag 519
QY 481 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAT 540
Db 520 ctgacgctttaaagacaagacacacacacacacacacacacacacacacacacacac 579
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTGCTAAAGTCCGCCCGGTAGA 600
Db 580 cgggaagcttcgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 639
QY 601 TTCGAGAGAACTTACTCAGAGTGCATAATACCAAGTTCGCCCAACCTTTCGCGGCAA 660
Db 640 ttgagagaatcttactcagagtcgcaaataccacagttccgcaaaccttgcgggcaa 699
QY 661 CAATCCATTCACCTGGGAGGAGTATTTGAATTCGAACCAAGGTGCTTCGGTGTTCGTCAT 720
Db 700 caatccattcacttggagaggtatttgattgcaaccagggtgctccgggtttgttcaat 759
QY 721 GTGACTGATCAAGCAAGTGAAGTGCATGCGCTGCTTACGCTCCCTTTGCGTTCATCAAA 780
Db 760 gtgactgatccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 819
QY 781 CTCTGA 786
Db 820 ctctga 825

RESULT 2
US-09-442-384B-457
; Sequence 457, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-457

Query Match 95.9%; Score 754; DB 5; Length 1816;
Best Local Similarity 97.5%; Pred. No. 1.1e-188;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCCAACCTTCCCGAGATCCGTCGCAACATCGGACTTCACCGGAGC 60
Db 40 atgatagaacatacaacacacacacacacacacacacacacacacacacacacacacacac 99
QY 61 ATGAAGATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATCAGCAATGATTTGGATCTGTG 120
Db 100 atgaagattttatgatttacttactgtttttcttataccacagatgatg99gcagca 159
QY 121 CTTTTTGTCTGTATCTTCTATGAAGTGGACAAGATGAAGATGAAGATGAAGATGAAGATGAAGAT 180
Db 160 ctttttgcgtgtatcttctatgagaaggttggacaagatagaagatagaagaaatcttcat 219
QY 181 GAAGATTTTATGATTTTATGATTTTACTTACTTCTTCTTATCACCCTTATCAGCAATGATTTTC 240
Db 220 gaagattttatgatttacttactgtttttcttataccacagatgatg99gcagca 279
QY 241 TTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 300

```



Db 133 ctttttgcgtgtatcttctcatagaagattggataaggtcgaagaggaaagtaaaccttcat 192  
Qy 181 GAAGATTTTGTATTATGAAACGATACAGACATGCACACAGGAGAAAGATCCTTATCC 240  
Db 193 gaagattttgtattcataaaagctaaagatgcaacaaggaagagatctttatcc 252  
Qy 241 TTAAGTGAAGTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 300  
Db 253 ttgtgaaactgtgagagatgagaagcaatttgaagaccttgcgaagataaagctta 312  
Qy 301 ACAAGAGGAGACGAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 360  
Db 313 aacaaagaaga---gaaaaagaacacagctttgaaatgcaaaaggtgatgagatcct 369  
Qy 361 CAAATTCGGGCAATGTCTATAGTCAGGCGACGCTGAAACAACTCTGTTCAGATGG 420  
Db 370 caaattgcagcacagttgttaagcgaagcccaacagtaataagcatccgtttctacagtg 429  
Qy 421 GCTGAAAAGGATACACACCATGAGCAACAACTTTGGTAACCCCTTGAAATGGGAAACAG 480  
Db 430 gccaaagaagatattatccatgaaagcaacttggtaagtctgaaatgggaaacag 489  
Qy 481 CTGACCGTTAAAGACAGGACTCTATTATATCTATGCGCAAGTCACTTCGTTCCTCAAT 540  
Db 490 ctgacggttaaagaagaagactctattatgtctacactcaagtcacactcttctctaat 549  
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCGGTAGA 600  
Db 550 cgggagccttcagtcacagcccttcctcgtcgcctctggtgaagccagcagtgga 609  
Qy 601 TTCGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCAA 660  
Db 610 tctgagaatcttactcaagcggcgaataaccacagttctccacagctttgcgagcag 669  
Qy 661 CAATCCATTCAGTTGGGAGGAGTATTGAAATGCAACAGGTCGTTCGGTGTTCGCAAT 720  
Db 670 cagtcgttcacttggcggagtggttgaattacaagctggtgctctgttctgtcaac 729  
Qy 721 GTGAGTATCCCAAGCAAGTGAAGCCATGCACCTGCCTTCAGCTTCCTTGGCTTACTCAA 780  
Db 730 gtagctgaagcgaagccagtgatccacagagtggtggtctctcatcttttggcttactcaa 789  
Qy 781 CTCTGA 786  
Db 790 ctcctga 795

RESULT 4  
US-09-911-904-131  
; Sequence 131, Application US/09911904  
; GENERAL INFORMATION:  
; APPLICANT: Farr, Spencer B.  
; APPLICANT: Pickett, Gavin G.  
; APPLICANT: Neft, Robin Eileen  
; APPLICANT: Dunn, II, Robert Thomas  
; TITLE OF INVENTION: CANINE TOXICITY GENES  
; FILE REFERENCE: 400742000200  
; CURRENT APPLICATION NUMBER: US/09/911,904  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US 60/220,057  
; PRIOR FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 386  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 131  
; LENGTH: 508  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-911-904-131

Query Match 45.9%; Score 360.6; DB 5; Length 508;  
Best Local Similarity 83.0%; Pred. No. 2.2e-85;  
Matches 424; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

Qy 267 CCAGTTTGAAGCTTTGTCAAGGATATATGTTAAACAAGAGGAGACCAAGAAAGAAA 326  
Db 1 ccaatttgaagctttctcaaggagataatgctaacaacgaatgaagaagaagaaaa 60  
Qy 327 CAGCTTTGAAATGCAAAAGAGTGATCAGAAATCCTCAAAATTCGGGCACATGTCTAAGTGA 386  
Db 61 ca---tgcgaatgcaaaaaggtgatcagagatctcgaattgcagccatgtcataagtg 117  
Qy 387 GCCCAGCAGTAAACAACATCTGTTCAGTGGGCTGAAAAGGATATCTACCATGAG 446  
Db 118 ggctagtagtaaccacagcgtccgttctcgttggcgccaaaggggtactaccataag 177  
Qy 447 CAAACATTTGGTAAACCTTCGAAATGGGAAACAGCTGACCGTTAAAGACAAAGGACTCTA 506  
Db 178 cagcaacctggcgagcctcagaaatgggaaacagttggcgtgaaagacagggactctca 237  
Qy 507 TTATATCTATATGCCCCAAGTACCTTCTGTTCCTCAATCGGAAAGCTTCAGTCAAGCTCCATT 566  
Db 238 ttaagctctatgcccaagtcaccttctcgtcccaatcggcgagcttcgagtcagctccgtt 297  
Qy 567 TATAGCCAGCTCTCGCTTAAAGTCCCGGCTAGATTCGAGAGAAATCTTACTCAGAGCTGC 626  
Db 298 cgtcgcagcctatgcctccattcccccagtggaacggagagagagcttactccgcgcgc 357  
Qy 627 AATATCCACAGTTCGCGCAACCTTCGCGGCAACAACTTCATTCACCTGGGAGGAGTATT 586  
Db 358 gagctcgcgcgcgtcgtccaaaccttgcgcaacagtcctccacttggggagagatt 417  
Qy 687 TCAATTTGAACACAGTGTCTCGTTCGTTCAATGTACTGATCAAGCAAGTGAAGCA 746  
Db 418 tgaattgcatccagtggtctcgttgcgtcaactgactgatccaagccaagtgagcca 477  
Qy 747 TGGCACTGGCTTCACGTCCTCTTTGGCTTACTC 777  
Db 478 cgggaccgcgttcacgtcttttggcttactc 508

RESULT 5  
US-09-875-453A-9  
; Sequence 9, Application US/09875453A  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jungshuh P.  
; APPLICANT: Starr, Douglas B.  
; APPLICANT: Tam, Albert W.  
; APPLICANT: Laurance, Megan E.  
; APPLICANT: Michelotti, Emil F.  
; APPLICANT: Veiligan, Mark D.  
; APPLICANT: Latour, Derek R.  
; APPLICANT: Thomas, Rita L.  
; APPLICANT: Kongpachith, Ana  
; APPLICANT: Sheppard, Liana T.  
; APPLICANT: Lim, Moon Young  
; APPLICANT: Brulice, Thomas W.  
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION  
; FILE REFERENCE: 54600-8135, US00  
; CURRENT APPLICATION NUMBER: US/09/875,453A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: US 60/209,549  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2395  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-875-453A-9

Query Match 16.0%; Score 125.4; DB 5; Length 2395;  
Best Local Similarity 80.3%; Pred. No. 2.6e-23;  
Matches 147; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY	1	ATGATAGAAACATACAGCCAACTTCCCAGATCCCTGGCAACTGGACTTCCAGCGAGC	60
Db	1939	atgatcgaaacatacaaccacactctcccgatctcggccactggaactggccatcagc	1998
QY	61	ATGAGATTTTATGTATTTACTTACTCTTTTCCTTATCACCCAAATGATTTGGATCTGTG	120
Db	1999	atgaaatttttatgtatcttacttactgttttcttaccaccacagatgattgggacaga	2058
QY	121	CTTTTTCGTGTATCTTCATAGAGGTTGGACAAGATAGAAATGAAAGCATCTTCAT	180
Db	2059	cttttctgtgtatcttcataaggctggaaggtaagatgaaccacaagccctttat	2118
QY	181	GAA	183
Db	2119	taa	2121

```

RESULT      6
PCT-US02-10421-202
; Sequence 202, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siqing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
; FILE REFERENCE: 210121 565PC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10421-202

```

	Query Match	5.8%	Score 45.6	DB 1	Length 569	
	Best Local Similarity	49.6%	Pred. No. 0.017			
	Matches 117	Conservative	0	Mismatches 119	Indels	Gaps 0
QY	238	TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGCGCTTGTGTAAGGATATAATG	297			
Db	165	ttcatacattacagtggttggataaaaaattggatgaatgggttcctccggagcgagatca	224			
QY	298	TTAAACAAGAGCAGACGAGAAAGAAAACAGCTTTGAAATGCCAAAAGGTGATCAGAAAT	357			
Db	225	ctcaaatacgtggagaccatttgcgaaacacgcgagaacttcaaaaagcccaatcaggag	284			
QY	358	CCTCAAAATTGGCGCACATGTCATAAGTGAAGCCAGCAGTAAACACATCTTGTTTACAG	417			
Db	285	cagtatcgagaggggaagatgagaggggctgccccagaaagaagacatctggtgtcgaa	344			
QY	418	TGGGCTGTAAAGAGGATCTACACCCNTAGGCAACAACCTTGGTACCCCTGGAAATAGG	473			
nb	345	cacaaaaatttgaagtgaacacgaaaaagaacacacacgaaacacacactggaaaatgg	400			

RESULT 7  
US-10-112-699-202  
: Sequence 202, Application US/10112699  
: GENERAL INFORMATION:  
: APPLICANT: Wang, Tongtong  
: APPLICANT: Wang, Siqing  
: APPLICANT: Bangur, Chaitanya S.  
: APPLICANT: Gaiger, Alexander  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
: TITLE OF INVENTION: AND DIAGNOSIS OF CANCER  
: FILE REFERENCE: 210121.565  
: CURRENT APPLICATION NUMBER: US/10/112.699  
: CURRENT FILING DATE: 2002-03-28

```

; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 202
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-699-202

Query Match          5.8%; Score 45.6; DB 6; Length 569;
Best Local Similarity 49.6%; Pred. No. 0.017;
Matches 117; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 238 TCCTTACTCACTGTGAGCAGATTAAAGCCAGTGTTCGAGGCTTTGTGAAGGATATAATG 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 ttcatactacagtgttggaataaaaattggagatgaatgggttcggagagacagLa 224
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 298 TTAACAAAGAGGAGCAGCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAT 357
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 ctcaaatatcgtggacaccaatttcgagaaacagcgagaaacttcaaaaagccaatcaggag 284
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 358 CCTTCAAAATTCGGGCACATGTCATAAGTGGAGGCGCAGCAGTAAACAAACATCTGTGTACAG 417
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 cagtatgcagaggggaaagtggaggggctgccccagaaagaagacatctgctctgcaa 344
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 418 TGGGCTGAATAAGGATACTACACCATGAGCAACAACTTGGTAAACCCCTCGAAATGG 473
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 cadagaaatgttgaagtgaacgaaaagaacaaacagaaacacacccctggaaatgg 400
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT      8
US-09-919-002-664
; Sequence 664, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Lesnikowicz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 664
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-664

```

Query Match	5.6%	Score 44	DB 5	Length 2127
Best Local Similarity	49.2%	Pred. No.	0.064	
Matches 116	Conservative	0	Mismatches 120	Indels
QY	238	TCCTTACTGAACCTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTGTGAAGGATATATATG	297	
Db	238	ttcatccattacagtggttggaataaaattggatgaatgggttcggagagcagagta	297	
QY	298	TTAAACAAGAGAGACGACGAAGAAAGNAACACGTTTGAANTGCAAAAAGGTGATCAGAAAT	357	
Db	298	ctcaaatcagtgagaccgaatttgagaaacsgcagagaacttcaaaaagccaatcaggag	357	
QY	358	CCTCAAAATTCGGCGACATGTCATAAGTGTAGGGCCAGCAGTAAACAACATCTGTGTTACAG	417	
Db	358	cagtatgcagaggggaagalgagaggggctgccccaggaaagacatctggtgtgcaa	417	
QY	418	TGGCGTGA AAAAGGATACACCATGACCAACCTTGGTAACTCGTGAATAAGG	473	
Db	418	cagaaaaatttgaagtgaataacgaaagaaacacacagaaaaaacaccttggaaatg	473	

```

RESULT 9
US-09-540-210B-7000
; Sequence 7000, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaby, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP.
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996

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; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7000
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00141818
; NAME/KEY: unsure
; LOCATION: 24,113
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-7000

Query Match 5.0%; Score 39.4; DB 5; Length 234;
Best Local Similarity 48.8%; Pred. No. 0.55;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 263 AAAGCCAGTTTGAAGGCTTTGTGAAGCATATATGTTAAACAAGAGGAGACGAAGAAG 322
Db 1 aaaaattgggatgaatgggttcgcnagagcagagtagtactcaataatcgtyggacaccaatttgc 60
QY 323 AAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCTCAAAATGCGGCACATGTCTATA 382
Db 61 agaaacagcgagaacttcaaaagccaatcaggagcagtagtcgagagggggaanattgagag 120
QY 383 GTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGGGCTGAAAAGGATACACTACACCA 442
Db 121 gggctgccccaggaaagagagacatctgctcgaacagaaaaaatgttgaatggaatacga 180
QY 443 TGAGCAACAACACTTGGTAAACCCCTGGAAAATGG 473
Db 181 aaagaacaacaacagaaaaacacctgggaatgg 211

RESULT 10
US-09-540-210B-14649
; Sequence 14649, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.

```

APPLICANT: Stuve, Laura L.  
APPLICANT: Mullahy, Sara J.  
APPLICANT: Naughton, Rebecca E.  
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE  
FILE REFERENCE: PD-1037 CIP  
CURRENT APPLICATION NUMBER: US/09/540,210B  
CURRENT FILING DATE: 2002-04-03  
PRIOR APPLICATION NUMBER: 08/972,899  
PRIOR FILING DATE: November 18, 1997  
PRIOR APPLICATION NUMBER: 08/395,244  
PRIOR FILING DATE: February 27, 1995  
PRIOR APPLICATION NUMBER: 08/722,922  
PRIOR FILING DATE: September 27, 1996  
PRIOR APPLICATION NUMBER: 60/005,526  
PRIOR FILING DATE: September 29, 1995  
PRIOR APPLICATION NUMBER: 08/824,029  
PRIOR FILING DATE: March 25, 1997  
PRIOR APPLICATION NUMBER: 60/014,010  
PRIOR FILING DATE: March 25, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/903,555  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/862,178  
PRIOR FILING DATE: May 22, 1997  
PRIOR APPLICATION NUMBER: 60/018,217  
PRIOR FILING DATE: May 23, 1996  
PRIOR APPLICATION NUMBER: 08/881,589  
PRIOR FILING DATE: June 24, 1997  
PRIOR APPLICATION NUMBER: 60/021,275  
PRIOR FILING DATE: June 25, 1996  
PRIOR APPLICATION NUMBER: 08/903,802  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/023,308  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/905,881  
PRIOR FILING DATE: August 1, 1997  
PRIOR APPLICATION NUMBER: 60/025,204  
PRIOR FILING DATE: August 1, 1996  
PRIOR APPLICATION NUMBER: 08/903,471  
PRIOR FILING DATE: July 30, 1997  
PRIOR APPLICATION NUMBER: 60/025,478  
PRIOR FILING DATE: July 31, 1996  
PRIOR APPLICATION NUMBER: 08/903,556  
PRIOR FILING DATE: July 31, 1997  
PRIOR APPLICATION NUMBER: 60/025,217  
PRIOR FILING DATE: August 22, 1996  
PRIOR APPLICATION NUMBER: 08/937,142  
PRIOR FILING DATE: September 23, 1997  
PRIOR APPLICATION NUMBER: 60/026,598  
PRIOR FILING DATE: September 24, 1996  
PRIOR APPLICATION NUMBER: 08/960,746  
PRIOR FILING DATE: October 29, 1997  
PRIOR APPLICATION NUMBER: 60/030,144  
PRIOR FILING DATE: October 30, 1996  
PRIOR APPLICATION NUMBER: 08/826,847  
PRIOR FILING DATE: April 10, 1997  
PRIOR APPLICATION NUMBER: 60/015,533  
PRIOR FILING DATE: April 10, 1996  
PRIOR APPLICATION NUMBER: 08/755,524  
PRIOR FILING DATE: November 22, 1996  
PRIOR APPLICATION NUMBER: 60/007,495  
PRIOR FILING DATE: November 22, 1995  
PRIOR APPLICATION NUMBER: 09/021,031  
PRIOR FILING DATE: February 10, 1998  
PRIOR APPLICATION NUMBER: 60/039,325  
PRIOR FILING DATE: February 13, 1997  
PRIOR APPLICATION NUMBER: 09/035,172  
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431  
PRIOR FILING DATE: March 5, 1997  
PRIOR APPLICATION NUMBER: 09/041,894  
PRIOR FILING DATE: March 12, 1998  
PRIOR APPLICATION NUMBER: 60/040,199  
PRIOR FILING DATE: March 14, 1997  
PRIOR APPLICATION NUMBER: 09/050,817  
PRIOR FILING DATE: March 30, 1998  
PRIOR APPLICATION NUMBER: 60/043,792  
PRIOR FILING DATE: April 11, 1997  
PRIOR APPLICATION NUMBER: 09/074,999  
PRIOR FILING DATE: May 8, 1998  
PRIOR APPLICATION NUMBER: 60/048,431  
PRIOR FILING DATE: May 29, 1997  
PRIOR APPLICATION NUMBER: 09/107,592  
PRIOR FILING DATE: June 30, 1998  
PRIOR APPLICATION NUMBER: 60/052,751  
PRIOR FILING DATE: July 1, 1997  
PRIOR APPLICATION NUMBER: 09/094,079  
PRIOR FILING DATE: June 9, 1998  
PRIOR APPLICATION NUMBER: 60/049,975  
PRIOR FILING DATE: June 13, 1997  
NUMBER OF SEQ ID NOS: 35654  
SOFTWARE: PERL Program  
SEQ ID NO 14649  
LENGTH: 230  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No: hu00678829  
US-09-540-210B-14649

Query Match 4.9%; Score 38.2; DB 5; Length 230;  
Best Local Similarity 50.8%; Pred. No. 1.1;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATG 297  
Db 32 ttcatattacagtggttggaataaaattggatgaatgggttccggagagcagagta 91  
QY 298 TTAACAAGAGGAGACGAGAGAGAAAGAACAGCTTTGAATCAAAAAGTGATCAGAAAT 357  
Db 92 ctcaaatagtggaacacatttgcagaaacgagcgaggaacttcaaaaagccaatcaggag 151  
QY 358 CCTCAAAATTCGGCACATGTCATAAGTCAGGCCAGCAGTAAACAAACATCTGTGTGTACA 416  
Db 152 cagtatgcagagggggaagatgagaggggctgccccgggaaagagacatctgtgtgca 210

RESULT 11  
US-10-123-155-120  
Sequence 120, Application US/10123155  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 120
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-120

Query Match
Best Local Similarity 4.9%; Score 38.2; DB 6; Length 775;
Matches 45; Conservative 192; Mismatches 404; Indels 0; Gaps 0;

QY 111 TGGATCTGCTGTTTGTGCTGATCTTCAAGAGAGGTTGGACAAGATGAGATGAAG 170
DB 134 WLRRHAIPDDKLTGYTIAAIGSEQRERLRRLARPGGPGGAQRKVRFFRSCLDMRI 193
QY 171 GAATCTTCATGAAGATTTGTTATTCATGAAGAGATGATGAGATGATGAGAGAG 230
DB 194 ERLGPRPMEVIEDCGGMDLGAERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLDD 253
QY 231 ATCCCTTACTTACTGAACTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGA 290
DB 254 RNSRVIRIDODGLTLPERTLYLAODESEKILAAIRVFMERVLSLLGADAVEKQAEI 313
QY 291 TATAATGTTAAACAAGAGGAGGACGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGA 350
DB 314 LOVEQOLANITVSEYDLDLRDSSMYNKVTLGLOKIPHLRWLLDQIFOEDFSEEE 373
QY 351 TCAGATCTCAATTCGCGGACATGTCATAGTGAGGCCACGACGATTAACACATCTGT 410
DB 374 VLLATDTMQVSQLIRSPHRLNLYLWVRVVVLSLSEHSPFREALHQAQWEGSDK 433
QY 411 GTTACAGTGGCGTGAAGAGGATGATACACCATGAGCAACACTTGGTAACCTGGAAAA 470
DB 434 POELARVCIGQANRHFAGALFVHEHFSAAKAKVQOLVEDIKYILQORLEELDWMDA 493
QY 471 TGGGAACAGCTGACCGTTAAAGACAGGACTCTATATATCTATATCTATGCTCCAGTACCTT 530
DB 494 ETRAARAKLOMMYVGVDFLLPDAVDKEYEVEVHEKTYFKNILNSIPESIOISVKK 553
QY 531 CTGTTCCATCGGAGCTTCGAGTCAAGCTCCATTTATAGCAGCTGCTGCTAAAGTC 590
DB 554 IQEVDKSTWLLPQALNAYILPNQWVFPAGILOPLTLYDPFQSLNYGGIGITLIGHE 613
QY 591 CCCGGTAGATTCGAGAGATCTTACTCAGAGCTGCAATATCCACAGTTCGCCCAACACC 650
DB 614 LTHGYDDMGQYDRSGLLHWWTEASYSRFLRKAECIVRLYDFTVYNQVNGKHTLGEN 673
QY 651 TTGCGGGCAACATCCATTCATCTGGGAGGAGTATTGAAATGCAACAGGCTGCTCGGT 710
DB 674 IADMGVLKYLAYHAYQKVRHEGPHPLRLKLYTHDQLEFFIAFAQNWCKIKRRSQSVLQVL 733
QY 711 GTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 734 TDKHAPEHYRVLGVSQFEFGAFHCPKDPSPMNAHKCSV 774

RESULT 12
US-10-632-206146
; Sequence 206146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206147
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206147

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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206146
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206146

Query Match
Best Local Similarity 4.8%; Score 38; DB 6; Length 663;
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 176 TTCATGACAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGAGAAAGATCCT 235
DB 173 ttaagagaaacccagtgaaacatcaagaaatgcaatgaacaaattcaacaaatgagaaa 232
QY 236 TATCCTTACTGAACTGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATA 295
DB 233 aacagttaagtcaggaatgagaaatttaacagagattgaaataattttaagaatcaaa 292
QY 296 TGTTTAAACAAACAGAGAGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTG 349
DB 293 gagatatcaggaggagctgaaataacataatgaataatgtgaaatgcaatgagag 346

RESULT 13
US-10-027-632-206147
; Sequence 206147, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206147
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206147

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Query Match 4.8%; Score 38; DB 6; Length 663;

Best Local Similarity 51.1%; Pred. No. 1.7; Indels 0; Gaps 0;  
Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
QY 176 TTCATCAAGATTGTTGATTCATGAACCATACAGAGATGCAACACAGGAGAAAGATCCT 235  
Db 173 ttaagaaaactcagtgagacatcaagaaaatgcaatgaacaatcaacaataatgagaaa 232  
QY 236 TATCCTTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGCAAGGATATAA 295  
Db 233 aacagtaagtgcacagaatgagaaaatttaacagagattgaaaataatttttaagaatcaaa 292  
QY 296 TGTTAAACAAGAGAGACGACGAAAGAAACAGCTTTTCAAATGCAAAAAAGGTG 349  
Db 293 gagatatcagggagctgaaaaataacataatgaataatgaaaaatgcaatagagag 346  
RESULT 14  
US-09-539-331D-26090  
; Sequence 26090; Application US/09539331D  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Deleane, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE  
; FILE REFERENCE: PD-1022 CIP  
; CURRENT APPLICATION NUMBER: US/09/539, 331D  
; CURRENT FILING DATE: 2000-03-30  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 40961  
; SOFTWARE: PERL Program  
; SEQ ID NO 26090  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc-feature  
; OTHER INFORMATION: Incyte-ID No: hu00341082  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 262, 268, 288, 330, 338, 353, 371  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-539-331D-26090

Query Match 4.7%; Score 36.8; DB 5; Length 438;  
Best Local Similarity 49.7%; Pred. No. 3.2;  
Matches 89; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 238 TCCTTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATG 297  
Db 112 ttcatacatcagtggttggaataaaaaattggatgaatgggtccggagagagagta 171  
QY 298 TTAACAAGAGGAGACGACGAAAGAAACAGCTTTGAATGCAAAAAGGTGATCAGAAAT 357  
Db 172 ctcaaatcgtggacaacaatttcgagaacagcagagaaacttcaaaaagcgaatcaggag 231  
QY 358 CTTCAATTCGCGACATGTCTATAGTCAGGCGACAGCTAAACAAACATCTGTGTACA 416  
Db 232 cagatgcagaggggaagatgaggggctnccccangaaagagacatctggtctnca 290  
RESULT 15  
US-10-105-299-1996/c  
; Sequence 1996; Application US/10105299  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, et. al  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS950  
; CURRENT APPLICATION NUMBER: US/10/105,299  
; CURRENT FILING DATE: 2002-03-26

NUMBER OF SEQ ID NOS: 15197  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1996  
; LENGTH: 1751  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (1741)-(1742)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-105-299-1996

Query Match 4.6%; Score 36.4; DB 6; Length 1751;  
Best Local Similarity 53.5%; Pred. No. 6.1;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 241 TTACTGAACGTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 300  
Db 1174 TAACTGAAGTGTGAATAACAAAGAAATGCATATAGTCCTGTTTAAAAATCCTGTGA 1115  
QY 301 AACAAAGAGGAGACGACGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 360  
Db 1114 CACAGAAAAAAGAAAAAAGAAACTGTTGAAATTTTAAATAGGTCTCTAAATCTGCT 1055  
QY 361 CAAATTCGCGCACATGTCTATAA 382  
Db 1054 GAAATTCGTTGTAATGTTTGA 1033  
Search completed: May 30, 2002, 05:40:08  
Job time: 16782 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:51:45 ; Search time 139.75 seconds  
(without alignments)  
1381.524 Million cell updates/sec

Title: US-08-982-272-7  
Perfect score: 786

Sequence: 1 ATGATAGAAACATACAGCCA.....TTGGCTTACTCAAACTCTGA 786

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCRTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	95.9	786	1	US-08-446-922-3
2	754	95.9	786	5	PCT-US93-10034-3
3	754	95.9	840	1	US-07-940-605A-1
4	754	95.9	840	1	US-08-184-422-7
5	754	95.9	840	1	US-08-360-923A-1
6	754	95.9	840	1	US-08-431-055-3
7	754	95.9	840	2	US-08-690-096-1
8	754	95.9	840	2	US-08-249-189-11
9	754	95.9	840	2	US-08-484-624A-11
10	754	95.9	840	2	US-08-477-733B-11
11	754	95.9	840	3	US-08-763-995-1
12	754	95.9	840	3	US-09-088-913A-11
13	754	95.9	840	3	US-08-589-771B-7
14	754	95.9	840	4	US-08-769-819-11
15	754	95.9	840	4	US-08-770-974-11
16	754	95.9	840	4	US-08-858-197-3
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18	638.2	81.2	1425	2	US-08-484-624A-15
19	638.2	81.2	1425	2	US-08-477-733B-15
20	638.2	81.2	1425	3	US-09-088-913A-15
21	638.2	81.2	1425	4	US-08-769-819-15
22	638.2	81.2	1425	4	US-08-770-974-15
23	637.2	81.1	929	1	US-08-446-922-10
24	637.2	81.1	929	2	US-08-249-189-20
25	637.2	81.1	929	2	US-08-484-624A-20
26	637.2	81.1	929	2	US-08-477-733B-20
27	637.2	81.1	929	3	US-09-088-913A-20

28	637.2	81.1	929	4	US-08-769-819-20
29	637.2	81.1	929	4	US-08-770-974-20
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33	594	75.6	783	2	US-08-477-733B-1
34	594	75.6	783	3	US-09-088-913A-1
35	594	75.6	783	4	US-08-769-819-1
36	594	75.6	783	4	US-08-770-974-1
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41	445.6	56.7	878	2	US-08-484-624A-22
42	445.6	56.7	878	2	US-08-477-733B-22
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44	445.6	56.7	878	4	US-08-769-819-22
45	445.6	56.7	878	4	US-08-770-974-22

#### ALIGNMENTS

RESULT 1  
US-08-446-922-3  
; Sequence 3, Application US/08446922  
; Patent No. 5716805  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,922  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/107,353  
; FILING DATE: 08-13-93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 1003-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 786 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; STRAIN: CD40-L  
; FEATURE:

us-08-982-272-7.rn1

TITLE OF INVENTION: PROCEEDINGS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle

05 09: score 754: DB 1: length 786:

COMPUTER TYPE: Floppy disk  
MEDIUM TYPE: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10034  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0614  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PCT-US93-10034-3

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Query Match          95.9%; Score 754; DB 5; Length 786;
Best Local Similarity 97.5%; Pred. No. 1.2e-209;
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY	1	ATGATAGAAACATACAGCCAACTTCCCCAGATCCGTGGCAACTGGCACTTCCAGCAGCAGC. 60
DB	1	ATGATGAAACATACAAACAACTTCTCCCGATCTGGGCCACTGGACTGCCCATCAGC 60
QY	61	ATGAAGATTTTATGTATTTACTTTACTGTGTTTCTTATCACCCAAATGATTGGATCTGTG 120
DB	61	ATGAAATTTTATGTATTTACTTTACTGTGTTTCTTATCACCCAGATGATTTGGGTCAACA 120
QY	121	CTTTTTCCTGTATCTTCATAGAAGTTGGACAGATAGAGAATGAAAGGAATCTTCAT 180
DB	121	CTTTTTCCTGTATCTTCATAGAAGTTGGACAAGATAGAGAATGAAAGGAATCTTCAT 180
QY	181	GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTTATCC 240
DB	181	GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTTATCC 240
QY	241	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTCAAGGATATATGTTA 300
DB	241	TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTTGTCAAGGATATATGTTA 300
QY	301	AACAAAGGAGGAGGAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCT 360
DB	301	AACAAAGGAGGAGGAGAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGAATCCT 360
QY	361	CAAAATTCGGGCACATGTCATAAGTTAGGCCGACGAGTAAACAACATCTGTGTTACAGTGG 420
DB	361	CAAAATTCGGGCACATGTCATAAGTTAGGCCGACGAGTAAACAACATCTGTGTTACAGTGG 420

RESULT 2  
PCT-US93-10034-3  
; Sequence 3, Application PC/TUS9310034  
; GENERAL INFORMATION:  
; \*APPLICANT: Spriggs, Melanie  
; APPLICANT: Srinivasan, Subhashini  
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric



Db 361 CAAATGGCGGCACATGTCATTAAGTGAGGCGCCAGCAGTAAACAAACATCTGTGTTACAGTGG 420  
Qy 421 GCTGAAAAGAGATACCTACACCATGAGCAACAACTTGGTAACCTCGAAATGGGAAACAG 480  
Db 421 GCTGAAAAGAGATACCTACACCATGAGCAACAACTTGGTAACCTCGAAATGGGAAACAG 480  
Qy 481 CTGACCGTTAAAGACAGGAGCTCTATTATCTATGTCCTCAAGTCAACCTTCCTTCCAAAT 540  
Db 481 CTGACCGTTAAAGACAGGAGCTCTATTATCTATGTCCTCAAGTCAACCTTCCTTCCAAAT 540  
Qy 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
Db 541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
Qy 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATATACCCACAGTTCGCGCAAACTTCGCGGGCAA 660  
Db 601 TTCGAGAGAACTTCTACTCAGAGCTGCAATATACCCACAGTTCGCGCAAACTTCGCGGGCAA 660  
Qy 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCAT 720  
Db 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCAT 720  
Qy 721 GTGACTGATCCCAAGCAAGTGCATGACCTGCGCTTCACTGCTTGGCTTACTCAAA 780  
Db 721 GTGACTGATCCCAAGCAAGTGCATGACCTGCGCTTCACTGCTTGGCTTACTCAAA 780  
Qy 781 CTCTGA 786  
Db 781 CTCTGA 786

RESULT 3  
US-07-940-605A-1  
; Sequence 1, Application US/07940605A  
; Patent No. 5540926  
; GENERAL INFORMATION:  
; APPLICANT: ARUFFO, ALEJANDRO  
; APPLICANT: HOLLENBAUGH, DIANE  
; APPLICANT: LEDBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940.605A  
; FILING DATE: 04-SEP-1992  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 22...807  
US-07-940-605A-1  
Query Match 95.9%; Score 754; DB 1; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 ATGATAGAAACATACAGCCCAACCTTCCCGCCAGATCCGTGGCACTCGACTTCCAGCGAGC 60  
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Qy 61 ATGCAAGATTTTATGTATTTACTTACTTGTTCCTTATCACCCAAATGATTTGATGCTG 120  
Db 82 ATGCAAAATTTTATGTATTTACTTACTTGTTCCTTATCACCCAGATGATTTGGTCA 141  
Qy 121 CTTTTTGTGTGTATCTTTCATAGAAGTTGGACAAGATAGAAGATGAAGAGGAATCTTCAT 180  
Db 142 CTTTTTGTGTGTATCTTTCATAGAAGTTGGACAAGATAGAAGATGAAGAGGAATCTTCAT 201  
Qy 181 GAAGATTTTGTATTCATGAAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 240  
Db 202 GAAGATTTTGTATTCATGAAGAGTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 261  
Qy 241 TTACTGAACCTGTGAGGAGATTAAGGCGAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 262 TTACTGAACCTGTGAGGAGATTAAGGCGAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 321  
Qy 301 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATCAAAAGAGTGATCAGAAATCCT 360  
Db 322 AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTGAAATCAAAAGAGTGATCAGAAATCCT 381  
Qy 361 CAAATTTGCGGCACATGTCATTAAGTGAGGCGCCAGTAAACACACATCTGTGTACAGTGG 420  
Db 382 CAAATTTGCGGCACATGTCATTAAGTGAGGCGCCAGTAAACACACATCTGTGTACAGTGG 441  
Qy 421 GCTGAAAAAGGATCTACTACACCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAG 480  
Db 442 GCTGAAAAAGGATCTACTACACCATGAGCAACAACTTGGTAACCTCGGAAATGGGAAACAG 501  
Qy 481 CTGACCGTTAAAGACAGAGCTCTATTATATATATGTCCTCAAGTCAACCTTCCTTCCAAT 540  
Db 502 CTGACCGTTAAAGACAGAGCTCTATTATATATGTCCTCAAGTCAACCTTCCTTCCAAT 561  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 600  
Db 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 621  
Qy 601 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCCGCGGCAA 660  
Db 622 TTCGAGAGAACTTCTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCCGCGGCAA 681  
Qy 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCAT 720  
Db 682 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACCAAGTCTTCGGTGTGTTGTCAT 741  
Qy 721 GTGACTGATCCCAAGCAAGTGCATGCGCTTCACTGCTTTCAGCTTCTTACTCAAA 780  
Db 742 GTGACTGATCCCAAGCAAGTGCATGCGCTTCACTGCTTTCAGCTTCTTACTCAAA 801  
Qy 781 CTCTGA 786  
Db 802 CTCTGA 807  
RESULT 4  
US-08-184-422-7  
; Sequence 7, Application US/08184422  
; Patent No. 5565321  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY

APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSCHAW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
TITLE OF INVENTION: IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,422  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-184-422-7

Query Match 95.98; Score 754; DB 1; Length 840;  
Best Local Similarity 97.58; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 1 ATGATAGAAACATACAGCAACCTTCCCGAGATCCGTTGGCAACTGGCACTGCCATGCCATCAGC 60  
DB 46 ATGATCGAACAATACCAACCACTTCCCGAGATCCGTTGGCAACTGGCACTGCCATGCCATCAGC 105  
QY 61 ATGAGATTTTATGATTTTACTGTTTCTTATCACCACCAATGATGATGCTGTG 120  
DB 106 ATGAAATTTTATGATTTTACTGTTTCTTATCACCACCAATGATGATGCTGTG 165  
QY 121 CTTTGTGCTGATCTTATGATAGAGTTGGCAAGATAGAGATGAAAGGAATCTTCAT 180  
DB 166 CTTTGTGCTGATCTTATGATAGAGTTGGCAAGATAGAGATGAAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCCACAGAGAGAAAGATCCCTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCCACAGAGAGAAAGATCCCTATCC 285  
QY 241 TTAGTAACTGTGAGAGATTTAAAGCCAGTTTGAGGCTTTGTGAGGATATATGTTA 300

DB 286 TTAGTAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATATGTTA 345  
QY 301 AACAAAGAGGAGACGAAAGAAAGAGCTTTTGAATGCAAAAAGGTGATCAGAACTCCT 360  
DB 346 AACAAAGAGGAGACGAAAGAAAGAGCTTTTGAATGCAAAAAGGTGATCAGAACTCCT 405  
QY 361 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGG 420  
DB 406 CAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGG 465  
QY 421 GCTGAAAAAGGATATACACCATGAGCAACAACTTGGTAACCCCTGGAATGGAACACAG 480  
DB 466 CTTGAAAAAGGATATACACCATGAGCAACAACTTGGTAACCCCTGGAATGGAACACAG 525  
QY 481 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAT 540  
DB 526 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 645  
QY 601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTTCGGGCAA 660  
DB 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAACTTTCGGGCAA 705  
QY 661 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACACAGTGTCTCGTGTGTTCAAT 720  
DB 706 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACACAGTGTCTCGTGTGTTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGGAGCATGCGCTGCTTACGCTTCTGCTTACTCAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGGAGCATGCGCTGCTTACGCTTCTGCTTACTCAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831  
RESULT 5  
US-08-360-923A-1  
Sequence 1, Application US/08360923A  
Patent No. 5674492  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MURPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,923A  
FILING DATE: December 21, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46...831

US-08-360-923A-1

Query Match 95.9%; Score 754; DB 1; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGAGCTTCCAGCGAGC 60  
DB 46 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGAGCTTCCAGCGAGC 105  
QY 61 ATGAGAGATTTTATGATTTACTTACTGTTTCTTATACACCAAAATGATGGATCTGTG 120  
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATACACCAAGATGATGGGTCAGCA 165  
QY 121 CTTTTTGTGTCTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 180  
DB 166 CTTTTTGTGTCTATCTTCATAGAGGTTGGACAGATAGAGATGAAAGGAATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGAGAGAAAGATCTTATCC 240  
DB 226 GAAGATTTTGTATTCATGAAACGATACAGATGCAACACAGAGAGAAAGATCTTATCC 285  
QY 241 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGGAGCAAGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 360  
DB 346 AACAAAGAGGAGCAAGAAAGAAACACAGCTTTGAAATGCAAAAGGTGATCAGATCTCT 405  
QY 361 CAAATTTGGGACATGTCATAGTGAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 420  
DB 406 CAAATTTGGGACATGTCATAGTGAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 465  
QY 421 GCTGAAAAGGATACCTACACCATGAGCAACACTTGGTAACCTGGAAATGGGAACAG 480  
DB 466 GCTGAAAAGGATACCTACACCATGAGCAACACTTGGTAACCTGGAAATGGGAACAG 525  
QY 481 CTGACGGTTAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCGTCTCCCAAT 540  
DB 526 CTGACGGTTAAAGACAAGGACTCTATTATATCTATGCCCAGTCACTTCGTCTCCCAAT 585  
QY 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCTTAAGTCCCGCGGTAGA 600  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCTTAAGTCCCGCGGTAGA 645  
QY 601 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCAGAGTTCCGCCAAACCTTCCGGGCAA 660  
DB 646 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCAGAGTTCCGCCAAACCTTCCGGGCAA 705

QY 661 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACAGGTCCTTGGTGTGTTGTCAAT 720  
DB 706 CAATCCATTCACTTGGGAGGAGTATTGAATGCAACAGGTCCTTGGTGTGTTGTCAAT 765  
QY 721 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 780  
DB 766 GTGACTGATCCAAAGCAAGTGAAGCCATGCGCACTGGCTTCACGTCCTTTGGCTTACTCAAA 825  
QY 781 CTCTGA 786  
DB 826 CTCTGA 831

RESULT 6

US-08-431-055-3  
Sequence 3, Application US/08431055  
Patent No. 5817516  
GENERAL INFORMATION:  
APPLICANT: KEHRY, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,055  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,580  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22...807  
US-08-431-055-3

Query Match 95.9%; Score 754; DB 1; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGAGCTTCCAGCGAGC 60  
DB 22 ATGATGAGAACATACAGCAACCTCCCGCCAGATCGGTGGCAACTGGAGCTTCCAGCGAGC 81  
QY 61 ATGAGATTTTATGATTTACTTACTGTTTCTTATACACCAAAATGATGGATCTGTG 120  
DB 82 ATGAAATTTTATGATTTACTTACTGTTTCTTATACCCAGATGATGGGTCAGCA 141

Qy	1	ATGCATAGAACATACAGCCAACTTCCCCCGACATCGTGGCAACTGGACCTTCCAGCGAGC	60
Db	22	ATGATCGAAACATACAAACAACTTCTCCCGATCTGCGCCACTGGACTGCCCATCAGC	81
Qy	61	ATGAAGATTTTATGTPATTACTTACTGTTTTCCTTATCACCCAATGATTGGATCTGTG	120
Db	82	ATGAAATTTTATGTATTACTTACTGTTTTTCTTATCACCAGATGATTTGGTGACGA	141
Qy	121	CTTTTTCGTGTATCTTCATAGAAGTTGGACAAGATAGAAGTGAAGGAATCTTTCAT	180
Db	142	CTTTTTCGTGTATCTTCATAGAAGTTGGACAAGATAGAAGTCAAAAGGAATCTTTCAT	201
Qy	181	GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACACAGGAGAAAGATCCTTATCC	240
Db	202	GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC	261
Qy	241	TTACTGCACTGTCCAGGAGATTAAACGCCAGTTTGAAGGCTTTTCTGAAGGATATAATGTTA	300

Qy	301	AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGNAATCCT	360
Db	322	AACAAAGAGGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGNAATCCT	381
Qy	361	CAAAATTGCGGCACATGTCATAAGTGAGGCCAGCNGTAAACAAACATCTGTGTTACAGTGG	420
Db	382	CAAAATTGCGGCACATGTCATAAGTGAGGCCAGCAGTAAACAAACATCTGTGTTACAGTGG	441
Qy	421	GCTGAAAAAGGATCTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAG	480
Db	442	GCTGAAAAAGGATCTACACCATGAGCAACAACCTTGGTAACCCCTGGAAAATGGGAAACAG	501
Qy	481	CTGACCCCTTAAAAAGACAAGGACTCTATTATATCTATGCCCCAGTCACCTTCGTGTCCCAAT	540
Db	502	CTGACCGGTTAAAGACAAGGACTCTATTATCTATGCCCCAGTCACCTTCGTGTCCCAAT	561
Qy	541	CGGGAAGCTTCGAGTCAAGCTCATTATAGCCAGCCTCTGCGCTCAAGTCGCCCGGTAGA	600
Db	562	CGGGAAGCTTCGAGTCAAGCTCATTATAGCCAGCCTCTGCGCTCAAGTCGCCCGGTAGA	621
Qy	601	TTCCGAGAGAAATCTTACTFCAGAGCTGCAAAATPACCACAGTTCCGCCAAACCTTCGCGGCAA	660

Db 622 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCAAACCTTCGGGCAA 681  
Qy 661 CAATCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTTCGGTCTTCTCAAT 720  
Db 682 CAATCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTTCGGTCTTCTCAAT 741  
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCATGGCCTTTCAGCTGCTTTCAGCTTCTTGGCTTACTCAA 780  
Db 742 GTGACTGATCCAAAGCAAGTGGAGCATGGCCTTTCAGCTGCTTTCAGCTTCTTGGCTTACTCAA 801  
Qy 781 CTCGA 786  
Db 802 CTCGA 807

RESULT 8  
US-08-249-189-11  
; Sequence 11, Application US/08249189  
; Patent No. 5961974  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,189  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,703  
; FILING DATE: October 23, 1992  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE: December 5, 1991  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/783,707  
; FILING DATE: October 25, 1991  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia A.  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2802-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 2065870430  
; TELEFAX: 2065870506  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens

IMMEDIATE SOURCE:  
; CLONE: CD40-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 46..831  
US-08-249-189-11  
  
Query Match 95.9%; Score 754; DB 2; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0:  
  
Qy 1 ATGATAGAAACATACAGCAACCTTCCGCCAGATCCGTGGCAACTGGACTTCCACGCGAGC 60  
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTGGCCACATGGACTGCCATCAGC 105  
Qy 61 ATGAAGATTTTATGTTTACTTACTGTTTTCCTTATCACCCTTATGATGGATCTGTG 120  
Db 106 ATGAAATTTTATGTTTACTTACTGTTTTCCTTATCACCCTTATGATGGATCTGTG 165  
Qy 121 CTTTTCCTGCTGATCTTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 180  
Db 166 CTTTTCCTGCTGATCTTTCATAGAGGTTGGACAGATAGAGATGAAGGAATCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACAGATACAGAGATGCAACACAGAGAGAAAGATCTTATCC 285  
Qy 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGCTTTTGAAGGATATAATGTTA 345  
Qy 301 AACAAAGAGGAGACGACGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCT 360  
Db 346 AACAAAGAGGAGACGACGAAAGAAACAGCTTTGAAATGCAAAAGGATGATCAGATCT 405  
Qy 361 CAAATTGCGGCACATGTCATAGTCAAGGAGCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
Db 406 CAAATTGCGGCACATGTCATAGTCAAGGAGCAGCAGTAAACCAACATCTGTGTACAGTGG 465  
Qy 421 GCTGAAAGAGGATACATCACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAAACAG 480  
Db 466 GCTGAAAGAGGATACATCACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAAACAG 525  
Qy 481 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCAGTCACTCTCTGTTCCTCAAT 540  
Db 526 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCAGTCACTCTCTGTTCCTCAAT 585  
Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTATTATAGCCAGCCTCTGCTTAAAGTCCCGGCTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTATTATAGCCAGCCTCTGCTTAAAGTCCCGGCTAGA 645  
Qy 601 TTCGAGAGAATCTTACTCAGAGCTCCAAATACCCACAGTTCGCCAAACCTTTCGGGGCAA 660  
Db 646 TTCGAGAGAATCTTACTCAGAGCTCCAAATACCCACAGTTCGCCAAACCTTTCGGGGCAA 705  
Qy 661 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTTCGGTCTTCTCAAT 720  
Db 706 CAATCCATTCTCTGGGAGGAGTATTTGAATTGCAACAGGTCTTCGGTCTTCTCAAT 765  
Qy 721 GTGACTGATCCAAAGCAAGTGGAGCATGGCCTTTCAGCTGCTTTCAGCTTCTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCCTTTCAGCTGCTTTCAGCTTCTTGGCTTACTCAA 825  
Qy 781 CTCGA 786  
Db 826 CTCGA 831  
  
RESULT 9  
US-08-484-624A-11  
; Sequence 11, Application US/08484624A  
; Patent No. 5962406







Thu May 30 05:46:23 2002

REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-763-995-1

Query Match 95.9%; Score 754; DB 3; Length 840;  
Best Local Similarity 97.5%; Pred No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	1	ATGATGAAACATACAGCCAACTTCCCGGATCTCGCGCCACTGGACTGCCATFCAGC	60
DB	46	ATGATGAAACATACAGCCAACTTCCCGGATCTCGCGCCACTGGACTGCCATFCAGC	105
QY	61	ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGATCTGTG	120
DB	106	ATGAGATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGATGATGATG	165
QY	121	CTTTTCTGTGATCTTCTAGAGGTTGGACAAGATAGAGATGAAAGGAACTTCAT	180
DB	166	CTTTTCTGTGATCTTCTAGAGGTTGGACAAGATAGAGATGAAAGGAACTTCAT	225
QY	181	GAAGATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGATCTGTG	240
DB	226	GAAGATTTTATGATTTTACTTACTTCTTCTTATCACCACCAATGATGATCTGTG	285
QY	241	TTACTGAATCTGAGGAGATTAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA	300
DB	286	TTACTGAATCTGAGGAGATTAAGCCAGTTTCAAGGCTTTGTGAAGGATATAATGTTA	345
QY	301	AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTCAATGCAAAAGGATGATCAGATCCT	360
DB	346	AACAAAGAGGAGAGCAAGAAAGAAACAGCTTTCAATGCAAAAGGATGATCAGATCCT	405
QY	361	CAAAATGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACACATCTGTGTACAGTGG	420
DB	406	CAAAATGCGGCACATGTCATAGTGAGGCGCAGCAGTAAACACATCTGTGTACAGTGG	465
QY	421	GCTGAAAAAGGATACACCATGACCAACTTGGTAAACCTTGGAAAAATGGAACAG	480
DB	466	GCTGAAAAAGGATACACCATGACCAACTTGGTAAACCTTGGAAAAATGGAACAG	525
QY	481	CTGACCGTTAAAGACAGGACTCTATTATCTATGCGGCGCAGTAAACCTTCTGTTCAT	540
DB	526	CTGACCGTTAAAGACAGGACTCTATTATCTATGCGGCGCAGTAAACCTTCTGTTCAT	585
QY	541	CGGAGCTTCGAGTCAAGCTCATTATATAGCGAGCCTCTGCCTAAAGTCCCGCGTGA	600
DB	586	CGGAGCTTCGAGTCAAGCTCATTATATAGCGAGCCTCTGCCTAAAGTCCCGCGTGA	645
QY	601	TTGAGAGAACTTCTACTCAGCTGCAATACCCACAGTTCCGCCAAACCTTGGCGGCA	660
DB	646	TTGAGAGAACTTCTACTCAGCTGCAATACCCACAGTTCCGCCAAACCTTGGCGGCA	705
QY	661	CAATCCATTCACTTGGGAGGATTTGTAATTCACCAAGGTCCTCGGTGTTTGTCAAT	720

DB	706	CAATCCATTCACTTGGGAGGATTTGTAATTCACCAAGGTCCTCGGTGTTTGTCAAT	765
QY	721	GTGACTGATCCCAAGCAAGTGGCTTCCAGCTGCTTCCAGCTTCTTGGCTTACTCAA	780
DB	766	GTGACTGATCCCAAGCAAGTGGCTTCCAGCTGCTTCCAGCTTCTTGGCTTACTCAA	825
QY	781	CTCTGA 786	
DB	826	CTCTGA 831	

RESULT 12  
US-09-088-913A-11  
: Sequence 11, Application US/09088913A  
: Patent No. 6087329  
: GENERAL INFORMATION:  
: APPLICANT: ARMITAGE, RICHARD  
: APPLICANT: FANSLAW, WILLIAM  
: APPLICANT: SPRIGGS, MELANIE  
: APPLICANT: SRINIVASAN, SUBHASHINI  
: APPLICANT: GIBSON, MARYLOU  
: APPLICANT: MORRIS, ARVIA E.  
: APPLICANT: MCGREW, JEFFERY  
: TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
: NUMBER OF SEQUENCES: 26  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: IMMUNEX CORPORATION  
: STREET: 51 UNIVERSITY STREET  
: CITY: SEATTLE  
: STATE: WASHINGTON  
: COUNTRY: USA  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: Apple Macintosh  
: OPERATING SYSTEM: Apple Operating System 7.5.5  
: SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/088,913A  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: PRIOR APPLICATION NUMBER: 08/484,624  
: FILING DATE:  
: APPLICATION NUMBER: 08/477,733  
: FILING DATE: June 07, 1995  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/969,703  
: FILING DATE: October 23, 1992  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/805,723  
: FILING DATE: December 5, 1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 07/783,707  
: FILING DATE: October 25, 1991  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Perkins, Patricia A.  
: REGISTRATION NUMBER: 34,693  
: REFERENCE/DOCKET NUMBER: 2802-D  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 2065870430  
: TELEFAX: 2065870606  
: INFORMATION FOR SEQ ID NO: 11:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 840 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: HYPOTHETICAL: NO  
: ANTI-SENSE: NO  
: ORIGINAL SOURCE:



ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-09-088-913A-11

Query Match 95.9%; Score 754; DB 3; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCGGTGGCAACCTGGACTTCCAGCGAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGCCACTGGACTGCCCATCAGC 105

Qy 61 ATGAAGATTTTATGTATTTACTTACTTACTTCTTATCCTTATCACCCTTATCGATCTGTG 120  
Db 106 ATGAAGATTTTATGTATTTACTTACTTCTTATCCTTATCACCCTTATCGATCTGTG 165

Qy 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 180  
Db 166 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 225

Qy 181 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 240  
Db 226 GAAGATTTTGTATTCATGAAACGATACAGAGATGCAACACAGGAGAAAGATCCTTATCC 285

Qy 241 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
Db 286 TTACTGAACTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345

Qy 301 AACAAAGGAGACCAAGAAACACAGCTTTGAAATGCAAAAGGATGATCAGATCTCT 360  
Db 346 AACAAAGGAGACCAAGAAACACAGCTTTGAAATGCAAAAGGATGATCAGATCTCT 405

Qy 361 CAAATTTGGGCGACATGTATAGTGGCGCAGCAGTAAACCAACATCTGTGTACAGTGG 420  
Db 406 CAAATTTGGGCGACATGTATAGTGGCGCAGCAGTAAACCAACATCTGTGTACAGTGG 465

Qy 421 GCTGAAAAGGATACACCATGAGCAACAACTTTGTAACCTTGGAAATGGGAAACAG 480  
Db 466 GCTGAAAAGGATACACCATGAGCAACAACTTTGTAACCTTGGAAATGGGAAACAG 525

Qy 481 CTGACCGTTAAAGACAAAGGACTTATATATCTATGCCCAAGTCACCTTCTGTTCCTCAT 540  
Db 526 CTGACCGTTAAAGACAAAGGACTTATATATCTATGCCCAAGTCACCTTCTGTTCCTCAT 585

Qy 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCCTTAAAGTCCCGCGGTAGA 600  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCCTTAAAGTCCCGCGGTAGA 645

Qy 601 TTCGAGAGAACTTTACTCAGAGCTCAATATACCCAGATTCGCCCAACCTTGGCGGCA 660  
Db 646 TTCGAGAGAACTTTACTCAGAGCTCAATATACCCAGATTCGCCCAACCTTGGCGGCA 705

Qy 661 CAATCCATTCACCTTGGGAGGATTTGAAATGCAACAGGTCCTTGGTGTGTTCTCAAT 720  
Db 706 CAATCCATTCACCTTGGGAGGATTTGAAATGCAACAGGTCCTTGGTGTGTTCTCAAT 765

Qy 721 GTGACTGTATCCAAAGCAAGTGGAGCATGGCCTGCTTCACTGCTTCTTGGCTTACTCAA 780  
Db 766 GTGACTGTATCCAAAGCAAGTGGAGCATGGCCTGCTTCACTGCTTCTTGGCTTACTCAA 825

Qy 781 CTCTGA 786  
Db 826 CTCTGA 831

RESULT 13  
US-08-589-771B-7  
Sequence 7, Application US/08589771B

Patent No. 6106832  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSHAW, WILLIAM  
APPLICANT: RENSLOW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING  
TITLE OF INVENTION: DEFECTIVE CD40L (as amended)  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589,771B  
FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JANIS C.  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-589-771B-7

Query Match 95.9%; Score 754; DB 3; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ATGATAGAACATACAGCAACCTTCCCGCAGATCGGTGGCAACCTGGACTTCCAGCGAGC 60  
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGCCACTGGACTGCCCATCAGC 105

Qy 61 ATGAAGATTTTATGTATTTACTTACTTCTTATCCTTATCACCCTTATCGATCTGTG 120  
Db 106 ATGAAGATTTTATGTATTTACTTACTTCTTATCCTTATCACCCTTATCGATCTGTG 165

Qy 121 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 180  
Db 166 CTTTTTGTCTGTATCTTATAGAGGTTGGACAAGATAGAGATCAAGAGGAATCTTCAT 225

181 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 240  
226 GAAGATTTTGTATTCATGAAACGATACAGAGATCAACACAGGAGAAAGATCCTTATCC 285  
241 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
286 TTACTCAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
301 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360  
346 AACAAAGAGAGACGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405  
361 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
406 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
421 GCTGAAAGAGATACACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAG 480  
466 GCTGAAAGAGATACACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAG 525  
481 CTGACCTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTCCCAAT 540  
526 CTGACCTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAGTCACCTTCTGTCCCAAT 585  
541 CGGAAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 600  
586 CGGAAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCTAAAGTCCCGCGGTAGA 645  
601 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAACTTCGCGGCA 660  
646 TTCGAGAGAACTTTACTCAGAGCTGCAAAATACCCACAGTTTCGCCAACTTCGCGGCA 705  
661 CAATCCATTCACTGGGAGGAGTATTTGAATGCAACCCAGGTCTCGGTGTTTGTCAAT 720  
706 CAATCCATTCACTGGGAGGAGTATTTGAATGCAACCCAGGTCTCGGTGTTTGTCAAT 765  
721 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTTCAGCTTTCGCTTACTCAAA 780  
766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTTCAGCTTTCGCTTACTCAAA 825  
781 CTCGA 786  
826 CTCGA 831

RESULT 14  
US-08-769-819-11  
; Sequence 11, Application US/08769819,  
; Patent No. 6264951  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; CITY: SEATTLE  
; STATE: WASHINGTON  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.1  
; SOFTWARE: Microsoft Word for Apple, version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,819  
; FILING DATE: 19-DEC-1996  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA: 07/969,703  
APPLICATION NUMBER: 07/805,723  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-769-819-11

Query Match 95.9%; Score 754; DB 4; Length 840;  
Best Local Similarity 97.5%; Pred. No. 1.3e-209;  
Matches 766; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGATAGAAACATACAGCCAACTTCCCGCAGATCCGCTGGCAACTGGAGCTTCCAGCGAGC 60  
DB 46 ATGATCGAAACATACAGCCAACTTCTCCCGATCTGCGGCACCTGGAGCTGCGCATCAGC 105  
QY 61 ATGAAGATTTTATGATTTACTTACTGTTTCTTATCACCACCAATGATTGATCTGTG 120  
DB 106 ATGAAAATTTTATGATTTACTTACTGTTTCTTATCACCACAGATGATTGGGTGCA 165  
QY 121 CTTTTTGTGTGATCTTCTTATAGAAAGTTGGCAAGATAGAAGATGAAAGGATCTTCA 180  
DB 166 CTTTTTGTGTGATCTTCTTATAGAAAGTTGGCAAGATAGAAGATGAAAGGATCTTCA 225  
QY 181 GAAGATTTTCTATTGATGAAAGCATACAGAGATGCAACACAGGAGAGAGATCCTTATCC 240  
DB 226 GAAGATTTTCTATTGATGAAAGCATACAGAGATGCAACACAGGAGAGAGATCCTTATCC 285  
QY 241 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 300  
DB 286 TTACTGAACTGTGAGGAGATTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345  
QY 301 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 360  
DB 346 AACAAAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405  
QY 361 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
DB 406 CAATTCGCGCATCTGATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
QY 421 GCTGAAAGAGATACACCATGAGCAACAACTTGGTAACCTGGAAATGGAAACAG 480



Thu May 30 05:46:23 2002

Db 706 CAATCCATTCACTTGGAGGAGTAATTGAATTGCAACCAGGTGCTTCGGTGTTCAT 765  
QY 721 GTGACTGATCCAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 780  
Db 766 GTGACTGATCCAGCCAACTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA 825  
QY 781 CTCTGA 786  
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:51:53  
Job time: 11617 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 02:49:14 ; Search time 6499.83 Seconds  
(without alignments)  
2520.909 Million cell updates/sec

Title: US-08-982-272-20  
Perfect score: 783  
Sequence: 1 ATGATCGAATACACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :	GenEmbl.*
1: gb_ba.*	187864 Sequence 3
2: gb_hgt.*	AR044779 Sequence
3: gb_in.*	AR076926 Sequence
4: gb_om.*	AR078316 Sequence
5: gb_ov.*	AR085419 Sequence
6: gb_pat.*	AR103375 Sequence
7: gb_ph.*	AR106246 Sequence
8: gb_pl.*	AR169232 Sequence
9: gb_pr.*	AR171647 Sequence
10: gb_ro.*	123893 Sequence 1
11: gb_sts.*	127345 Sequence 7
12: gb_sy.*	167828 Sequence 1
13: gb_un.*	AX090039 Sequence
14: gb_vi.*	215017 H.sapiens m
15: em_ba.*	X67878 H.sapiens m
16: em_fun.*	L07414 Human CD40-
17: em_hum.*	X68550 H.sapiens T
18: em_in.*	AF344841 Cercocebu
19: em_mu.*	AF344859 Macaca mu
20: em_om.*	X96710 H.sapiens m
21: em_or.*	AF344860 Aotus tri
22: em_ov.*	AF344844 Callithri
23: em_pat.*	AF013985 Rattus no
24: em_ro.*	AR076918 Sequence
25: em_sts.*	AR078308 Sequence
26: em_sy.*	AR085411 Sequence
27: em_un.*	AR103367 Sequence
28: em_vi.*	AR169224 Sequence
29: gb_ba.*	187865 Sequence 5
30: gb_hgt.*	X65453 M.musculus
31: gb_in.*	AF116582 Rattus no
32: gb_om.*	AR044778 Sequence
33: gb_ov.*	AR171646 Sequence
34: gb_pat.*	AX208160 Sequence
35: gb_ph.*	248469 B.taurus mr
36: gb_pl.*	AF079105 Felis cat
37: gb_pr.*	AF086711 Canis fam
38: gb_ro.*	AR076929 Sequence
39: gb_sts.*	AR078319 Sequence
40: gb_sy.*	AR085422 Sequence
41: gb_un.*	AR103378 Sequence
42: gb_vi.*	AR169235 Sequence
43: em_ba.*	AR076932 Sequence
44: em_fun.*	AR078322 Sequence
45: em_hum.*	AR085425 Sequence

ALIGNMENTS

RESULT	1	786 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	187864	Sequence 3 from patent US 5716805.			
DEFINITION	187864	Sequence 3 from patent US 5716805.			
ACCESSION	187864	GI:3407804			
VERSION	187864.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 786)				
AUTHORS	Srinivasan,S...and Spriggs,M.K.				
TITLE	Methods of preparing soluble, oligomeric proteins				
JOURNAL	Patent: US 5716805-A 3 10-FEB-1998;				
FEATURES	Location/Qualifiers				
source	1..786				
BASE COUNT	250 a	168 c	200 t		
ORIGIN	/organism="unknown"				

Query Match 92.8%; Score 726.8; DB 6; Length 786;  
Best Local Similarity 96.2%; Pred. No. 2,7e-170;

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Query	Match	Length	ID	Description
NO.	Score	Match	Length	ID	Description

JOURNAL		Patent: US 5817516-A 3 06-OCT-1998;	
FEATURES		Location/Qualifiers	
source		1..840	
BASE COUNT		263 a 182 c 181 g 214 t	
ORIGIN		/organism="unknown"	
Query Match		92.8%; Score 726.8; DB 6; Length 840;	
Best Local Similarity		96.2%; Pred. No. 2.7e-170;	
Matches 736; Conservative		0; Mismatches 27; Indels 3; Gaps 1;	
QY	1	ATGATCGAAACATACAAACAACTTCCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC	60
Db	22	ATGATCGAAACATACAAACAACTTCCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC	81
QY	61	ATGAAATTTTATGTATTTACTTTACTTGTCTTCTTATCACCCAGATGATTGGGTGCAGCA	120
Db	82	ATGAAATTTTATGTATTTACTTTACTTGTCTTCTTATCACCCAGATGATTGGGTGCAGCA	141
QY	121	CTTTTTCGTGTATCTTCATAGAAATTCGATTAAGGTTCGAGGAGGAAGTAAACCTTCAT	180
Db	142	CTTTTTCGTGTATCTTCATAGAAATTCGATTAAGGTTCGAGGAGGAAGTAAACCTTCAT	201
QY	181	GAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACAAGGAGAGAGATCTTTATTC	240
Db	202	GAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACAAGGAGAGATCTTTATTC	261
QY	241	TTGCTGTAACCTGTGAGGAGATGAGAGCAATTTTGAAGACCTTGTCAAGGATATAACGTTA	300
Db	262	TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTTGTGAAGGATATAATGTTA	321
QY	301	AACAAGNAGA: --GAAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	357
Db	322	AACAAGAGGAGCAAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT	381
QY	358	CAAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	417
Db	382	CAAAATTGCGGCACATGTCATAAGTGAGCCAGCAGTAAACAACATCTGTGTTACAGTGG	441
QY	418	GCTGAAAGAGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAAATGGGAAACAG	477
Db	442	GCTGAAAGAGATACTACACCATGAGCAACAACCTTGGTAAACCTCGAAAATGGGAAACAG	501
QY	478	CTGACCGTTAAAGAACARAGGACTCTATTATATCTATGCCAAGTCACCTTCGTTCCAAT	537
Db	502	CTGACCGTTAAAGAACARAGGACTCTATTATATCTATGCCAAGTCACCTTCGTTCCAAT	561
QY	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCCCGGTAGA	597
Db	562	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCCTCTGCCTAAAGTCCCCCGGTAGA	621
QY	598	TTGAGAGAAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTCGCGGCA	657
Db	622	TTGAGAGAAATCTTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAACCTTCGCGGCA	681
QY	658	CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAT	717
Db	682	CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGAGTCTTCGGTGTGTTGTCAT	741
QY	718	GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACGTCCTTTGGCTTTACTCAA	777
Db	742	GTGACTGATCCAAAGCAAGTGAAGCCATGGCACTGGCTTCACGTCCTTTGGCTTTACTCAA	801
QY	778	CTCTGA 783	
Db	802	CTCTGA 807	

RESULT	3
AR076926	
Locus	
DEFINITION	840 bp DNA linear PAT 31-AUG-2000 Sequence 11 from patent US 5961974..

ACCESSION AR076926  
VERSION AR076926.1 GI:10003672  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.  
TITLE Monoclonal antibodies to CD40 ligand, pharmaceutical composition comprising the same and hybridomas producing the same  
JOURNAL Patent: US 5961974-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..840

BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATTGGGTTCAGCA 120  
DB 106 ATGAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATTGGGTTCAGCA 165  
QY 121 CTTTTGCTGTGATCTATAGAGATTTGATAGGTTCGAAGGAGGAGTAAACCTTCAT 180  
DB 166 CTTTTGCTGTGATCTATAGAGATTTGATAGGTTCGAAGGAGGAGTAAACCTTCAT 225  
QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAGAGAGGATCTTTATTC 240  
DB 226 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAGAGAGGATCTTTATTC 285  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300  
DB 286 TTACTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 345  
QY 301 AACAAAGAAGAA--GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACCT 357  
DB 346 AACAAAGAGGAGACGAGAAAGAAAGCAAGCTTTGAAATGCAAAAGGTGATCAGAACCT 405  
QY 358 CAATTCGGGACATGTATAGGTGAGGCAAGCTTTGAAATGCAAAAGGTGATCAGAACCT 417  
DB 406 CAATTCGGGACATGTATAGGTGAGGCAAGCTTTGAAATGCAAAAGGTGATCAGAACCT 465  
QY 418 GCTGAAAGAGGATCTACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 477  
DB 466 GCTGAAAGAGGATCTACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 525  
QY 478 CTGACCGTTTAAAGCAAGGAGTCTATATATCTATGATGCCCAAGTCACTCTGTTCCTCAAT 537  
DB 526 CTGACCGTTTAAAGCAAGGAGTCTATATATCTATGATGCCCAAGTCACTCTGTTCCTCAAT 585  
QY 538 CGGGAAGCTTCGAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGGTAGA 597  
DB 586 CGGGAAGCTTCGAGTCAAGCTTCAATTTATAGCCAGCTCTGCCTTAAAGTCCCGCGGTAGA 645  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 657  
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTGGGGGCAA 705  
QY 658 CAATCCATTCCTTGGGAGGAGTATTTGAATTTGAACAGAGTCTCGGTGTTGTCAAT 717  
DB 706 CAATCCATTCCTTGGGAGGAGTATTTGAATTTGAACAGAGTCTCGGTGTTGTCAAT 765  
QY 718 GTGACTGATCCAGCCAAAGTGAGCCATGGCACTGGCTTCAAGTCTTGGCTTACTCAA 777  
DB 766 GTGACTGATCCAGCCAAAGTGAGCCATGGCACTGGCTTCAAGTCTTGGCTTACTCAA 825

QY 778 CTCTGA 783  
DB 826 CTCTGA 831

RESULT 4  
AR078316  
LOCUS AR078316  
DEFINITION Sequence 11 from patent US 5962406.  
ACCESSION AR078316  
VERSION AR078316.1 GI:10005062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE Recombinant soluble CD40 ligand polypeptide and pharmaceutical composition containing the same  
JOURNAL Patent: US 5962406-A 11 05-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATTGGGTTCAGCA 120  
DB 106 ATGAAATTTTATGTATTTACTTACTGTTTTCTTATCACCAGATGATTGGGTTCAGCA 165  
QY 121 CTTTTGCTGTGATCTATAGAGATTTGATAGGTTCGAAGGAGGAGTAAACCTTCAT 180  
DB 166 CTTTTGCTGTGATCTATAGAGATTTGATAGGTTCGAAGGAGGAGTAAACCTTCAT 225  
QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAGAGAGGATCTTTATTC 240  
DB 226 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAGAGAGGATCTTTATTC 285  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300  
DB 286 TTACTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 345  
QY 301 AACAAAGAAGAA--GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAACCT 357  
DB 346 AACAAAGAGGAGACGAGAAAGAAAGCAAGCTTTGAAATGCAAAAGGTGATCAGAACCT 405  
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DB 406 CAATTCGGGACATGTATAGGTGAGGCAAGCTTTGAAATGCAAAAGGTGATCAGAACCT 465  
QY 418 GCTGAAAGAGGATCTACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 477  
DB 466 GCTGAAAGAGGATCTACACCATGAGCAACAACTTTGGTAAACCTTGGAAATGGGAAACAG 525  
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DB 526 CTGACCGTTTAAAGCAAGGAGTCTATATATCTATGATGCCCAAGTCACTCTGTTCCTCAAT 585  
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598 TTCGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 657  
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646 TTCGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTGGGGCAA 705  
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706 CAATCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGCAAT 765  
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778 CTCTGA 783  
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RESULT 5  
AR085419 AR085419 840 bp DNA linear PAT 01-SEP-2000  
LOCUS  
DEFINITION Sequence 11 from patent US 5981724.  
ACCESSION AR085419  
VERSION AR085419.1 GI:10012188  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S.,  
Gibson,M.G., Morris,A.E. and McGrew,J.T.  
TITLE DNA encoding CD40 ligand, a cytokine that binds CD40  
JOURNAL Patent: US 5981724-A 11 09-NOV-1999;  
FEATURES  
Location/Qualifiers  
1..840  
source  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN  
  
Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
  
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGGCCACTGGACTGCCCATCAGC 105  
  
QY 61 ATGAAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120  
DB 106 ATGAAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165  
  
QY 121 CTTTTTGTCTGTATCTTCTATAGAGATTTGATAAGTTCGAAGACCTTGTCAAGGATATAACGTTA 180  
DB 166 CTTTTTGTCTGTATCTTCTATAGAGATTTGATAAGTTCGAAGACCTTGTCAAGGATATAACGTTA 225  
  
QY 181 GAAGATTTTGTATTTATCAAAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTTATCC 240  
DB 226 GAAGATTTTGTATTTATCAAAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTTATCC 285  
  
QY 241 TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 286 TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 345  
  
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DB 346 AACAAAGAAGAAGAAGAAGAAAGCACTTTGAAATGCAAAAAGGTGATCAGATCCT 405  
  
QY 358 CAAATTCGGGCACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 417  
DB 406 CAAATTCGGGCACATGTCTAAGTGGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 465  
  
QY 418 GCTGAAAAGGATATACACCTAGCAACACTTGGTAAACCTTGGAAATGGGAACAG 477  
DB 477 GCTGAAAAGGATATACACCTAGCAACACTTGGTAAACCTTGGAAATGGGAACAG 525

466 GCTGAAAAGGATATACACCTAGCAACACTTGGTAAACCTTGGAAATGGGAACAG 525  
QY 478 CTGACCGTTAAAAAGAGAGAGTCTTATATATCTATGCCCCAAGTACCTTCTGTGTTCCAAAT 537  
DB 526 CTGACCGTTAAAAAGAGAGAGTCTTATATATCTATGCCCCAAGTACCTTCTGTGTTCCAAAT 585  
QY 538 CGGGAAGCTTCGAGTCAAGCTCATTATAGCCAGAGCTCTGCCTAAAGTCCGCCGGTAGA 597  
DB 586 CGGGAAGCTTCGAGTCAAGCTCATTATAGCCAGAGCTCTGCCTAAAGTCCGCCGGTAGA 645  
QY 598 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCCGGGCAA 657  
DB 646 TTCGAGAGAAATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAACCTTCCGGGCAA 705  
QY 658 CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGCAAT 717  
DB 706 CAATCCATTCTTGGGAGGAGTATTTGAATTTGCAACAGAGTGTTCGGTGTTCGCAAT 765  
QY 718 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTGCTTGGCTTGTACTCAA 777  
DB 766 GTGACTGATCCAAAGCAAGTGGAGCCATGGCTGCTTGGCTTGTACTCAA 825  
QY 778 CTCTGA 783  
DB 826 CTCTGA 831  
  
RESULT 6  
AR103375 AR103375 840 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 11 from patent US 6087329.  
ACCESSION AR103375  
VERSION AR103375.1 GI:12814963  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C. and Spriggs,M.K.  
TITLE CD40 ligand polypeptide  
JOURNAL Patent: US 6087329-A 11 11-JUL-2000;  
FEATURES  
Location/Qualifiers  
1..840  
source  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN  
  
Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
  
QY 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGGCCACTGGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGGCCACTGGACTGCCCATCAGC 105  
  
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DB 106 ATGAAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165  
  
QY 121 CTTTTTGTCTGTATCTTCTATAGAGATTTGATAAGTTCGAAGACCTTGTCAAGGATATAACGTTA 180  
DB 166 CTTTTTGTCTGTATCTTCTATAGAGATTTGATAAGTTCGAAGACCTTGTCAAGGATATAACGTTA 225  
  
QY 181 GAAGATTTTGTATTTATCAAAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTTATCC 240  
DB 226 GAAGATTTTGTATTTATCAAAAAAGCTTAAAGATGCAACAAAGGAGAGATCTTTATCC 285  
  
QY 241 TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 286 TTGCTGAACTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 345  
  
QY 301 AACAAAGAAGA ---GAAAAAGAAAAAGCACTTTGAAATGCAAAAAGGTGATCAGATCCT 357



Db 346 AACAAAGGAGAGACCAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAATCCT 405  
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Db 406 CAAATTCGGGCACATGTCTAAGTGAGCCAGCAGTAAACAAACATCTGTCTTACAGTGG 465  
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Qy 538 CGGGAAGCTTCGAGTCAAGCTTCAATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 597  
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Qy 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTTCGCGGCAA 657  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTTCGCGGCAA 705  
Qy 658 CAATCCATTCATTCGGGAGGAGTATTCATTTGCAACAGAGTCTCGGTCTTTGTCTCAAT 717  
Db 706 CAATCCATTCATTCGGGAGGAGTATTCATTTGCAACAGAGTCTCGGTCTTTGTCTCAAT 765  
Qy 718 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCCTTTCAGCTCTTTCGCTTACTCAAA 777  
Db 766 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCCTTTCAGCTCTTTCGCTTACTCAAA 825  
Qy 778 CTCTGA 783  
Db 826 CTCTGA 831

RESULT 7  
AR106246  
LOCUS AR106246 840 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 7 from patent US 6106832.  
ACCESSION AR106246  
VERSION AR106246.1 GI:12820776  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.  
TITLE Treatment of individuals exhibiting defective CD40L  
JOURNAL Patent: US 6106832-A 7 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGGGCACTGGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGGGCACTGGACTGCCCATCAGC 105  
Qy 61 ATGAAATTTTATGTATTTACTTACTGTCTTTTCTTATCACCAGATGATTGGGTACAGCA 120  
Db 106 ATGAAATTTTATGTATTTACTTACTGTCTTTTCTTATCACCAGATGATTGGGTACAGCA 165  
Qy 121 CTTTTTGTGTGTATCTTCTATAGAGATTTGGATAAGTTCGAAGAGAGAAAGTAAACCTTCAT 180  
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Qy 181 GAAGATTTTGTATTATCAAAAAAGCTAAAGAGATCAACAAAGAGAGATCTTTTATCC 240  
Db 236 GAAGATTTTGTATTATCAAAAAAGCATACAGAGATCAACACAGAGAAAGATCTTTATCC 285  
Qy 241 TTGCTGAATGTGAGGAGATGAGAAGGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300  
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Qy 418 GCTGAAAGAGATACACCATGAGCAACAACTTGGTAAACCCCTGGAAATGGGAAACAG 477  
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Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGGTAGA 597  
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Qy 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCCCAAAACCTTTCGCGGCAA 657  
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Qy 658 CAATCCATTCATTCGGGAGGAGTATTTGAATTCGAAACAGAGTCTTCGGTCTTTGTCTCAAT 717  
Db 706 CAATCCATTCATTCGGGAGGAGTATTTGAATTCGAAACAGAGTCTTCGGTCTTTGTCTCAAT 765  
Qy 718 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCCTTTCAGCTCTTTCGCTTACTCAAA 777  
Db 766 GTGACTGATCCAAAGCAAGTGGCAGTGGCAGTGGCCTTTCAGCTCTTTCGCTTACTCAAA 825  
Qy 778 CTCTGA 783  
Db 826 CTCTGA 831

RESULT 8  
AR169232  
LOCUS AR169232 840 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 11 from patent US 6290972.  
ACCESSION AR169232  
VERSION AR169232.1 GI:17907047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 840)  
AUTHORS Armitage,R.J., Fanslow,W.C., Spriggs,M.K., Srinivasan,S. and Gibson,M.G.  
TITLE Method of augmenting a vaccine response by administering CD40 ligand  
JOURNAL Patent: US 6290972-A 11 18-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..840  
BASE COUNT 266 a 185 c 175 g 214 t  
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-170;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACACCAAACTTCTCCCGGATCTGGGGCACTGGACTGCCCATCAGC 60

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Best Local Similarity	96.2%; Pred. No. 2.7e-170;				
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QY	61	ATGAAATTTTATGATTTTACTTACTGTTTTCCTATCACCAGATGATTTGGTGACGA	120		
DB	82	ATGAAATTTTATGATTTTACTTACTGTTTTCCTATCACCAGATGATTTGGTGACGA	141		
QY	121	CTTTTTCCTGTGATCTTTCATAGAAGATTGGATAAGCTCGAAGAGGAAAGTAACCTTCAT	180		
DB	142	CTTTTTCCTGTGATCTTTCATAGAGTTGGACAAGATAGAAGATGAAGAAATCTTCAT	201		
QY	181	GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAGAGAGAAGATCTTATCC	240		
DB	202	GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAGAGAGAAGATCTTATCC	261		
QY	241	TTGCTGAACCTGTGAGGAGATGAGAAGCAATTGGAAGACCTTGTCAAGGATATAACGTTA	300		
DB	262	TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA	321		
QY	301	AACAAGAGA --GAAAGAAACACAGCTTTGAATGCAAAAAGGTGATCAGAACTCT	357		
DB	322	AACAAGAGGAGAGAGAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	381		
QY	358	CAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGG	417		
DB	382	CAAAATTCGGGCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTACAGTGG	441		
QY	418	GCTGAAAAGGATACATACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAG	477		
DB	442	GCTGAAAAGGATACATACCATGAGCAACAACCTTGGTAACCTGGAAAATGGGAAACAG	501		
QY	478	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTTCCAAT	537		
DB	502	CTGACCGTTAAAGACAGGACTCTATTATATCTATGCCCAAGTCACCTCTCTGTTCCAAT	561		
QY	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	597		
DB	562	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGGTAGA	621		
QY	598	TTGAGAGAATCTTACTCAGAGCTCCAAATACCCACAGTTCGCGCAAACTTTGCGGGCAA	657		
DB	622	TTGAGAGAATCTTACTCAGAGCTCCAAATACCCACAGTTCGCGCAAACTTTGCGGGCAA	681		
QY	658	CAATCCATTCACCTTCGGGAGGAGTATTGAAATGCAACCAGGTGCTTCGGTGTGTTGTCAT	717		

QY	718	GTGACTGATCCAAAGCCCAAGTGAAGCCTGGCACTGGCTTCACGTCTCTTGCGCTTACTCAA	777
Dd	742	GTGACTGATCCAAAGCCCAAGTGAAGCCTGGCACTGGCTTCACGTCTCTTGCGCTTACTCAA	801
QY	778	CTCTGA 783	
Dd	802	CTCTGA 807	
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DEFINITION	Sequence 1 from patent US 5540926.		
ACCSSION	I23893		
VERSION	I23893.1 GI:1603763		
KEYWORDS			



Thu May 30 05:45:51 2002

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Db 706 CAATCATTACCTTGGAGGAGTATTGCAATTGCAACAGGTGCTTGGTGTCTCAAT 765
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Db 766 GTGACTGATCCAAAGCAAGTGGACCTGCTTACGCTCTTGGCTTACTCAAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

RESULT 12
LOCUS I67828 840 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 1 from patent US 5674492.
ACCESSION 167828
VERSION 167828.1 GI:2829950
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 840)
AUTHORS Armitage, R.J., Fanslow, W.C. III, Longo, D.L. and Murphy, W.J.
TITLE Method of preventing or treating disease characterized by
neoplastic cells expressing CD40
JOURNAL Patent: US 5674492-A 1 07-OCT-1997;
FEATURES
Location/Qualifiers
source
1..840
/organism="unknown"
BASE COUNT 266 a 185 c 175 g 214 t
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 840;
Best Local Similarity 96.2%; Pred. No. 2.7e-170;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGCCACTGGACTGCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATGGGTGACGA 120
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QY 121 CTTTGTGCTGTATCTTCATAGAGATTTGGATAGGTTCGAGAGAGATTAACCTTCAT 180
Db 166 CTTTGTGCTGTATCTTCATAGAGATTTGGACAGATGATGAAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTTCATTAAGAGCTTAAGAGATGCAACAAAGAGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTTCATTAAGAGCTTAAGAGATGCAACAAAGAGAGAGATCTTATCC 285
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300
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QY 301 AACAAAGAGA ---GAAAAGAGAAACAGCTTTGAATGCAAAAGGTGCATCAGATCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
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QY 418 GCTGAAAAGAGGATACACCATGAGCAACAACTTGGTAAACCTTGAAGTGGGAACAG 477
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Db 826 CTCTGA 831

RESULT 13
LOCUS AX090039 879 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 1 from Patent WO0116180.
ACCESSION AX090039
VERSION AX090039.1 GI:13444004
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 879)
AUTHORS Ahuja, S.U. and Bonewald, L.U.
TITLE CD40 agonist compositions and methods of use
JOURNAL Patent: WO 0116180-A 1 08-MAR-2001;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES
Location/Qualifiers
source
1..879
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BASE COUNT 274 a 193 c 190 g 222 t
ORIGIN

Query Match 92.8%; Score 726.8; DB 6; Length 879;
Best Local Similarity 96.2%; Pred. No. 2.7e-170;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

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QY 241 TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300
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QY 301 AACAAAGAGA ---GAAAAGAGAAACAGCTTTGAAATGCAAAAGGTGCATCAGATCCT 357
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742 GTGACTGATCCAAAGCAAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 801
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778 CTCCTGA 783
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802 CTCCTGA 807

RESULT 14
HSGP39MR      HSGP39MR      879 bp      mRNA      linear      PRI 01-SEP-1996
LOCUS
DEFINITION H.sapiens mRNA for glycoprotein 39 (gp39).
ACCESSION 215017 S49392
VERSION 215017.1 GI:38483
KEYWORDS glycoprotein 39.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Hollenbaugh, D., Grosmaire, L.S., Kullas, C.D., Chalupny, N.J.,
            Braesch-Andersen, S., Noelle, R.J., Stamenkovic, I., Ledbetter, J.A.
            and Aruffo, A.
TITLE The human T cell antigen gp39, a member of the TNF gene family, is
            a ligand for the CD40 receptor: expression of a soluble form of
            gp39 with B cell co-stimulatory activity.
            EMBO J. 11 (12), 4313-4321 (1992)
JOURNAL 93049181
MEDLINE 2 (bases 1 to 879)
REFERENCE Hollenbaugh, D.L.
            Direct Submission
            Submitted (27-AUG-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
            PRI, Seattle, WA, 98121
JOURNAL 3 (bases 1 to 879)
REFERENCE Hollenbaugh, D.
            Direct Submission
            Submitted (21-SEP-1992) Diane L Hollenbaugh, Bristol-Myers Squibb
            PRI, Seattle, WA, 98121
JOURNAL The original submission [1] reported 934bp.
            Location/Qualifiers
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CDS

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LTVRKQGLYIYIAQVTFCSNREASQAPFIASLCLKSPREFRILLRAANTHSSAKPC
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BASE COUNT 274 a 193 c 190 g 222 t
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Best Local Similarity 96.2%; Pred. No. 2.7e-170;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
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Db 82 ATGAAAATTTTATGTTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 141
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QY 121 CTTTTTGTGTGTATCTTCTATAGAGATTTGGAATAGGTGCGAAGAGAGAACTTCAAT 180
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QY 181 GAAGATTTTGTATTCATTAATAAGCTTAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240
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QY 358 CAAATTCGGGCACATGTCTATAAGTGAAGGCGCAGCAGTAAACCAACATCTCTGTGTACAGTGG 417
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Db 442 GCTGAAAAGGATACATACACATGAGCAACAACTTGGTAAACCCCTGGAAAATGGGAAACAG 501
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QY 718 GTGACTGATCCAAAGCAAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 777
      |||
Db 742 GTGACTGATCCAAAGCAAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGT 801
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778 CTCCTGA 783
      |||
802 CTCCTGA 807

RESULT 15

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Search completed: May 30, 2002, 02:49:21.  
Job time: 22040 sec

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LOCUS	830 bp		
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ACCESSION	X67878.S50586		
VERSION	X67878.1 GI:38411		
KEYWORDS	glycoprotein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	Spriggs M.		
JOURNAL	Direct Submission		
TITLE	Submitted (28-JUL-1992) M. Spriggs, Immunex Res & Development Corporation, 51 University Street, Seattle WA 98101, USA		
REFERENCE	2 (bases 1 to 1803)		
AUTHORS	Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N., Macduff B.M., Sato T.A., Maliszewski C.R. and Fanslow W.C.		
TITLE	Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion		
JOURNAL	J. Exp. Med. 176 (6), 1543-1550 (1992).		
MEDLINE	93094757		
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Best Local Similarity	96.2%; Pred. No. 2.6e-170;		
Matches	756; Conservative 0; Mismatches 27; Indels 3; Gaps:		
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Qy	61 ATGAAATTTTATGTATTACTTACTGTTTTTCTTATCACCCAGATGATTGGGTACGA 120		
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	106 ATGAAATTTTATGTATTACTTACTGTTTTTCTTATCACCCAGATGATTGGGTACGA 165		
Qy	121 CTTTTTCCTGCTATCTTCATAGAAGATTGGATAAGGTGCGAAGAGAGTAACCTTCAT 180		
Db			
	166 CTTTTTCCTGCTATCTTCATAGAAGTTGGACAAGATAGAAAGATGAAAGGAATCTTCA 225		
Qy	181 GAAGATTTTGTATCATAAAAGCTTAAAGAGATGCACAAAGAGAGAAGGATCTTTATPC 240		
Db			
	226 GAAGATTTTGTATCATGAAACATACAGATGCACACAGAGAAAGATCTTTATCC 285		
Qy	241 TTGCTGAACCTGTGAGGAGATGAGAAGCCAAATTGGAAGACCTTGTCAAGGATATAAGTTA 309		
Db			
	286 TTACTGAACCTGTGAGGAGATTAAGAACGCCAGTTTGAAGGCTTTGTCAAGGATATAAGTTA 345		
Qy	301 AACAAAGNAG-- --GAAAAGAAAAACAGCTTTGAAATGCAAAAAGAGGTGATCAGAATCCT 357		
Db			
	346 AACAAAGAGGAGACACAGAAAGAAACAGCTTTGAAATGCAAAAAGAGGTGATCAGAATCCT 405		
Qy	358 GAAATTCGGGCACATGTCATAAGTGGGCCAGCAGTAAACAACATCTGTGTTCAGTAGG 417		

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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 01:00:16 ; Search time 5112.58 Seconds  
(without alignments)  
2067.081 Million cell updates/sec

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Perfect score: 783  
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Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31.8	42.4	492	10	BF599437 263218 MA
2	256.4	32.7	398	9	AW486605 75217 MAR
3	69.6	8.9	638	9	AI982044 pat.pk007
4	54	6.9	797	9	AL534423
5	52	6.6	1101	12	CNS00039G
6	51.4	6.6	1043	12	CNS0145P
7	50.8	6.5	889	12	CNS006MT
8	50.2	6.4	997	12	CNS005TE
9	48	6.1	807	12	CNS0119V
10	47.4	6.1	799	12	CNS011SA
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13	46.2	5.9	858	12	CNS0127J
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17	45.8	5.8	597	9	AL514721

C 18	45.6	5.8	974	12	CNS00ITT
C 19	45.4	5.8	1084	12	CNS021NO
C 20	45.2	5.8	458	9	AL514085
C 21	45.2	5.8	559	12	AQ373239
C 22	45	5.7	633	9	AL513979
C 23	45	5.7	878	12	CNS0187R
C 24	44.6	5.7	534	12	CNS03DHB
C 25	44.4	5.7	814	12	AZ203738
C 26	44.4	5.7	828	12	CNS011YX
C 27	44.2	5.6	805	9	AI557564
C 28	44.2	5.6	959	12	CNS00655
C 29	44	5.6	802	12	CNS0383B
C 30	43.8	5.6	330	9	AL513817
C 31	43.8	5.6	901	12	CNS02PN3
C 32	43.8	5.6	1099	12	CNS06PVL
C 33	43.6	5.6	588	12	AQ451757
C 34	43.6	5.6	629	12	CNS04EYX
C 35	43.6	5.6	920	12	AZ691914
C 36	43.6	5.6	926	12	CNS006YV
C 37	43.4	5.5	472	12	AZ045586
C 38	43.4	5.5	596	10	BF558745
C 39	43.4	5.5	625	12	CNS036A2
C 40	43.4	5.5	899	12	CNS00D8F
C 41	43.4	5.5	955	12	BH136744
C 42	43.2	5.5	644	12	AG134982
C 43	43	5.5	277	12	CNS00DFP
C 44	43	5.5	468	9	AL514541
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## ALIGNMENTS

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LOCUS 263218 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION BF599437  
ACCESSION BF599437.1 GI:11695919  
VERSION BF599437.1  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 492)  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGAC  
Plate: 33 row: N column: 5  
Seq primer: ATTTAGGTGACACTAG.  
Location/Qualifiers  
1. 492  
/organism="Bos taurus"  
/db\_xref="taxon:9913"



Thu May 30 05:45:58 2002

Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@mail.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAAACAGCTATGACCAAT  
BACKWARD: GTTTCCTCCAGTCACGACG  
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Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."  
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Matches 297; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
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QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATACGTTA 300  
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AI982044  
LOCUS  
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VERSION  
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SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE

AI982044 638 bp mRNA linear EST 07-MAY-2001  
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AI982044  
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EST  
chicken.  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 638)  
Tirunagaru.V.G., Sofer,L., Cui,J. and Burnside,J.  
An expressed sequence tag database of T-cell-enriched activated  
chicken splenocytes: sequence analysis of 5251 clones  
Genomics 66 (2): 144-151 (2000)  
20318616

Thu May 30 05:45:58 2002

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Library made from pooled tissue from marrow, alveolar  
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BASE COUNT 163 a 103 c 104 g 122 t  
ORIGIN

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Best Local Similarity 85.5%; Pred. No. 3.9e-56;  
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QY 61 ATGAAATTTTATGATTTTACTTTTCTTATCACCAGATGTTGGGTACGCA 120  
DB 106 ATGAAATTTTATGATTTTACTTTTCTTATCACCAGATGTTGGGTACGCG 165  
QY 121 CTTTGTGCTGATCTTCATAGAGATTTGATTAAGTTCGAAGAGAGTAACCTTCAT 180  
DB 166 CTTTGTGCTGATCTTCATAGAGATTTGATTAAGTTCGAAGAGAGTAACCTTCAT 225  
QY 181 GAAGATTTTATGATTTTATGATTTTACTTTTCTTATCACCAGATGTTGGGTACGCA 240  
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DB 346 AACAAAGAGTAAGAAGAAAGAAACCTTTGAAATGCAACAAAGGAGAGGCTTATCC 405  
QY 358 CAATTTGGCGCACATGTCATAGTGAAGCGGAGGAGTAAACACATCTGTGTACAGTGG 417  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

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AW486605  
AW486605.1 GI:7056711  
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 398)  
Smith,T.P.L., Freking,W.M., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,  
Perlee,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
Keefe,J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4): 626-630 (2001)  
21180013  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA.



## COMMENT

Contact: Joan Burnside  
Molecular Endocrinology  
University of Delaware  
40 Townsend Hall, Newark, DE 19717, USA  
Tel: 302-831-1345  
Fax: 302-831-3411  
Email: joan@udel.edu, www.chickest.udel.edu  
Seq primer: 17.

## FEATURES

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Best Local Similarity 57.6%; Pred. No. 0.00038;  
Matches 167; Conservative 0; Mismatches 114; Indels 9; Gaps 2;  
QY 495 AGGACTCTATTATCTATCCCAAGTCACCTTCTCTGTTCCAAATCGGGAAGCTTCGAGTCA 554  
Db 2 AGGCTCTACTACTACTACTACAGTTCAGCTTCTGCAACCAAGCGCGGCTTCG----- 56  
QY 555 AGCTCATTTATAGCAGCCTCTGCTTAAAGTCCCGGGTAGATTTCAGAGAGATCTTACT 614  
Db 57 -GGCCATTACCTCTATATTTATTTGTACCTCCCATGGAAGAGCGGCTCTCTGAT 115  
QY 615 CAGAGTGCAAAATACCCACAGTTCGCGCAACCT---TGCGGGCAACAATCCATTCACTT 671  
Db 116 GAAGGACTTGACAGCAGCAGCAGCTCCAGGCTCTCTGTGAGCTCAGTCCATCCGGGA 175  
QY 672 GGGAGGAGTATTTGAATGTCAACAGGTGCTTCGGTGTGTTGTCAGTGAAGTCAAG 731  
Db 176 GGGCGGTGCTTCGAGTGGCGGAGCGACATGGTCTTTGTCAATGTGACGGACTCAAC 235  
QY 732 CCAAGTGAGCATGGCAGTGGCTTCAGTCTGCTTGGCTTACTCAACTCT 781  
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## RESULT 4

AL534423 797 bp mRNA linear EST 13-FEB-2001  
LOCUS AL534423 LTI\_FL013\_FBrnl Homo sapiens cDNA clone CS0DF004YD24 5  
DEFINITION prime, mRNA sequence.

ACCESSION AL534423.1 GI:12797916

VERSION AL534423

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 797)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .797

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DF004YD24"

/clone\_lib="LTI\_FL013\_FBrnl"

## FEATURES

source

/dev\_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"  
/lab\_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 407 a 43 c 120 g 152 t 75 others  
ORIGIN

Query Match 6.9%; Score 54; DB 9; Length 797;  
Best Local Similarity 39.3%; Pred. No. 0.45;  
Matches 168; Conservative 35; Mismatches 225; Indels 0; Gaps 0;

QY 140 ATAGAAGATTGGATAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTTGTATTCTATAA 199  
Db 240 AGAAGAAWAAAAAAWATTTAAAAAGAAAAAATAATTAATGAAAAAGAAAAATAA 299  
QY 200 AAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTCTGCTGAACTGTGAGGAGA 259  
Db 300 AGGAAAAATTTAAAAAAGTAAATTAATTTAAATTTAAATTTAAATTTAAATTTAA 359  
QY 260 TGAGAAGGCAATTTGAAGACCTTGTCAAGGATATTAAGCTTTAAACAAGAGAGAAAAAG 319  
Db 360 TGRAWAAAGAGGAAAGGAAAGAAATTAATGAATAAAAAAAGAAAAAARGAAAAA 419  
QY 320 AAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCTCAAAATTCGCGCACATGTCATA 379  
Db 420 AAAAAAGTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 479  
QY 380 GTGAGGCGCAGAGTAAACACATCTGTGTACAGTGGGTGAAAAAGGATGATACACCA 439  
Db 480 AAGGARATGGAATAATGAATTAATAAAAAATTAATAAAWAAAAAATAATTTGAAAAA 539  
QY 440 TGACCAACAACCTTGGTAACCTCGAAATGGAACAGCTGACCTTAATAAGACAAGGAC 499  
Db 540 TAAAAAATWAAAAATGAAAWGAAAAAAGAAAAAATAATTAATAAAAAAAGAAAAA 599  
QY 500 TCTATTATATCTATGCCCAAGTACCTTCTGTTCCAAATCGGGAAGCTTCGAGTCAAGCTC 559  
Db 600 MTATTCCTTTTMMTMTAAAGMMMTTMMTTTMMTMMTMTTCCCAATTTTATTTTGT 659  
QY 560 CATTTATA 567  
Db 660 TMTMMMTA 667

## RESULT 5

CNS0039G/c

LOCUS

DEFINITION

BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.

ACCESSION AL063921

VERSION AL063921.1 GI:4941778

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

TITLE

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr





Thu May 30 05:45:58 2002

ACCESSION	AL099997	fly), genomic survey sequence.	
VERSION	AL099997.1	GI:5611608	
KEYWORDS	GSS.		
SOURCE	fruit fly.		
ORGANISM	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 807)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.		
FEATURES	Location/Qualifiers		
source	1..807		
	organism="Drosophila melanogaster"		
	/plasmid="pBelobAC11"		
	/db_xref="taxon:7227"		
	/clone_lib="DrosBAC"		
	/clone="BACN05C05"		
	/note="end : 17"		
BASE COUNT	157 a	38 c	17 g
ORIGIN			287 t 308 others

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Query Match          6.1%; Score 48; DB 12; Length 807;
Best Local Similarity 27.1%; Pred. No. 6.9; Mismatches 0; Gaps 0;
Matches 117; Conservative 88; Pseudomismatches 227; Indels
68 TTTTATGTAATTACTACTACTGTTTTCTTATCACCCAGATGATGGTCAGACACTTTTG 127
11111 1111 11 11111 11 11 11 11 11 11 11 11 11 11 11 11 11 11
315 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 374
128 CTGTGTATCTTCATAGAGATTGGATAGGTCGAAGAGGAAGTAAACCTTCATGAAGATT 187
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
375 NNNNTNNNTTTTATTTATTTATTAATTAAGAAANCAANGNWTGNNTTTNNNNNTNN 434
188 TTGTATTCTATAAAAAAGCTAAAGAGATGCACAAAGGAGAGAGGATCTTATCTCTCTGA 247
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
435 NTNNNTNTNTTTCMSCCCRSACACASGCMCASGCVGMSSVAMAGMAAMSAVTSAMAS 494
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
248 ACTGTGAGAGATGAGAGAGCAATTTGAAGACCTTTCTCAAGGATATAACCTTAAACAAAG 307
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
495 MSARMAAVAVSARRARAASAGVSVVAVSVSVSVSVSVSVSVSVSVSVSVSVSVSVSV 554
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
308 AAGAGAAAAAGAAACACAGCTTTTGAATTCGAAAAAGGTGATCAGAAATCCTCAAAATGCGG 367
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
555 AAAAAAASAAAAAAMACMACAVNMTACMCMAACCMCYAVSAAHAAHAAVAAASASAMAM 614
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
368 CATCTCTATAAGTGAGGCGCAGCATAAACACATCTGTGTTTACATGTGGGCTGAAAAG 427
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
615 AMVAVVASASASASAMASAAASNSSVSVASAASAVAVANSAASASASAAHAAVAAVAA 674
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
428 GATACTACCATGAGCAGCAACACTTGGTAAACCTGGGAAAAATGGGAAACACCTGACCGCTTA 487
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
675 MACACVMSMWCAACAMCACACACACMACAMCMMTMACCMCCSSMASSSNAASASYVTIV 734
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
488 AAAGACAAGGAC 499
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
735 HABMTSASMSAV 746
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
RESULT 10

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CNS001ISA
LOCUS .....
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

FEATURES  
source

BASE COUNT	333 a	123 c	104 g	140 t	99 others
ORIGIN					

Query Match	6.1%;	Score 47.4;	DB 12;	Length 799;	
Best Local Similarity	35.9%;	Pred. No. 9.1;			
Matches 139;	Conservative 48;	Mismatches 200;	Indels 0;	Gaps 0;	

QY	140	ATAGAAGATTGGATPAAGTCGAAGAGGAGTAAACCTTCATGAAGATTTTGTATTCATAA	199
DB	13	AAAGAAGAWAAAAHAATAAAACAAAAAAWAAWAAATTTAAWMTATGGGAW	72
QY	200	AAAAGCTTAAAGAGATGCAACAAGGAGGAAGATCTTTATCCTTCCTGCACTGTGAGGAGA	259
DB	73	AWATMMCAAMWAWATAMCAWAAAAAAWAAAGGGAAAAAAWAAWAAWATATATANWAA	132
QY	260	TGAGAAGCAATTTGAAGACCTTTGTCAGGATATAACGTTAAACAAAGCAAGAGAAAAAAG	319
DB	133	AAATAAAAAWAAAAWAAAAACWAAAAAAWAAAGCWAACAAAGWAAWAAWMAAAWAGAW	192
QY	320	AAAACAGCTTTGAAATGCAAAAAGGTGATCAGATPCTTCAAATTCGGCGCATGTCTATAA	379
DB	193	AAAAAAACWCGAAATWATAWAAAAAAGCWAACAAWAAATPAGAAAAACAWAAWATAAAMAAAAA	252
QY	380	GTGAGGCGCAGATTAACACACATCTGTGTACAGTGGCTGAAAAAGGATACTACACCA	439
DB	253	AAAAAAWAAAAAAWMAAATAAACAWMGWAWACAAWAAACAAAAWMAAAAAWMAA	312
QY	440	TGAGCAACAACTTGGTAAACCCCTGGAAAAATGGGAAACAGCTGACCGTTTAAAGACAAGAC	499
DB	313	AAAAAAWAAAAAAWMAAAWAAAAATRTAAAAAAWAAAAAAGGAMMCAAAAAA	372
QY	500	TCTATTATATCTATGCCCAAGTCACCT	526
DB	373	AWAAAAATAAAACACGGAAACMCRCAT	399

RESULT 11

RESULT 11

AL514085/c  
LOCUS  
DEFINITION AL514085 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CL0BA004ZE10 3  
prime, mRNA sequence.  
ACCESSION AL514085  
VERSION AL514085.1 GI:12777579  
KEYWORDS EST.  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 458)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
Location/Qualifiers  
1..458  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CL0BA004ZE10"  
/clone\_lib="LTI\_NFL006\_PL2"  
/tissue\_type="placenta"  
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 207 t 49 others  
ORIGIN

Query Match 6.08; Score 46.8; DB 9; Length 458;  
Best Local Similarity 42.58; Pred. No. 14;  
Matches 117; Conservative 14; Mismatches 144; Indels 0; Gaps 0;

Qy 68 TTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTGCAGCACTTTTGG 127  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 304 TTTTATGATTTTWWTTCTTTTYYTYYTYYTYYTYYTYYTYYTYYTYYTYYT 245  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 128 CTGTGATCTTCATAGAGATTGATAGGTCGAAGAGAGTAACCTTCATGAAGATT 187  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 244 TTTTATGATTTTAAAGCAAGGTCGGGAAAAAANNNNNNNNNNNNNNNNNNN 185  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 188 TTGATTCATAAAAAGCTAAGAGATGCAACAAGAGAGAGATCTTATCCTGCTGA 247  
||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 184 AATAAATAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 125  
||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 248 ACTGTGAGGAGATGAGAGGCAATTTTGAAGACCTTGTCAAGGATATACGTTAAACAAG 307  
||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 124 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 65  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 308 AAGAGAAAAAAGAACAGCTTTTGAATGCAAAAA 342  
||| ||||| ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 64 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 30  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

RESULT 12  
CNS015HX/c  
LOCUS  
DEFINITION CNS015HX melanogaster genome survey sequence T7 end of BAC  
BACN14C18 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL105471  
VERSION AL105471.1 GI:5617485

CNS015HX  
LOCUS  
DEFINITION CNS015HX melanogaster genome survey sequence T7 end of BAC  
BACN14C18 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL105471  
VERSION AL105471.1 GI:5617485

GSS.  
fruit fly.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1064)  
Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelOBAC11.  
Location/Qualifiers  
1..1064  
/organism="Drosophila melanogaster"  
/plasmid="pBelOBAC11"  
/db\_xref="taxon:7227"  
/clone\_lib="DrosBAC"  
/clone="BACN14C18"  
/notes="end : T7"

BASE COUNT 262 a 216 c 154 g 263 t 169 others  
ORIGIN

Query Match 5.98; Score 46.4; DB 12; Length 1064;  
Best Local Similarity 32.48; Pred. No. 13;  
Matches 93; Conservative 61; Mismatches 133; Indels 0; Gaps 0;

Qy 207 AAAGAGATGCAACAAAGAGAGAGAGATCTTATCTCTGCTGAACCTGTGAGGAGATGAGAG 266  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 968 AARRWADKGRAAAAGAAAGAAWTTTWTWTWTWTWTWTWTWTWTWTWTWTWT 909  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 267 GCAATTTGAAGACCTTGTCAAGGATATACGTTAAACAAAGAGAGAGAGAGAGAGAG 326  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 908 RRRRDDDDAAAAGGKKKTTWWTTTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 849  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 327 CTTTGAATGCAAAAGGTGATGAGATCTCAATCTCGGCACATGTCATAGTGAGGC 386  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 848 TTBGGAGGGGGTWWCNGDITAKKDAATTAMATTGGTMMAGTGCANATTATGRARA 789  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 387 CAGCAGTAAACACACATCTGTGTACAGTGGCTGAAAGAGTACTACACCATGAGCAA 446  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 788 KGRAAADAKKKGAG 729  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

Qy 447 CACTTGGTAACCTCGGAAATGGAACACAGCTGACCGTTAAAGAC 493  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||  
Db 728 TTTACCGCAAGCAARGKKDKKVVAAAGGGGSGSCMTMTAATGGAC 682  
||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| ||| : : |||||

RESULT 13  
CNS0127J  
LOCUS  
DEFINITION CNS0127J melanogaster genome survey sequence T7 end of BAC  
BACN07D07 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL101209  
VERSION AL101209.1 GI:5612820  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 858)  
Genoscope.

**TITLE**  
JOURNAL

**COMMENT**

**FEATURES**  
source

**BASE COUNT**  
ORIGIN

**Query Match**  
Best Local Similarity 5.9%; Score 46; DB 12; Length 1101;  
Matches 82; Conservative 134; Mismatches 184; Indels 0; Gaps 0;

**QY** 74 TGTATTACTTACTTCTTTTATCACCAGATGTTGGTTCAGCAGCTTTTCTCTGT 133  
Db 630 YBKTTTBTGTTTCTTGGGTYTTTGYGAGVGTCTTCTGKGGTCTTTTCTTTTCT 689  
QY 134 ATCTTCATAGAGATTCGATAGCTGCAAGAGAGAACTTCATCAAGATTTCTAT 193  
Db 690 MAAADARGAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAGVAG 749  
QY 194 TCATAAAAAAGCTTTTCAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 253  
Db 750 WAAAAAAG 809  
QY 254 AGGAGATGAG 313  
Db 810 GRR 869  
QY 314 AAAAAAG 373  
Db 870 RRR 929  
QY 374 TCATAAGTGGCCAGCAGTAAACACATCTGCTTACAGTGGCTGAAAGAGAGACT 433  
Db 930 RRR 989  
QY 434 ACACCATGAGCAACCACTTGTGTAACCTTGAACCTTGAACCTTGAACCTTGAAC 473  
Db 990 GARRRAAGRRARR 1029

**RESULT** 15  
AL513719 329 bp mRNA linear EST 13-FEB-2001  
LOCUS AL513719 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CU0BA007ZH01 3  
DEFINITION prime, mRNA sequence.  
ACCESSION AL513719  
VERSION AL513719.1 GI:12777213  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 329)  
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
JOURNAL Full-length cDNA libraries and normalization  
Unpublished (2001)

**TITLE**  
JOURNAL

**COMMENT**

**FEATURES**  
source

**BASE COUNT**  
ORIGIN

**Query Match**  
Best Local Similarity 5.9%; Score 46.2; DB 12; Length 858;  
Matches 141; Conservative 41; Mismatches 199; Indels 0; Gaps 0;

**QY** 140 ATAGAAGTTGGTAAAGTTCGAGAGAGAGTAAACCTTCATGAAGATTTTGTATTCA 199  
Db 39 ATATAAAAAAAMMGAAGAAAAAACAACAAAMMMAAAMMMAAAMMMAAAMMMAA 98  
QY 200 AAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTTCTTCTGCTGCTGAGGAGA 259  
Db 99 GAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 158  
QY 260 TGAGAGGCAATTTGAGACCTTCTCANGATATACGTTTAAACAAAGAGAGAGAGAG 319  
Db 159 AAAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 218  
QY 320 AAAACAGCTTTGAAATGCAAAAGAGTGCATCAATCTTCAATTTGGGCGCATAT 379  
Db 219 AAAAAAG 278  
QY 380 GTAGGCGCAGTAAACACATCTGTTTACAGTGGCTGAAAGAGAGAGAGAGAGAGAG 439  
Db 279 MAGAAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 338  
QY 440 TGACCAACAACCTTGGTAACCTTGGAAACAGCTTGACCGTTTAAAGAGAGAGAGAG 499  
Db 339 AAAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 398  
QY 500 TCTATTATCTATGCCCAAG 520  
Db 399 AAGMATAMAAATAAGMMAMR 419

**RESULT** 14  
AL513719 1101 bp DNA linear GSS 26-JUL-1999  
LOCUS CNS0181N  
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACN37P10 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL108773  
VERSION AL108773.1 GI:5629077  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
AUTHORS 1 (bases 1 to 1101)  
JOURNAL Genoscope.

COMMENT

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers  
1. 329  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CLOBA0072H01"  
/clone\_lib="LRI\_NFL006\_PL2"  
/tissue\_type="placenta"  
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 186 a 13 c 3 g 60 t 67 others  
ORIGIN

Query Match 5.8%; Score 45.8; DB 9; Length 329;  
Best Local Similarity 36.1%; Pred. No. 23;  
Matches 105; Conservative 44; Mismatches 142; Indels 0; Gaps 0;

Qy 68 TTTTATGTAATTTACTGTTTCTTATCACCAGATGATGGTCAGCACATTTTGG 127  
Db 9 TTTTATGTAATTTACTGTTTCTTATCACCAGATGATGGTCAGCACATTTTGG 68

Qy 128 CTGCTATCTTCATAGACATGGATAAGTCGACAGAGAGTAACCTTCATGAAGATT 187  
Db 69 WWT 128

Qy 188 TTGTATTCATAAAAGCTAAAGAGATGCACAAAGAGAGAGATCTTTATCCTTGCTGA 247  
Db 129 AA 188

Qy 248 ACTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAACGTTAAACAAAG 307  
Db 189 MAA 248

Qy 308 AAGACAAAAACAAACACAGCTTTGAAATGCCAAAAGGTGATCAGATCCCTC 358  
Db 249 AAMCCCCC 299

Search completed: May 30, 2002, 01:00:20  
Job time: 22230 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 03:03:39 ; Search time 680.87 seconds  
(without alignments)  
1974.450 Million cell updates/sec

Title: US-08-982-272-20

Perfect score: 783

Sequence: 1 ATGATCGAATACATAACCA.....TTGGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

- 1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.\*
- 2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.\*
- 3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.\*
- 4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.\*
- 5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.\*
- 6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.\*
- 7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.\*
- 8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.\*
- 9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.\*
- 10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.\*
- 11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.\*
- 12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.\*
- 13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.\*
- 14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.\*
- 15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.\*
- 16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.\*
- 17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.\*
- 18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.\*
- 19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.\*
- 20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.\*
- 21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.\*
- 22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	783	100.0	783	19	AAV42184
2	726.8	92.8	786	15	AAO63959
3	726.8	92.8	786	19	AAV38997
4	726.8	92.8	786	19	AAV12852
5	726.8	92.8	840	14	AAO41506
6	726.8	92.8	840	15	AAO67123
7	726.8	92.8	840	16	AAT05763
8	726.8	92.8	840	18	AAT93782
9	726.8	92.8	840	19	AAV61062

10	726.8	92.8	840	20	AAZ27525
11	726.8	92.8	879	22	AAF55539
12	726.8	92.8	1816	21	AAAS1745
13	726.8	92.8	1816	23	AAS86571
14	723.8	92.4	840	18	AAT59122
15	723.6	92.4	840	15	AAQ57984
16	722	92.2	840	16	AAQ94091
17	717.2	91.6	786	19	AAV39000
18	704.4	90.0	786	19	AAV39002
19	694.8	88.7	786	19	AAV39003
20	648.6	82.8	783	19	AAV38999
21	639	81.6	783	19	AAV39001
22	618.2	79.0	783	15	AAO63960
23	618.2	79.0	783	19	AAV12853
24	618.2	79.0	783	20	AAZ27524
25	616.6	78.7	783	19	AAV38998
26	616.6	78.7	818	19	AAV61062
27	614.8	78.5	864	19	AAV39004
28	614	78.4	782	14	AAO41507
29	602.2	76.9	885	21	AAZ55540
30	602.2	76.9	885	21	AAZ55541
31	599.2	76.5	780	21	AAZ55542
32	599.2	76.5	780	21	AAZ55543
33	589	75.2	1552	22	AAH25525
34	583.6	74.5	865	22	AAF82933
35	583.6	74.5	906	22	AAF82932
36	583.6	74.5	2209	22	AAF82929
37	583.6	74.5	2252	22	AAF82928
38	583	74.5	1878	21	AAZ55534
39	583	74.5	1878	21	AAZ55535
40	580.6	74.2	1425	14	AAO41516
41	580.6	74.2	1425	20	AAZ27534
42	580	74.1	780	21	AAZ55536
43	580	74.1	780	21	AAZ55537
44	579.6	74.0	929	18	AAT58123
45	579.6	74.0	929	20	AAZ27537

#### ALIGNMENTS

RESULT 1  
AAV42184  
ID AAV42184 standard; DNA; 783 BP.

XX AC AAV42184;

XX DT 23-SEP-1998 (first entry)

XX DE Exemplary nucleotide sequence of a chimeric accessory molecule.

XX KW Human; alteration; immunoreactivity; human cell;

XX KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

XX KW autoimmune disorder; rheumatoid arthritis; vaccine; chimera; ss.

XX OS Chimeric - Homo sapiens.

XX OS Chimeric - Mus sp.

XX PN WO9826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-US22740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

XX



Db 1 atgctgaacacatacaacaaacttctcccgatctgcgccactggactgcccacatcagc 60  
Qy 61 ATGAAATTTTATGATATTTACTTACTTCTTTCTTTCTTATCATCCAGATGATGGGTACGA 120  
Db 61 atgaaattttatgtatttacttactgttttcttctatcaccacagatgattgggtcagca 120  
Qy 121 CTTTTGCTGTGATCTTCTATAGAGATGGATAGAGTTCGAAGTTCGAAGAGTAACCTTCAT 180  
Db 121 ctttttgcgtgctatcttcatagagggttgacaagatgagaagaaatcttctcat 180  
Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCACAAAGGAGGATCTTTTATCC 240  
Db 181 gaagattttgtattcatataaagcagcttggaagatgagaagaaatcttctcat 240  
Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGCAATTTGTAAGACCTTGTCAAGATATACGTTA 300  
Db 241 ttactgaaactgtgaggagatataaagccagtttgaagccttggtaagagataatgtta 300  
Qy 301 AACAAAGAAGA---GAAAAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCT 357  
Db 301 acaaaaggagagacgaagaagaacagcttgaatgcaaaaggtgacagaatcct 360  
Qy 358 CAAATTTGCGGCACATGTCATAGTCCAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417  
Db 358 caaattgcccacatgtcatagtgaggccagcagtaaaacaacatctgtgtacagtgg 420  
Qy 418 GCTGAAAAGGATACTACACCATGAGCAACAACTTTGGTAACCTCGGAAATGGGAAACAG 477  
Db 421 gctgaaaaggatactacacatgagcaacaacttggtaaccctggaaatgggaaacag 480  
Qy 478 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGCCCAGTCACCTCTGTGTCCAA 537  
Db 481 ctgaccgttaaaagacaaggactctattatctatgcccagtcacactctgttccaat 540  
Qy 538 CGGGAAGCTTCAGTCAAGCTCCATTTATPAGCCAGCCTCTGCCTAAAGTCCGCCGCTAGA 597  
Db 541 cgggaagcttgagtcagctccattatagccagcctctgcctaaagtcgcccgtaga 600  
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAATATCCACAGTTCGCCCAACCTTGGCGGCA 657  
Db 601 ttcgagaatcttactcagagctgcaaataccacagcttcgcccaaccttgcgggcaa 660  
Qy 658 CAATCCATTCACCTGGGAGGAGTATTGAAATGCAACAGGTCCTCGGTGTTGTCAAT 717  
Db 661 caatccattcacttgaggaggatattgaattgcaaccaggtgcttcgggtttgtccaat 720  
Qy 718 GTGACTGATCCCAAGCAAGTGAAGCCATGGCAGTGGCTTCACGTCCTTTGGCTTACTCAA 777  
Db 721 gtgactgatcccaagccaagtggccatggcactggcttcacgtccttggcttactcaaa 780  
Qy 778 CTCTGA 783  
Db 781 ctctga 786

## RESULT 3

AAV38997  
ID AAV38997 standard; DNA; 786 BP.

XX  
XX  
XX AAV38997;

XX  
XX  
XX 23-SEP-1998 (first entry)

XX  
XX  
XX CD40 ligand gene used in the course of the invention.

XX  
XX  
XX CD40 ligand; alteration; immunoreactivity; human cell;  
KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX  
XX  
XX Mus sp.

XX  
XX  
XX W09826061-A2.

XX  
XX  
XX

PD 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

XX (RECC ) UNIV CALIFORNIA.

PI Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for  
PT altering immunoreactivity of cells, particularly for treatment of  
PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
XX Disclosure; Page 104; 167pp; English.

XX The present sequence represents the CD40 ligand gene. The sequence is  
CC used to exemplify the method of the invention. The specification  
CC describes a method for altering the immunoreactivity of human cells  
CC which comprises introducing a gene encoding an accessory molecule  
CC ligand (AML) into the cells so that the AML is expressed on the surface  
CC of the cells. Vectors containing the AML genes can be used in gene  
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
CC arthritis. They can also be used for vaccination to produce immunity  
CC against a virus cell, bacteria, protein, fungus or neoplasia.

SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;

Query Match 92.8%; Score 726.8; DB 19; Length 786;

Best Local Similarity 96.2%; Pred. No. 2.6e-191;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAATATACCAACCAACTTCTCCCGATCTGCGCCACATGGAGTCCCATCAGC 60

Db 1 atgacgaacacatacaacaaacttctcccgatctgcgccacatggagtcgccatcagc 60

Qy 61 ATGAAATTTTATGATATTTACTTACTTCTTTCTTTATCACCAGATGATGGGTACGA 120

Db 61 atgaaattttatgtatttacttactgttttcttctatcaccacagatgattgggtcagca 120

Qy 121 CTTTTGCTGTGATCTTCTATAGAGATGGATAGGTCGAAGAGGAAGTAACCTTCAT 180

Db 121 ctttttgcgtgctatcttcatagagggttgacaagatgagaagaaatcttctcat 180

Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCACAAAGGAGGATCTTTATCC 240

Db 181 gaagattttgtattcatataaagcagcttggaagatgagaagaaatcttctcat 240

Qy 241 TTGCTGAAGTGTGAGGAGATGAGAGCAATTTGTAAGACCTTGTCAAGATATACGTTA 300

Db 241 ttactgaaactgtgaggagatataaagccagtttgaagccttggtaagagataatgtta 300

Qy 301 AACAAAGAAGA---GAAAAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCT 357

Db 301 aacaaaggagagacgaagaagaacacagcttgaatgcaaaaggtgatcagaatcct 360

Qy 358 CAAATTTGCGGCACATGTCATAGTGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417

Db 361 caaattgcccacatgtcataagtggccagcagtaaaacacactgtgttccagtgg 420

Qy 418 GCTGAAAAGGATGACTACACCATGAGCAACAACTTGGTAAACCTCGGAAATGGGAAACAG 477

Db 421 gctgaaaaggatatacaccatgagcaaacacttggtaaccctggaaaatgggaaacag 480

Qy 478 CTGACCGTTAAAGACAAAGGACTCTATTATATCTATGCCCCAACAGTCACTTCTGTCCAA 537

Db 481 ctgaccgttaaaagacaaggactctattatctatgcccagtcacactctgttccaat 540

Qy 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGCTAGA 597

Db 541 cgggaagcttcgagtcgaagctccattatagccagcctctgctcaaatcccccggtaga 600  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAAAACCTTGCAGGCAA 657  
Db 601 ttcagagagaatctactcagagctgcaaataccacagttccgcgaacaccttgccgggcaa 660  
QY 658 CAATCCATTTCACATGCGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCGTAAT 717  
Db 661 caatccatttcacttgaggaggtatttgaaatgcaaccagggtcttcggtgtttgtcaat 720  
QY 718 GTGACTGATCCAGCAAGTACGACCTGCGTTCACGTCCTTTGCGCTTACTTCAAA 777  
Db 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttggtactcaaa 780  
QY 778 CTCTGA 783  
Db 781 ctctga 786  
RESULT 4  
ID AAV12852 standard; cDNA to mRNA; 786 BP.  
XX AC AAV12852;  
XX DT 13-MAY-1998 (first entry)  
XX DE CD40 ligand coding sequence.  
XX KW Leucine zipper; fusion protein production; soluble oligomeric protein;  
XX KW heterologous mammalian type II transmembrane protein; activated T cell;  
XX KW heterologous mammalian type I transmembrane protein; antibody production;  
XX KW CD40-L; B-cell proliferation; CD27-L; lymphocyte antigen; ss.  
XX OS Homo sapiens.  
XX FH Key  
XX FT Location/Qualifiers  
XX FT 1..786  
XX FT /\*tag= a  
XX PN US5716805-A.  
XX PD 10-FEB-1998.  
XX PF 18-MAY-1995; 95US-0446922.  
XX PR 18-MAY-1995; 95US-0446922.  
XX PR 25-OCT-1991; 91US-0783707.  
XX PR 05-DEC-1991; 91US-0805723.  
XX PR 23-OCT-1992; 92US-0969703.  
XX PR 13-AUG-1993; 93US-0107353.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Spriggs MK, Srinivasan S;  
XX WPI; 1998-144799/13.  
XX P-PSDB; AAW41178.  
XX Soluble oligomeric fusion proteins - comprising leucine zipper fused  
XX to extracellular region of transmembrane protein  
XX Example 1; column 19-20; 21pp; English.  
XX This sequence is the coding sequence for the human CD40 ligand (CD40-L).  
XX The encoded protein can be used in a fusion protein produced using the  
XX method of the invention. The method is for preparing soluble oligomeric  
XX protein by culturing a host cell transfected with a vector for the  
XX fusion protein. The soluble oligomeric proteins comprise a leucine zipper  
XX fused to the N terminus of the extracellular region of a heterologous  
XX mammalian type II transmembrane protein or to the C terminus of the  
XX extracellular region of a heterologous mammalian type I transmembrane

CC protein, where the leucine zipper is a peptide comprising at least part  
CC of AAW41171 or AAW41172, optionally with conservative amino acid  
CC substitutions, provided that the peptide trimerises in solution. A  
CC soluble fusion protein comprising the leucine zipper of AAW41171 linked  
CC to the extracellular region of CD40-L (a type II transmembrane protein  
CC that is found on activated T cells and acts as a ligand for the B-cell  
CC antigen CD40) stimulates B-cell proliferation and antibody production in  
CC a similar manner to membrane-bound CD40-L. A soluble fusion protein  
CC comprising the leucine zipper of AAW41172 linked to the extracellular  
CC region of CD27-L (a type II transmembrane protein that binds to the  
CC lymphocyte antigen CD27) inhibits binding of CD27c (a fusion protein  
CC comprising the extracellular region of CD27 and a human IgG1 Fc region)  
CC to EBV-transformed B cells expressing CD27-L.  
XX SQ Sequence 786 BP; 250 A; 168 C; 168 G; 200 T; 0 other;  
Query Match 92.8%; Score 726.8; DB 19; Length 786;  
Best Local Similarity 96.2%; Pred. No. 2.6e-191;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGATCTCGGGCCACTGGACTGCCCATCAGC 60  
Db 1 atgatcgaaacatacaacaaacttctcccgatctcgcgcactggactgcccacagc 60  
QY 61 ATGAAATTTTATGTATTACTTACTTCTTCTTATCACCAGATGATTGGGTGACGA 120  
Db 61 atgaaattttatgtatttacttactgtttcttcttaccacccagatgattgggtcagca 120  
QY 121 CTTTTCGTGCTATCTTCATAGAGATTGGATAGAGTTCGAGAGAGTAAACCTTCAT 180  
Db 121 cttttcgtgctatcttcataagaagttgcaagaatagaagaatgaagaacttctcat 180  
QY 181 GAAGATTTTGTATTATATAAAGCTAAAGATGCAACAAAGAGAGAGATCTTTATCC 240  
Db 181 gaagattttgtattcatgaaacagatcacagatgataacacagagagaagatccctccc 240  
QY 241 TTCTCACTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGATATATACGTTA 300  
Db 241 ttactgaaactgtgaggagattaaaagccagtttgaagcttgtggaagataataatgta 300  
QY 301 AACAAAGAGA---GAAAGAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357  
Db 301 aacaaagaggagacgaagaagaagaaacagctttgaaatgcaaaaggtgatcagaatcct 360  
QY 358 CAATTCGCGCAGTCATATAAGTGAGGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 417  
Db 361 caaattgcgcacatgcatcactacacccatgagcaacactgtgttacagtgg 420  
QY 418 GCTGAAAAAGGATACATACACCATGAGCAACAACTTGGTAACTGGAAATGGGAACAG 477  
Db 421 gctgaaaaaggatactacacccatgagcaacactgtgttaacctgggaaacag 480  
QY 478 CTGACGTTTAAAGACAAAGGACTCTATTATATATATATATATATATATATATATAT 537  
Db 481 ctgaccgttaaaagacaagagactctattatatactatgcccacagtcaccttcttccaat 540  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATATAGCCAGCCTCTGCCTAAAGTCCCGGTAGA 597  
Db 541 cgggaagcttcgagtcgaagctccattatagccagcctctgctcaaatcccccggtaga 600  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAAAACCTTGCAGGCAA 657  
Db 601 ttcgagagaaatcttactcagagctgcaaataccacagttccgcgaacaccttgccgggcaa 660  
QY 658 CAATCCATTTCACATGCGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCGTAAT 717  
Db 661 caatccatttcacttgaggaggtatttgaaatgcaaccagggtcttcggtgtttgtcaat 720  
QY 718 GTGACTGATCCAGCAAGTACGACCTGCGTTCACGTCCTTTGCGCTTACTTCAAA 777  
Db 721 gtgactgatccaaagccaagtgagccatggcactggcttcacgtcccttggtactcaaa 780

QY 778 CTCTGA 783  
 Db 781 ctctga 786

RESULT 5  
 ID AA041506 standard; DNA; 840 BP.  
 AC AA041506;  
 DT 12-AUG-1993 (first entry)  
 XX CD40-L DNA.  
 DE  
 XX Human; CD40-L; CD40; type II; membrane; polypeptide; extracellular;  
 KW transmembrane; region; intracellular; soluble; activity; B cell;  
 KW proliferation; induction; antibody; secretion; IgE; agonist;  
 KW antagonist; binding assay; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 46..831  
 FT /\*tag= a  
 FT  
 XX WO9308207-A.  
 XX PD 29-APR-1993.  
 XX PF 23-OCT-1992; 92WO-US08990.  
 XX PR 25-OCT-1991; 91US-0783707.  
 XX PR 05-DEC-1991; 91US-0805723.  
 XX PA (IMV) IMMUNEX CORP.  
 XX PI Armitage RJ, Fanslow WC, Spriggs MK;  
 DR WPI; 1993-152417/18.  
 DR P-PSDB; AAR36701.  
 XX New cytokine CD40-L as CD40 agonist and antagonist - is used for  
 PT treating allergies, lupus, rheumatoid arthritis,  
 PT graft-versus-host disease and insulin-dependent diabetes mellitus  
 XX  
 PS Claim 1; Fig 2; 80pp; English.  
 CC This sequence encodes a human CD40-L polypeptide which binds to CD40.  
 CC CD40-L is a type II membrane polypeptide which has an extracellular  
 CC region at its C-terminus, a transmembrane region and an  
 CC intracellular region at its N-terminus. A soluble form of CD40-L  
 CC lacks the transmembrane domain. CD40-L activity is mediated by  
 CC binding with CD40 and induces B cell proliferation and induction of  
 CC antibody secretion, including IgE. Membrane bound CD40-L acts as a  
 CC CD40 agonist and soluble CD40-L acts as a CD40 antagonist. CD40-L  
 CC can be used in a binding assay to detect cells expressing CD40.  
 XX  
 SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 92.8%; Score 726.8; DB 14; Length 840;  
 Best Local Similarity 96.2%; Pred. No. 2.7e-191;  
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACAACTTCTCCCGATCTGGGCCACTGGACTGCCATCAGC 60  
 Db 46 atgacgaacatacaacaaactctcccgatctgggccactggactgccatcagc 105  
 QY 61 ATGAAATTTTATCTTACTTCTTCTTATCACCACAGATGATGGTCA 120  
 Db 106 atgaaatatttatctattactgtttctttattatccaccagatgattgggtcagca 165

QY 121 CTTTTGCTGTATCTTTCATAGAGATTGGATAGGTCGAGAGAAAGTAAACCTTCAT 180  
 Db 166 ctttttgcgtgtatcttcatatagaaggttgacaagatagaagatgaagaaatcttcat 225  
 QY 181 GAAGATTTTGTATCATAAAGAAAGCTTAAGAGATGCAACAAGAGAGAGATCTTTATCC 240  
 Db 226 gaagatttgcattcatgaaacacacacagagatgcaacacagagagaaagatcccttacc 285  
 QY 241 TTGCTGAATCTGTGAGGAGATGAGAGCAATTTTGAAGACCTTTGTCAAGGATATAACGTTA 300  
 Db 286 ttactgaactgtgaggagattaaaagccagtttgaagcctttgtgaagatataatgta 345  
 QY 301 AACAAAGAAGA--CAAAAAGAAACACCTTTGAAATGCAAAAAGCTGATCAGAAATCCT 357  
 Db 346 acaaaagaggacgaagaagaacagcttgaatgcaaaaaggtgatcagaatcct 405  
 QY 358 CAAATTCGGGCACATGTCTAAGTGAGCGCAGCAGTAAACAAACATCTGTGTACAGTGG 417  
 Db 406 caaatctgcggcacatgtcataagtgaggccagcagcaacaacacatctgtgtacagctgg 465  
 QY 418 GCTGAAAAAGGATACACCATGAGCAACAACACTTGGTAAACCTTGAAAAATGGGAAACAG 477  
 Db 466 gctgaaaaagagatactacacatgagcaacaacttggtaacctggaaaaatgggaaacag 525  
 QY 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCAACCTTCTGTTCAT 537  
 Db 536 ctgaccgttaaaagacaaggaactctattatctatgcccgaagtcaccttctgttccaat 585  
 QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 597  
 Db 586 cgggaagcttcgagtcgaagctcatttatagccagcctctgctcctaaagtcctcccggtaga 645  
 QY 598 TTCGAGAGAATCTTACTCAGAGCTGCAATACCCACAGTTCGCGCAAACTTTCGGGCAA 657  
 Db 646 ttcgagagaatcttactcagagctgcaaatccccacagctccgcgcaaaccttgcgggcaa 705  
 QY 658 CAATCCATTTCACCTTGGGAGGAGTATTGAAATGCAACCAAGTGCTTCGGTGTTCAT 717  
 Db 706 caatccatttcacttgggaggagatttgaattgcaaccaggtgcttcgggtgttgcacat 765  
 QY 718 GTGACTGATCCAAAGCAAGTGAAGCCATGCGACTGCTCAGCTGCTTGGCTTACTCAAA 777  
 Db 766 gtgactgatccaaagccaaagtggccatggcactggcttcacgtcccttggcttactcaaa 825  
 QY 778 CTCTGA 783  
 Db 826 ctctga 831

RESULT 6  
 ID AA067123 standard; DNA; 840 BP.  
 AC AA067123;  
 XX 23-MAR-1995 (first entry)  
 DE CD40 ligand gene.  
 KW Probe; primer; PCR; amplify; polymerase chain reaction; detection;  
 KW mutation; CD40 ligand gene; IgM; ss.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH CDS 46..831  
 FT /\*tag= a  
 FT /product= CD40 ligand  
 XX WO9417196-A.  
 XX PD 04-AUG-1994.  
 XX

538 CGGAAGCTTCGAGTCAAGCTCATTATAGCCAGAGCTTGCTAAAGTCCCGGTAGA 597  
586 cggagagcttcgagtcgaagctccattatagccagctctgctaaagtcctcccggtaga 645  
598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTCGCGGCA 657  
646 ttcgagagaatcttactcagagctgcaaa caccacacagttcccgcaaaccttcgcgga 705  
658 CAATCCATTCACTGGGAGGAGTATTTGAATTGCAACACAGTCTTCGGTGTGTTCAAT 717  
706 caatccattcacttggagagatttgaattgcaacacagttcttcggtgttgcatt 765  
718 GTGACTGATCAAGCCAAAGTGAGCCATGGCAGCTTGCTTACGCTTCTTACTCAAA 777  
766 gtgactgatccaagccaagtgcagctggcagctgcttcagcttccttggcttactcaaa 825  
778 CTCTGA 783  
826 cctctga 831

RESULT 7  
AAT05763  
ID AAT05763 standard; DNA; 840 BP.  
AC AAT05763;  
DT 18-MAR-1996 (first entry)  
DE Human CD40 ligand DNA.  
KW High density membrane-bound CD40 ligand; B-lymphocyte; B-cell;  
KW differentiation; proliferation; baculovirus; Spodoptera frugiperda;  
KW Sf9; insect cell culture; tumour necrosis factor receptor; ss.  
OS Homo sapiens.  
FH Key  
FT CDS .22..807  
FT /\*tag= a  
XX W09529935-A1.  
XX 09-NOV-1995.  
XX 28-APR-1995; 95WO-US05448.  
XX 28-APR-1994; 94US-0234580.  
XX (BOEHRINGER INGELHEIM PHARM INC.  
XX Castle BE, Kehry M;  
XX WPI; 1995-393038/50;  
XX P-PSDB; AAR85486.  
XX High density membrane bound CD40 ligand - for stimulating the  
XX proliferation of B cells in vitro or in vivo, partic. for producing  
XX differentiated cells  
XX Disclosure; Fig 1: 74pp; English.  
XX The nucleotide sequence given in AAT05763 encodes a human high-density,  
XX membrane-bound (hmb) CD40 ligand (AAR85486) that induces long-term  
XX proliferation of B-cells in culture. These proliferating B-cells  
XX can be induced to differentiate into antibody-prod. cells. The  
XX nucleotide sequence is incorporated into a baculovirus vector that  
XX is used to transfect Sf9 insect cells for prodn. of recombinant  
XX hmbCD40.  
XX Sequence 840 BP; 263 A; 182 C; 181 G; 214 T; 0 other;

21-JAN-1994; 94WO-US00786.  
22-JAN-1993; 93US-0009258.  
20-JAN-1994; 94US-0184422.  
(IMMV ) IMMUNEX CORP.  
Armitage RJ, Davison BL, Fanslow WC, Renshaw BR;  
Spriggs MK, Wildmer MB;  
WPI: 1994-264109/32.  
P-PSDB; AAR57469.  
Method for detecting mutation in CD 40 ligand gene - comprises  
amplification of nucleic acid, and mutational analysis  
Disclosure: Page 22-24; 38pp; English.  
This sequence represents the CD40 ligand gene. Mutations within  
this gene were identified by the method of the invention. The  
method comprises isolating DNA from an individual and selectively  
amplifying the isolated DNA derived from the CD40 ligand gene. The  
amplification product is then analysed to determine if there is a  
mutation present and determining if a protein expressed from the  
ligand gene will bind CD40. The detection of mutations in the CD40  
ligand gene allows subsequent treatment of a syndrome resulting in  
elevated levels of serum IgM and diminished levels of other Ig  
isotypes, due to mutation in the CD40 ligand gene. ie. X-linked  
hyperIgM syndrome.  
Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 92.98; Score 726.8; DB 15; Length 840;  
Best Local Similarity 96.28; Pred. No. 2.7e-191;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

1 ATGATCGAATCATCAACCAACCTTCCTCCCGATCTCGGCCACTGCGACATGCCCATCAGC 60  
46 atgacgaatacacaacccaactctcccgatctcgcgactcgcgacgagcagcagcagc 105  
61 ATGAAATTTTATGTTATTTACTTCTTTCTTCTTATCACCAGATGATTGGTTCAGCA 120  
106 atgaatattttatgtatttacttactgttttcttcttaccacagatgattgggtcagca 165  
121 CTTTTCGCTGTATCTTCATAGAGATTGGATAGGTTCGAGAGAGAGTAACCTTCAT 180  
166 ctttttgcgtgtatcttcataagatttgcgaggttgcaacagatagaagatgaaggaatcttcat 225  
181 GAAGATTTTGTATTCATATAAAGCTAAGAGATGCAACAGAGAGAGAGATCTTTATCC 240  
226 gaagattttgtattcatgaaacagatagagatgcaacacagagagaaagatccttatcc 285  
241 TTGCTGAACTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAGGATATAACGTTA 300  
286 ttactgaactgtgagagattataaagccagtttgagggcttggagagataataatgta 345  
301 AACAAAGAAGA--GAAAGAAAGAAACAGCTTTGAAATGCAAAAGAGTGCAGAACTCT 357  
346 acaaaagaggagacgaagaagaacacagcttggaaatgcaaaaggatcagaatcct 405  
358 CAAATTCGCGGCACATGTCTAATAGTGAAGCCAGCAGTAAACACATCTGTGTACAGTGG 417  
406 caaatgcgacatgtcataagtgaggccagcagtaaaacacatctgtgtacagtgg 465  
418 GCTGAAAAGGATACACTACACATGACACACTTGGTAACCTCGAAAATGGGAACAG 477  
466 gctgaaaaaggatctacacacatgagcaacacttggtaacctggaaatgggaaacag 525  
478 CTGACCGTTAAAGACAAAGACTCTATTATCTATGCTCCCAAGTCAACCTCTGTTCCAAAT 537  
526 ctgaccgttataaagacaaggactctattatctatgcccacagtcacacctctgttccaat 585

Query Match		92.8%; Score 726.8; DB 16; Length 840;
Best Local Similarity		96.2%; Pred. No. 2.7e-191;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;		
Qy	1	ATGATCGAAACATACAAACAACTCTCCCGAGTCTGGGCGCACTGGAGTGGCCATCAGC 60
Db	22	atgatcgaaacatacaacaaactctcccgatctgcccactggcactggactgccatcagc 81
Qy	61	ATGAAATTTTATCTATTTACTTCTTCTTCTTATCACCCAGATGATGGGTACCA 120
Db	82	atgaaaattttatgtatttacttactgttttcttatacaccagatgatgggtcagca 141
Qy	121	CTTTTGTCTGTATCTTCATAGAGATTGGATAGGTGCAAGAGAGTAACCTTCAT 180
Db	142	cttttctgtgtattcttcatagaaggttgcaacagatagaagatgaagaattctcat 201
Qy	181	GAAGATTTTGTATCTATAAAGCTTAAAGAGATGCACAAAGAGAGGATCTTTATCC 240
Db	202	gaagattttgtattcatgaaacagatagacagatgcaacacagggagaagatccttacc 261
Qy	241	TTGCTGAACCTGTGAGGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300
Db	262	ttactgaactgtgaggagattcaaaagccagtttgaagcgtttgtgaagataataatgta 321
Qy	301	AACAAAGAGA--GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357
Db	322	aacaaagaggagacgaagaaagaaacagctttgaaatgcataaagggtgatcagaatcct 381
Qy	358	CAAAATTCGGGCACATGTCATTAAGTGAGGCCAGCAGTCAAAACACATCTGTGTACAGTGG 417
Db	382	caaatgcggcacatgtcatagtgagggccagcagcaaaacacatctgtgtacagtcgg 441
Qy	418	GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCCTGCAAAATGGGAAACAG 477
Db	442	gctgaaaaaggatactacacatgagcaacaacttggtaaccctggaataagggaacag 501
Qy	478	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCCAAGTCACCTCTGTGTTCCAA 537
Db	502	ctgaccgttaaaagacaaggactctattatctatgcccgaagtcacactctctgttcccaat 561
Qy	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAATCCCGGTGAGA 597
Db	562	cgggaagcttcgagtcagctcccacttatagccagcctctgcctaaagtcctcccggtaga 621
Qy	598	TTGAGAGAACTTACTCAGAGCTCAAAATACCCACAGTTCGCCAAACCTTTGCGGGCAA 657
Db	622	ttcagagaactcttactcagagctgcaataaccacaggttcgcgaacaccttgcgggcaa 681
Qy	658	CAATCCATTCTACTTGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTTCATCAT 717
Db	682	caatccattcacttggggaggatttgaattgcaaccaggtgcttcggtgttgcatt 741
Qy	718	GTGACTGTATCAAGCAAGTGAAGCCATGGCCTTTCAGCTTCTCAGCTCTCTTGGCTTACTCAA 777
Db	742	gtgactgtatcaagcaagtcgaagtgagccatggcactggcttcacgtctcttggcttactcaaa 801
Qy	778	CTCTGA 783
Db	802	ctctga 807
RESULT 8		
AAT93782		
ID	AAT93782	standard; cDNA; 840 BP.
XX	AC	AAT93782;
XX	AC	AAT93782;
XX	DE	16-FEB-1998 (first entry)
XX	DE	cDNA of CD40L, a novel cytokine ligand for CD40.
XX	DE	Cytokine; activated CD4+ T cell; CD40; CD40L; monoclonal antibody;
XX	DE	neoplastic cell proliferation; B-cell lymphoma; immune deficiency; AIDS;
KW		

melanoma; carcinoma; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
CDS 46..831  
FT /\*tag= a

XX US5674492-A.

XX 07-OCT-1997.

XX 21-DEC-1994; 94US-0360923.

XX 23-DEC-1993; 93US-0172664.

XX (IMMUNEX CORP.  
USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Armitage RJ, Fanslow WC, Longo DL, Murphy WJ;

XX WPI: 1997-502273/46.  
P-PSDB; AAW34669.XX Treating or preventing neoplastic disease associated with  
CD40-expressing cells - particularly B-cell lymphoma, by  
administration of CD40-binding protein, preferably antibody or  
soluble CD40-ligand

XX Claim 3; Columns 19-22; 21pp; English.

XX The present sequence represents the cDNA sequence of a novel cytokine  
ligand for CD40 called CD40L. CD40L is a type II membrane polypeptide,  
which is expressed by activated CD4+ T cells, and causes B cell  
proliferation and induction of antibody secretion. The protein can be  
used to produce monoclonal antibodies, which in turn bind to  
CD40-expressing cells. This inhibits binding of soluble CD40 to its  
ligand CD40L. The monoclonal antibody against CD40L is used to inhibit  
proliferation of neoplastic cells, and is particularly useful in treating  
B-cell lymphoma (e.g. where induced after transplants or in other cases  
of immune deficiency such as AIDS), and also melanoma or carcinoma. Since  
the monoclonal antibodies inhibit neoplastic cells directly, they may not  
need to be coupled to a toxin or radioisotope, avoiding toxic effects on  
normal B cells.

XX Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 Other;

Query Match 92.8%; Score 726.8; DB 18; Length 840;  
Best Local Similarity 96.2%; Pred. No. 2.7e-191;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATACAAACAACTCTCCCGATCTGGGCGCACTGGAGTGGCCATCAGC 60

Db 46 atgatcgaaacatacaacaaactctcccgatctgcccactggcactggactgccatcagc 105

Qy 61 ATGAAATTTTATGTATTTACTTACTTCTTCTTATCACCAGATGATGGGTACCA 120

Db 106 atgaaaattttatgtatttacttactgttttcttatacaccagatgatgggtcagca 165

Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGGTGCGGAAGAGAGTAACCTTCAT 180

Db 166 cttttgtctgtatcttcatagaaggttggaacagatagaagatgaagggaatctcat 225

Qy 181 GAAGATTTTGTATTCATAAAGAGCTAAAGAGATGCAACAAAGAGAGGATCTTTATCC 240

Db 226 gaagattttgtattcatgaaacagatagacagatgcaacacagggagaagatcccttacc 285

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

Db 286 ttactgaactgtgaggagatttaaaagccagtttgaagcgtttgtgaagagataatgta 345

Qy 301 AACAAAGAAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAGAGGTGATCAGAACTCT 357







Db 682 caatccattcacttgaggagatttgaattgcaaccagggtgcttcggtgtttgtcaat 741

Qy 718 GTGACTGATCCAGCAAGTCCAGCATGGCTTCAGCTCCAGTCTCTGGCTTACTCAAA 777

Db 742 gtgactgatccaaagcaagtgagccatggcactggttcaogtctcttggcttactcaaa 801

Qy 778 CTCTGA 783

Db 802 ctctga 807

RESULT 10

AAZ27525

ID AAZ27525 standard; cDNA; 840 BP.

XX AC

XX AAZ27525;

DT 13-DEC-1999 (first entry)

XX DE Human CD40-L coding sequence.

XX KW CD40-L; CD40 receptor ligand; anti-human CD40-L monoclonal antibody;

XX KW binding inhibitor; trimeric CD40-L; anti-Immunoglobulin M;

XX KW peripheral blood B cell; proliferation inhibitor; ss.

XX OS Homo sapiens.

XX US5961974-A.

XX PD 05-OCT-1999.

XX PF 24-MAY-1994; 9AUS-0249189.

XX PR 25-OCT-1991; 9IUS-0783707.

XX PR 05-DEC-1991; 9IUS-0805723.

XX PR 23-OCT-1992; 92US-0969703.

XX PA (IMMUNEX) IMMUNEX CORP.

XX PI Spriggs MK; Fanslow WC; Armitage RJ;

XX DR WPI; 1999-579604/49.

XX DR P-PSDB; AAY39938.

XX PT Anti-human CD40-Ligand monoclonal antibodies -

XX PS Disclosure; Fig 2; 59pp; English.

CC This sequence encodes the human CD40 receptor ligand (CD40-L). The

CC invention relates to anti-human CD40-L monoclonal antibodies M90 secreted

CC by hybridoma hCD40L-M90 (ATCC HB-12055) and M91 secreted by hybridoma

CC hCD40L-M91 (ATCC HB-12056). M90 and M91 inhibit CD40-L binding to CD40

CC and the ability of trimeric CD40-L and anti-Immunoglobulin M to induce

CC proliferation of peripheral blood B cells.

XX SQ Sequence 840 BP; 266 A; 185 C; 175 G; 214 T; 0 other;

Query Match 92.8%; Score 726.8; DB:20; Length 840;

Best Local Similarity 96.2%; Pred. No. 2.7e-191;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAACATACCAACAACTTCCTCCCGATCTGGCGCACATGGACTGCCCATCAGC 60

Db 46 atgacgaacatacaacaaactctcccgatctgcgccactggactgcccacagc 105

Qy 61 ATGAAATTTATCTATTACTTCTCTTCTTATCACCACAGATGATGGGTACCA 120

Db 106 atgaaaattttatgtatttactactgttttcttattacaccagatgattgggtcagca 165

Qy 121 CTTTTCGTGTGATCTTCATAGAGATTGGATAGGTTCGAGAGAGTAACCTTCAT 180

Db 166 ctttttgcgtgtatcttcataagaaggttggaacaagatagaagatgaagaatcttc 225

Qy 181 GAAGATTTTGTATTTCATATAAAGCTAAAGAGATCCAAAGAGGAGAGGATCTTTATCC 240

Db 226 gaagattttgtattcatgaaacacgatacagagatcaacacagagagaagaatccattatcc 285

Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAGACCTTGTCAAGCATATAACGTTA 300

Db 286 ttacttgactgtgaggagattaaagccagtttgaagccttctgtgaagataataatgta 345

Qy 301 AACAAAGAAAGA---CAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGAAATCCT 357

Db 346 acaaaaggagagagagaaagaaacagctttgaaatgcaaaaagggtgatcagaaatcct 405

Qy 358 CAATTTGCGGCACATGTCTAATAGTGAGGCCAGCAGTCAAAACAACTCTGTGTACAGTGG 417

Db 406 caaatgcgacatgtcataagtgaggccagcagtaaaacaacatctgtgttacagtgg 465

Qy 418 GCTGAAAAGGATACTACACCATGAGCAACAACACTTGGTAAACCTCGAAAATGGGAAACAG 477

Db 466 gctgaaaaggatactacaccatgagcaacaacttggtaaccctggaaaatgggaaacag 525

Qy 478 CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACTCTCTGTTCCAAAT 537

Db 526 ctgaccgttaaaagacaaggactctattatctatgcccagtcacactctctgttccaaat 585

Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCTCTGCCTAAAGTCCGCCCGGTAGA 597

Db 586 cgggaagcttcgagtcgaagctccattatagccagcctctgctaaagtcccccgttaga 645

Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTCCGCCAAACCTTGGCGGCAA 657

Db 646 ttcgagagaatcttactcagagctgcaaataccacagcttcgcgcaaaccttgcg99gcaa 705

Qy 658 CAATCCATTCACTTGGGAGGAGTATTGAAATGCAACAGAGTCTTCGCTGTTTGTCAAT 717

Db 706 caatccattcacttgggaggagatttgaattgcaacaggtgcttcggtgttgcataat 765

Qy 718 GTGACTGATCCAGCCAAAGTGGCCATGGCAGCTGCTTCACGTCTCTTGGCTTACTCAAA 777

Db 766 gtgactgatccaagccaagttagccatggcactggcttcacgtctcttggcttactcaaa 825

Qy 778 CTCTGA 783

Db 826 ctctga 831

RESULT 11

AAF55539

ID AAF55539 standard; DNA; 879 BP.

XX AC

XX AAF55539;

DT 29-MAY-2001 (first entry)

XX DE Nucleotide sequence of human gp39 protein, a CD40 ligand.

XX KW gp39; CD40 ligand; osteoblast cell death; apoptosis; bone loss;

XX KW osteoporosis; osteonecrosis; inflammatory arthritis; estrogon loss;

XX KW ovariectomy; histiocytoma; lupus nephritis; Takayasu's arteritis;

XX KW Wegener's granulomatosis; nephritis; myositis; scleroderma;

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 22..807

XX FT /\*tag= a

XX FT /product= "gp39"

XX PN WO200116180-A2.

XX PD 08-MAR-2001.

PF 24-AUG-2000; 2000WO-US23276.  
 XX PR 27-AUG-1999; 99US-0151250.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PI Ahuja SS, Bonewald LF;  
 XX WPI; 2001-169007/17.  
 DR P-PSDB; AAB67612.  
 XX CD40 agonist containing composition, used to reduce bone cell death or  
 PT apoptosis associated with osteoporosis, osteonecrosis and inflammatory  
 PT arthritis  
 XX PS Disclosure; Page 113; 118pp; English.  
 XX CC The present sequence encodes a gp39 protein. It is a CD40 ligand.  
 CC CD40 ligands are used for reducing osteoblast cell death or apoptosis,  
 CC and for treating or preventing bone loss in animals, preferably humans,  
 CC at risk of, or undergoing, bone loss. The bone loss is associated with  
 CC osteoporosis, osteonecrosis, inflammatory arthritis, post-menopausal  
 CC osteoporosis, estrogen loss due to ovariectomy, total hysterectomy,  
 CC lupus nephritis, Takayasu's arteritis, Wegener's granulomatosis,  
 CC anti-glomerular basement membrane nephritis, myositis, scleroderma,  
 CC idiopathic autoimmune thrombocytopenia, asthma, a chronic obstructive  
 CC lung disease, nephrotic/nephritic syndrome, or cancer. They may also be  
 CC used to treat or prevent bone loss in a subject undergoing, or scheduled  
 CC for, an organ or bone marrow transplant.  
 XX SQ Sequence 879 BP; 274 A; 193 C; 190 G; 222 T; 0 other;  
 Query Match 92.8%; Score 726.8; DB 22; Length 879;  
 Best Local Similarity 96.2%; Pred. No. 2.7e-191;  
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps. 1;  
 QY 1 ATGATCGAAGACATACCAACATCTCCCGGATCTCGGGCCACTGCGACTGCCATCAGC 60  
 DB 22 atgacgaacatacaacaaactctcccgatctcgccactgagctgacatgccatcagc 81;  
 QY 61 ATGAATTTTATGTTACTTACTTCTTCTTATCACCAGATGATTGGTTCAGCA 120  
 DB 82 atgaatttttattgtatttacttactgtttttcttattatccacagatgattgggtcagca 141  
 QY 121 CTTTTTGTGTATCTTCATAGAGATTTGGATAAGTTCGAGAGAGAACTTCAT 180  
 DB 142 ctttttgcgtatcttctcatalagaaggttggaacagatagaagatgaagaaatcttcat 201  
 QY 181 GAAGATTTTGTATCAATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240  
 DB 202 gaagatttgcgtatcttctcatalagaaggttggaacagatagaagatgaagaaatcttcat 261  
 QY 241 TTGCTGAAGTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGCAAGGATATAACGTTA 300  
 DB 262 ttactgaactgtgagagatataaagccagtttgaagcgttggtaagagatataatgta 321  
 QY 301 ACAAAGAGA--CAAAAAGAAACAGCTTGAATGCAAAAGGTGATCAGAATCCT 357  
 DB 322 acaaaagagagacgaagaagaacacagcttgaatgcgaagaaggtgaacagaaatcct 381  
 QY 358 CAAATTCGGCCACATGTCATAGTGGCCGACGATCAAAACAAACATCTGTTCAGTGG 417  
 DB 382 caaattgcgcacatgtcatagtgagccagcagtagtaaaacacatctgtttacagtg 441  
 QY 418 GCTGAAAAGGATACACCATGAGCAACACTTTGGTAAACCTCGGAATATGGGAACAG 477  
 DB 442 gctgaaaagagatactacacatgagcaacacttggttaacccctggaaatgggaacag 501  
 QY 478 CTGACCGTTAAAGACAGGACTCTATTATCTATGCCCCAGTCAACCTCTGTTCCTCAAT 537  
 DB 502 ctgaccgttaaaagacagagactctattatctatgcccagtcacactctgttcccaat 561  
 QY 538 CGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTTGCTTAAGTCCCGGTAGA 597  
 DB 562 cgggaagcttcgagctcaagctccatttatagccagctctgctaaagtcgccggtaga 621  
 QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCAACAGTTCGGCCAAACCTTGGGGCAA 657  
 DB 622 ttcgagagaattcttactcagagctgcaaataccacacagttccgccaaaccttgcgggcaa 681  
 QY 658 CAATCCATTCCTTGGGAGGAGTATTTGAATTCGAACAGTCTGCTGGTGTTCCTCAAT 717  
 DB 682 caatccattcacttgggagagatttgaattgcaaccaggtgcttcggtgttgcataat 741  
 QY 718 GTGACTGATCAACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 777  
 DB 742 gtgactgatccaagccaagtgagccatggcactgctcactgcttggcttactcaaa 801  
 QY 778 CTCTGA 783  
 DB 802 ctctga 807  
 RESULT 12  
 AAA51745  
 ID AAA51745 standard; cDNA; 1816 BP.  
 XX AAA51745;  
 AC AAA51745;  
 XX 31-OCT-2000 (first entry)  
 DT Human CD40 ligand cDNA.  
 DE  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 40..825  
 FT CDS  
 FT /\*tag= a  
 FT /product= Human\_CD40\_ligand  
 XX WO200039283-A1.  
 XX 06-JUL-2000.  
 XX 22-DEC-1999; 99WO-US30930.  
 XX 29-DEC-1998; 98US-0114106.  
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 XX Newell MK, Wagner D, Newell E;  
 PI WPI; 2000-452387/39;  
 DR P-PSDB; AAY96993.  
 DR Inducing T cell receptor gene rearrangement for treating autoimmune  
 PT diseases comprises contacting T cells with a CD40-binding agent.  
 PT  
 XX Disclosure; Page 46; 50pp; English.  
 XX CD40 engagement on T cells can be used to induce T cell receptor  
 CC rearrangement and enhance T cell affinity for a particular antigen. CD40  
 CC engagement can be brought about by contacting CD40 with a CD40-binding  
 CC agent, e.g. human CD40 ligand. The CD40-binding agents can also be used  
 CC in methods for promoting T cell maturation, inhibiting T cell receptor  
 CC rearrangement, inhibiting environmental stress-induced cell death,  
 CC altering the specificity of a T cell towards an antigen, inducing T cell  
 CC reactivity towards an antigen or enhancing environmental stress-induced  
 CC cell death (all claimed). T cell affinity maturation towards a specific



FT		or Lys"
FT	mutation	
FT	625..627	b
FT	/*tag=	"wild-type TGC (Cys) codon is mutated to
FT	/note=	a codon for Trp, Ser, Asp or Lys".
FT		
WT		
PX	W09640918-A2.	
PN		
PD	19-DEC-1996.	
PP		
XX	-06-JUN-1996;	96WO-USO9632.
XX	07-JUN-1995;	95US-0484624.
PR	07-JUN-1995;	95US-0477733.
PA	(IMV ) IMMUNEX CORP.	
XX		
PI	Armitage RJ, Fanslow WC, Gibson MG, Spriggs MK;	
PI	Srinivasan S;	
XX		
DR	WPI; 1997-052320/05.	
XX	P-PSDB; AAW091113, AAW091114, AAW091115, AAW091116.	
DR		
PT	New CD40 ligand mutein with higher CD40 affinity than native ligand	
PT	- useful in binding assays, and for therapy of disorders and	
PT	diseases involving low levels of B cells and antibody secretion .	
XX		
CC	Claim 1; Page -; 3lpp; English.	
XX		
CC	This sequence covers cDNA coding for human CD40L mutein polypeptides	
CC	in which the wild-type Cys residue at position 194 has been	
CC	replaced by a Trp, Ser, Asp or Lys residue. The muteins, designated	
CC	C194W, C194S, C194D and C194K, are functional analogues of CD40L	
CC	and as such are useful to induce B cell proliferation and antibody	
CC	secretion. This property may be used to treat disorders associated	
CC	with low levels of B cells or antibody secretion. The new CD40L	
CC	muteins have a higher binding affinity for human CD40 than native	
CC	CD40L and can be used in binding assays.	
CC	(Note: The present sequence does not appear in the specification;	
CC	it has been produced by modifying the wild-type coding sequence,	
CC	which is given on pages 19-20, at codon 194).	
XX		
SQ	Sequence 840 BP; 266 A; 184 C; 174 G; 213 T; 3 other;	
Query Match                  92.4%;    Score 723.8;   DB 18;   Length 840;		
Best Local Similarity    95.8%;   Pred. No. 1.8e-190;		
Matches 753; Conservative     0; Mismatches 30; Indels     3; Gaps		
Qy	1	ATGATCGAAACATACAAACCAAATTCTCCCGATCTGCCGGCTGAGTGGACTGCCCATCAGC 60
Db	46	atgatcgaaacatacaaccaaaccttcccgcagtctgcccactggagctgccatcaggc 105
Qy	61	ATGAATAATTTTAIGTATTTCATTACTGTGTTTTCTTATCACCCAGATGATTTGGGTCAGCA 120
Db	106	atgaataattttaigtatttacttactgttttttccttatccaccagatgattgggtcagca 165
Qy	121	CTTTTGTGCTGTATCTTCATAGAAGATTGGATAAGGTGCAAGAGGAAGTAACCTTCAT 180
Db	166	ctttttgtctgtatcttctcatagaagtttgacaagatatgaagatgaaggaaatcttcat 225
Qy	181	GAAATTTTGTTATTATATAAAAAGCTTAAGAGATGCAACAAGGAGAAGAGATCTTTATCC 240
Db	226	gaagatttgttattcatgaaacgatacacagagatgcaacacaggaagaagatccctatcc 285
Qy	241	TTCGTCACTGTGGAGAGATCAGAGGCAATTTGAAGACCTTCTCAAGGATATAAGCTTGA 300
Db	286	tactgtacctgtgaggagattcaaaagccagtttgaaagcgtttgaaagcgtttgaaagataaagtta 345
Qy	301	AACAAGAGAAGA ---GAAAAAGAAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357
Db	346	aacaagaggagacgaagaagaacacagcgtttgaaatgcgaagaaggtgatcagaatccct 405

QY 358 CAAATTGGCGGCACATGTCATATAAGTGAGCCAGCAGTAAACAACTCTGTGTACAGTGG 417  
 CC |||||||  
 Db 406 caaattgcgccacatgtcataagtgaggccagcagtaaaacaacatctgtgtacagtg 465  
 CC |||||||  
 QY 418 GCTGAAAAGGATACACCATGAGCACAACACTTGGTAACCTCGAAATCGGAAACAG 477  
 CC |||||||  
 Db 466 gctgaaaaaggatatacacaccatgagcaacaacttggttaaccctggaaaatgggaaacag 525  
 CC |||||||  
 QY 478 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGCCCCAAGTCACCTTCGTTCCTCAAT 537  
 CC |||||||  
 Db 526 ctgacgcttaaaagacaaggactcattatatactatgccccagtcacctctctgttcccaat 585  
 CC |||||||  
 QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCGCCGTAGTA 597  
 CC |||||||  
 Db 586 cgggaagcttcgagtcgaagctccattatagccagcctcnnnctaaagtcccccggtaga 645  
 CC |||||||  
 QY 598 TTCGAGAGAACTTACTCAGAGCTCAATACCCAGTTCGCCCAAACTTGGCGGCA 657  
 CC |||||||  
 Db 646 ttcgagagaatcttactcagagctgcaaatatacccaagttccgcgaaccttgcgggcaa 705  
 CC |||||||  
 QY 658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGTGCTTCGGTGTGTTCAT 717  
 CC |||||||  
 Db 706 caatccattcacttgggaggagtatttgaattgcaaccagggtctcggttbtgtcaat 765  
 CC |||||||  
 QY 718 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGGCTTCACGCTCTGCTTGGCTTACTCAA 777  
 CC |||||||  
 Db 766 gtgactgatcccaagccaagtgagccatggcactggcttcacgtccttggcttactcaaa 825  
 CC |||||||  
 QY 778 CTCTGA 783  
 CC |||||||  
 Db 826 cctctga 831

## RESULT 15

AAQ57984  
 ID AAQ57984 standard; DNA; 840 BP.  
 XX AC AAQ57984;  
 XX DT 20-AUG-1994 (first entry)  
 XX DE Genomic sequence of human gp39.  
 XX KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation;  
 XX KW B-cell differentiation; ss.  
 XX OS Homo sapiens.  
 XX FH Key  
 XX FT CDS  
 XX PD Location/Qualifiers  
 XX FT 22..807  
 XX FT /\*tag= a  
 XX PN EP585943-A.  
 XX PD 09-MAR-1994.  
 XX PF 03-SEP-1993; 93EP-0114153.  
 XX PR 04-SEP-1992; 92US-0940605.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Aruffo AA, Hollenbaugh D, Ledbetter JA, Aruffo A;  
 XX WPI; 1994-076264/10.  
 XX DR P-PSDB; AAR59548.  
 XX PT New nucleic acid encoding human gp39 T cell antigen - which is a  
 XX PT ligand for the CD40 receptor, causing proliferation and  
 XX PT differentiation of B cells and some cancer cells  
 XX PS Claim 1; Fig 1; 39pp; English.

CC The complete nucleic acid sequence of human gp39 (hgp39) protein  
 (corresp. to cDNA) and the complete AA sequence of hgp39 are  
 CC presented in AAQ57984 and AAR49548 respectively and contd. in plasmid  
 CC CD8-hgp39, deposited with the ATCC as E. coli, CD8 MC1061/p3-hgp39  
 CC and assigned accession No. 69050. The human T cell antigen gp39 is a  
 CC ligand for the CD40 receptor. Soluble gp39 may be produced using the  
 CC expression vector CD8-gp39.  
 XX  
 SQ Sequence 840 BP; 263 A; 180 C; 183 G; 214 T; 0 other;  
 Query Match 92.4%; Score 723.6; DB 15; Length 840;  
 Best Local Similarity 95.9%; Pred. No. 2e-190;  
 Matches 754; Conservative 0; Mismatches 29; Indels 3; Gaps 1;  
 QY 1 ATGATCGAAACATACAAACCACTTCTCCCGATCTGCGGCCACTGGAGTCCCATCAGC 60  
 CC |||||||  
 Db 22 atgagggaaacatacaaacactctcccagatctcgggccactggagatgccatcagc 81  
 CC |||||||  
 QY 61 ATGAAATTTTATGTATTTACTTACTGTGTTTTCATCACCAGATGATGGGTGAGCA 120  
 CC |||||||  
 Db 82 atgaaaattttatgtatttacttactgttttttcttaccacagatgattgggtcagca 141  
 CC |||||||  
 QY 121 CTTTTCGTGTATCTTCATAGAGATTGGATAGGTGCAAGAGGAAGTAACCTTCAT 180  
 CC |||||||  
 Db 142 ctttttgcgtgtatcttcataagaggttggaacaagatagaagatgaaggaaatctcat 201  
 CC |||||||  
 QY 181 GAAGATTTTGTATTATATAAAAGCTTAAAGAGATGCAACAAAGGAGCAAGTCTTTATCC 240  
 CC |||||||  
 Db 202 gaagatttctgtattcattgaaacgatacagagatgcaacacagggagaaagatccctatcc 261  
 CC |||||||  
 QY 241 TTGCTCAACTGTGAGGAGATGAGAAGGCAATTTGAGAGCTTGTCAAGGATATAAGCTTA 300  
 CC |||||||  
 Db 262 ttaactgaactgagagagattaaaagccagtttgaagctttgtgaagatataatgtta 321  
 CC |||||||  
 QY 301 AACAAAGAAGA--GAAAAAGAAAACACGCTTTGAAATCCAAAAGGTGATCAGAACTCT 357  
 CC |||||||  
 Db 322 aacaaaggaggagacgaagaagaaacagctttgaatgcaaaagcgtgatcagaatcct 381  
 CC |||||||  
 QY 358 CAAATTTGCGGCACATGTCATTAAGTGAGGCCAGCAGTAAACAACTCTCTGTGTACAGTGG 417  
 CC |||||||  
 Db 382 caaattgcgcacatgcatagtgaggtgagccagcagtaaaacaacatctgtgtacagtgg 441  
 CC |||||||  
 QY 418 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTCGGAAATCGGAAACAG 477  
 CC |||||||  
 Db 442 gctgaaaaaggatatacacaccatgagcaacaacttggtaaccctggaaaatgggaaacag 501  
 CC |||||||  
 QY 478 CTGACCGTTAAAGACACAGGACTCTATTATATCTATGCCCCAAGTCACCTTCGTTCCTCAAT 537  
 CC |||||||  
 Db 502 ctgacgcttaaaagacaaggactctattatatactatgccccagtcacctctctgttcccaat 561  
 CC |||||||  
 QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCGCCGTAGTA 597  
 CC |||||||  
 Db 562 cgggaagcttcgagtcgaagctccattatagccagcctctgcctaaagtcctcccggtaga 621  
 CC |||||||  
 QY 598 TTCGAGAGAACTTACTCAGAGCTGCAATACCCAGTTCGCCCAAACTTGGCGGCA 657  
 CC |||||||  
 Db 622 ttcgagagaatcttactcagagctgcaaatatacccaagttccgcgaaccttgcgggca 681  
 CC |||||||  
 QY 658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGTGCTTCGGTGTGTTCAT 717  
 CC |||||||  
 Db 682 caatccattcacttgggaggagtatttgaattgcaaccagggtcttcggttbtgtcaat 741  
 CC |||||||  
 QY 718 GTGACTGATCCAAAGCAAGTGAGCCATGGCTTCACGCTCTGCTTGGCTTACTCAA 777  
 CC |||||||  
 Db 742 gtgactgatcccaagccaagtgagccatggcactggcttcacgtccttggcttactcaaa 801  
 CC |||||||  
 QY 778 CTCTGA 783  
 CC |||||||  
 Db 802 cctctga 807

Search completed: May 30, 2002, 03:03:47  
Job time: 11276 sec

43: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq

## SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	726.8	100.0	783	13	Sequence 20, Appli
2	726.8	92.8	786	5	Sequence 3, Appli
3	726.8	92.8	786	13	Sequence 1, Appli
4	726.8	92.8	840	1	Sequence 7, Appli
5	726.8	92.8	840	1	Sequence 1, Appli
6	726.8	92.8	840	1	Sequence 1, Appli
7	726.8	92.8	840	3	Sequence 10, Appli
8	726.8	92.8	840	3	Sequence 11, Appli
9	726.8	92.8	840	3	Sequence 11, Appli
10	726.8	92.8	840	4	Sequence 7, Appli
11	726.8	92.8	840	5	Sequence 1, Appli
12	726.8	92.8	840	6	Sequence 1, Appli
13	726.8	92.8	840	6	Sequence 3, Appli
14	726.8	92.8	840	7	Sequence 1, Appli
15	726.8	92.8	840	8	Sequence 11, Appli
16	726.8	92.8	840	8	Sequence 11, Appli
17	726.8	92.8	840	9	Sequence 7, Appli
18	726.8	92.8	840	10	Sequence 1, Appli
19	726.8	92.8	840	11	Sequence 11, Appli
20	726.8	92.8	840	14	Sequence 11, Appli
21	726.8	92.8	840	17	Sequence 11, Appli
22	726.8	92.8	840	17	Sequence 11, Appli
23	726.8	92.8	840	17	Sequence 11, Appli
24	726.8	92.8	840	17	Sequence 11, Appli
25	726.8	92.8	840	17	Sequence 1, Appli
26	726.8	92.8	840	17	Sequence 1, Appli
27	726.8	92.8	840	17	Sequence 1, Appli
28	726.8	92.8	840	17	Sequence 11, Appli
29	726.8	92.8	840	17	Sequence 11, Appli
30	726.8	92.8	840	18	Sequence 1, Appli
31	726.8	92.8	840	21	Sequence 7, Appli

32 726.8 92.8 840 21 US-09-545-993A-7  
33 726.8 92.8 879 25 US-09-645-926A-1  
34 726.8 92.8 1803 18 US-09-469-519-31  
35 726.8 92.8 1803 34 US-09-909-595-3  
36 726.8 92.8 1803 71 US-60-329-393-3  
37 726.8 92.8 1816 1 PCT-US01-08631-22375  
38 726.8 92.8 1816 1 PCT-US01-08655-373  
39 726.8 92.8 1816 1 PCT-US99-30930-1  
40 726.8 92.8 1816 18 US-09-442-384A-457  
41 726.8 92.8 1816 18 US-09-470-494-1  
42 726.8 92.8 1816 18 US-09-470-494A-1  
43 726.8 92.8 1816 25 US-09-645-926A-5  
44 725.2 92.6 786 1 PCT-US01-07009-6  
45 725.2 92.6 1833 1 PCT-US01-14827-3489

ALIGNMENTS

RESULT 1  
US-08-982-272-20  
: Sequence 20, Application US/08982272  
: GENERAL INFORMATION:  
: APPLICANT: Kipps, Thomas J.  
: APPLICANT: Sharma, Sanjai  
: APPLICANT: Cantwell, Mark  
: TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
: TITLE OF INVENTION: CONTAINING ACCESSORY  
: TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
: TITLE OF INVENTION: THEIR USE FOR IMMUNO-  
: TITLE OF INVENTION: MODULATION AND TREATMENT OF  
: TITLE OF INVENTION: MALIGNANCIES  
: NUMBER OF SEQUENCES: 44  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Lyon & Lyon  
: STREET: 633 West Fifth Street  
: CITY: Los Angeles  
: STATE: California  
: COUNTRY: U.S.A.  
: ZIP: 90071-2066  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5" Diskette,  
: MEDIUM TYPE: 1.44 Mb storage  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: IBM P.C. DOS 5.0.  
: SOFTWARE: FastSeq Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/982,272  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 60/132145  
: FILING DATE: 12/9/96  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Guise, Jeffrey W.  
: REGISTRATION NUMBER: 34,613  
: REFERENCE/DOCKET NUMBER: 231/003  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (213) 489-1600  
: TELEFAX: (213) 955-0440  
: TELEX: 67-3510  
: INFORMATION FOR SEQ ID NO: 20:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 783 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear

Query Match 100.0%; Score 783; DB 13; Length 783;  
Best Local Similarity 100.0%; Pred. No. 7.9e-174;

Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGCATGCGGCCACTGGACTGCCCATCAGC 60  
DB 1 ATGATCGAAACATACAAACAACTTCTCCCGCATGCGGCCACTGGACTGCCCATCAGC 60  
QY 61 ATGAAAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTTCAGCA 120  
DB 61 ATGAAAAATTTTATGATTTACTTACTTCTTATCACCAGATGATGGGTTCAGCA 120  
QY 121 CTTTTCGCTGCTATCTTATGATTAAGATTTGATTAAGTTCGAAGAGGAAGTAACCTTCA 180  
DB 121 CTTTTCGCTGCTATCTTATGATTAAGATTTGATTAAGTTCGAAGAGGAAGTAACCTTCA 180  
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATCAACAAGAGGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATCAACAAGAGGAGAGATCTTTATCC 240  
QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
DB 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
QY 301 AACAAAG 360  
DB 301 AACAAAG 360  
QY 361 ATTGGGACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
DB 361 ATTGGGACATGTCATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420  
QY 421 GAAAAAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGGAAACAGCTG 480  
DB 421 GAAAAAGGATCTACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGGAAACAGCTG 480  
QY 481 ACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAATCG 540  
DB 481 ACCGTTTAAAGACAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAATCG 540  
QY 541 GAAGCTTCGATCAAGCTCCATTTATAGCAGGCTTGCCTTAAGTCCCGGTCAGATTC 600  
DB 541 GAAGCTTCGATCAAGCTCCATTTATAGCAGGCTTGCCTTAAGTCCCGGTCAGATTC 600  
QY 601 GAGAGATCTTACTCAGAGCTGCAAAATACCCAGCTTCCGCCCCAACCTTTCGCGGCAACAA 660  
DB 601 GAGAGATCTTACTCAGAGCTGCAAAATACCCAGCTTCCGCCCCAACCTTTCGCGGCAACAA 660  
QY 661 TCCATTTCATTTGGGAGGAGTATTTGAATTCGAACACAGGCTTCGGTGTTCATATG 720  
DB 661 TCCATTTCATTTGGGAGGAGTATTTGAATTCGAACACAGGCTTCGGTGTTCATATG 720  
QY 721 ACTGATCCCAAGCCCAAGTGAAGCTGAGCCATGCTTCCAGCTTCCCTTTCCTTCAAACTC 780  
DB 721 ACTGATCCCAAGCCCAAGTGAAGCTGAGCCATGCTTCCAGCTTCCCTTTCCTTCAAACTC 780  
QY 781 TGA 783  
DB 781 TGA 783

RESULT 2  
US-08-107-353-3  
: Sequence 3, Application US/08107353  
: GENERAL INFORMATION:  
: APPLICANT: Spriggs, Melanie  
: APPLICANT: Srinivasan, Subhashini  
: TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
: TITLE OF INVENTION: Proteins  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle  
: STATE: WA



COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/107.353  
FILING DATE: 19930813  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
US-08-107-353-3

Query Match 92.8%; Score 726.8; DB 5; Length 786;  
Best Local Similarity 96.2%; Pred. No. 1.3e-160;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy	1	ATGATCGAAACATACCAACCAACTTCTCCCGATCTGCGGCACGTGGACTGCCCATCAGC	60
Db	1	ATGATCGAAACATACCAACCAACTTCTCCCGATCTGCGGCACGTGGACTGCCCATCAGC	60
Qy	61	ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA	120
Db	61	ATGAAATTTTATGATTTTACTTACTCTTTTCTTATCACCAGATGATTGGGTCAGCA	120
Qy	121	CTTTTGTCTGTATCTTCATAGAGATTGGATAGGTGCGAGAGAGTAAACCTTCAT	180
Db	121	CTTTTGTCTGTATCTTCATAGAGATTGGATAGGTGCGAGAGAGTAAACCTTCAT	180
Qy	181	GAAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
Db	181	GAAGATTTTGTATTTCATATAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
Qy	241	TTGCTGAAGTGTGAGAGATGAGAGGCAATTGGAAGACCTTTGTCAGGATATAACGTTA	300
Db	241	TTACTGAAGTGTGAGAGATTAAGAGCCAGTTGAAGCTTTGTGAAGGATATAATGTTA	300
Qy	301	AACAAAGAAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	357
Db	301	AACAAAGAGAGACAGAAAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT	360
Qy	358	CAAAATGCGGCACATGTCATAGTCAGCCAGCAGTCAACAAACATCTGCTTACAGTGG	417
Db	361	CAAAATGCGGCACATGTCATAGTCAGCCAGCAGTCAACAAACATCTGCTTACAGTGG	420
Qy	418	GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTGCAAAAATGGGAAACAG	477
Db	421	GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAAACCTGCAAAAATGGGAAACAG	480
Qy	478	CTGACCGTTAAAGACAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTTCCAAT	537

Db	481	CTGACCGTTAAAGACAAGGACTCTATTATATCTATGCCAAGTCACCTTCTGTTTCCAAT	540
Qy	538	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTTGCTTAAGTCCCGCGTAGA	597
Db	541	CGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGCCTTGCTTAAGTCCCGCGTAGA	600
Qy	598	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGCGGGCAA	657
Db	601	TTGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAACCTTTGCGGGCAA	660
Qy	658	CAATCCATTCACTTCGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTCAAT	717
Db	661	CAATCCATTCACTTCGGGAGGAGTATTGAAATGCAACAGGTGCTTCGGTGTGTTCAAT	720
Qy	718	GTGACTGATCCAAGCAAGTGAAGCCATGGCACTGCTTCACGTCTCTTTGGCTTACTCAA	777
Db	721	GTGACTGATCCAAGCAAGTGAAGCCATGGCACTGCTTCACGTCTCTTTGGCTTACTCAA	780
Qy	778	CTCTGA 783	
Db	781	CTCTGA 786	

RESULT 3  
US-08-982-272-1  
Sequence 1, Application US/08982272  
GENERAL INFORMATION:  
APPLICANT: Kipps, Thomas J.  
APPLICANT: Sharma, Sanjai  
TITLE OF INVENTION: NOVEL EXPRESSION VECTORS  
TITLE OF INVENTION: CONTAINING ACCESSORY  
TITLE OF INVENTION: MOLECULE LIGAND GENES AND  
TITLE OF INVENTION: THEIR USE FOR IMMUNO-  
TITLE OF INVENTION: MODULATION AND TREATMENT OF  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette.  
MEDIUM TYPE: 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq, Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/982,272  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/132145  
FILING DATE: 12/9/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 231/003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-982-272-1

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Query Match          92.8%; Score 726.8; DB 13; Length 786;
Best Local Similarity 96.2%; Pred No. 1.3e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 60
DB 1 ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC 60

QY 61 ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGTTCAGCA 120
DB 61 ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGTTCAGCA 120

QY 121 CTTTCTGCTGTGTATCTTCATAGAACTGGATAGGTCGAAGGAGGAAGTAAACCTTCAT 180
DB 121 CTTTCTGCTGTGTATCTTCATAGAACTGGATAGGTCGAAGGAGGAAGTAAACCTTCAT 180

QY 181 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
DB 181 GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240

QY 241 TTCTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300
DB 241 TTCTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTGTGAAGATATAAGCTTA 300

QY 301 AACAAAGAGA ---GAAAAGAGAAACAGCTTTGAAATGCAAAAAGGTGATCAGAACTCT 357
DB 301 AACAAAGAGAGAGAGAGAGAGAGAGAGATGCAACAAAGGAGAGATCAGAACTCT 360

QY 358 CAATTCGCGGCACATGTCATAGTGGAGGCGAGCAGTAAACACATCTGTTTACAGTGG 417
DB 361 CAAATTCGCGGCACATGTCATAGTGGAGGCGAGCAGTAAACACATCTGTTTACAGTGG 420

QY 418 GCTGAAAAGGATACACCATGAGCAACACTTGGTAACTCGGAAAATGGGAAACAG 477
DB 421 GCTGAAAAGGATACACCATGAGCAACACTTGGTAACTCGGAAAATGGGAAACAG 480

QY 478 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTTCCTTCCAAT 537
DB 481 CTGACCGTTTAAAGACAGGACTCTATTATATCTATGCCCAGTCACTTCCTTCCAAT 540

QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGTAGA 597
DB 541 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGCGTAGA 600

QY 598 TTCGAGAGATCTTACTCAGAGTGCATATACCCAGATTTCCGCCAAACCTTCGGGCAA 657
DB 601 TTCGAGAGATCTTACTCAGAGTGCATATACCCAGATTTCCGCCAAACCTTCGGGCAA 660

QY 658 CAATCCATTCACCTGGGAGGATTTGAAATGCAACAGGTGCTCGGTGTTTGTCAAT 717
DB 661 CAATCCATTCACCTGGGAGGATTTGAAATGCAACAGGTGCTCGGTGTTTGTCAAT 720

QY 718 GTGACTCATCCAGCCAAAGTGCAGCTGGCTGCTTCAAGTCTTGGCTTACTCAAA 777
DB 721 GTGACTCATCCAGCCAAAGTGCAGCTGGCTGCTTCAAGTCTTGGCTTACTCAAA 780

QY 778 CTCCTGA 783
DB 781 CTCCTGA 786
```

RESULT 4  
PCT-US94-00786-7  
Sequence 7, Application PC/TUS9400786  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSCH, BLAIR  
APPLICANT: SPRIGGS, MELANIE

APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/00786  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/009,258  
APPLICATION NUMBER: 01/22/93  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
PCT-US94-00786-7

Query Match 92.8%; Score 726.8; DB 1; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1.4e-160;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY	DB	QY	DB	QY	DB	QY	DB	QY	DB
1	46	61	106	121	166	181	226	241	286
ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC	ATGATCGAAACATACAAACAACTCTCCCGATCTGGCGGCACCTGGAGTGCCTATCAGC	ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGTTCAGCA	ATGAAAATTTTATGATTTACTTACTGTTTTCTTATCACCAGATGATGGTTCAGCA	CTTTTCTGCTGTGTATCTTCATAGAACTGGATAGGTCGAAGGAGGAAGTAAACCTTCAT	CTTTTCTGCTGTGTATCTTCATAGAACTGGATAGGTCGAAGGAGGAAGTAAACCTTCAT	GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC	GAAGATTTTGTATTCATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC	TTCTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTGAAGATATAAGCTTA	TTACTGTAACCTGTCAGAGATGAGAGCAATTTGAAGACCTTGTGAAGATATAAGCTTA



QY 718 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTTCAGCTCCTTTGGGTTACTCAA 777  
 Db 766 GTGACTGATCCAAAGCAAGTGGAGCATGGCTTTCAGCTCCTTTGGGTTACTCAA 825  
 QY 778 CTCTGA 783  
 Db 826 CTCTGA 831

RESULT 6

PCT-US97-11956-1  
 ; Sequence 1, Application PC/TUS9711956  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Power Macintosh 7200/90  
 ; OPERATING SYSTEM: Apple Operating System 7.6  
 ; SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US97/11956  
 ; FILING DATE: 09-JUL-1997  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/677,762  
 ; FILING DATE: 10-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/763,995  
 ; FILING DATE: 12-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia A.  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2845-WO  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)233-0644  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 840 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; IMMEDIATE SOURCE:  
 ; CLONE: CD40-L  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 46..831  
 ; PCT-US97-11956-1

Query Match 92.8%; Score 726.8; DB 1; Length 840;  
 Best Local Similarity 96.2%; Pred. No. 1.4e-160;  
 Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
 QY 1 ATGATCAACATACACCAAACTTCTCCCGGATCTGGCCCACTGGCTGCTCCATCAGC 60  
 Db 46 ATGATCAACATACACCAAACTTCTCCCGGATCTGGCCCACTGGCTGCTCCATCAGC 105

QY 61 ATGAAATTTTATGTATTACTTACTTGTCTTCTTATCACCAGATGATTGGGTACGA 120  
 Db 106 ATGAAATTTTATGTATTACTTACTTGTCTTCTTATCACCAGATGATTGGGTACGA 165  
 QY 121 CTTTTCCTGTGTATCTTATAGAAAGTTCGATTAAGTTCGAAAGAGGAAGTAAACCTTCAT 180  
 Db 166 CTTTTCCTGTGTATCTTATAGAAAGTTCGATTAAGTTCGAAAGAGGAAGTAAACCTTCAT 225  
 QY 181 GAAGATTTTGTATTATTAATAAAGCTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240  
 Db 226 GAAGATTTTGTATTATTAATAAAGCTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 285  
 QY 241 TTGCTGACTGTGAGGAGATGAGAAGGCAATTTTGAAGACCTTTGCAAGGATATAACCTTA 300  
 Db 286 TTGCTGACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGGATATAATGTTA 345  
 QY 301 AACAAAGAAGA- ---GAAAAAGAAACAGCTTTTGAATGCAAAAAAGGTGATCAGAACTCT 357  
 Db 346 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTTGAATGCAAAAAAGGTGATCAGAACTCT 405  
 QY 358 CAAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417  
 Db 406 CAAATTCGGGCACATGTCATTAAGTGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
 QY 418 GCTGAAAAAGGATATACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 477  
 Db 466 GCTGAAAAAGGATATACACCATGAGCAACAACTTGGTAAACCTTGGAAAAATGGAAAAACAG 525  
 QY 478 CTGACCGTTAAAGCAAGAGCTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 537  
 Db 526 CTGACCGTTAAAGCAAGAGCTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCCTCAAT 585  
 QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 597  
 Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTTATAGCCAGCCTCTGCTTAAAGTCCCGCGGTAGA 645  
 QY 598 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCACAGTTCGCCCAACCTTGGGGGCAA 657  
 Db 646 TTCGAGAGAAATCTTACTCAGAGTGCATAATACCCACAGTTCGCCCAACCTTGGGGGCAA 705  
 QY 658 CAATCCATTCTGCTGGGAGGAGTATTTCAATTGCAACAGGTGCTTCGGTGTCTTCTCAAT 717  
 Db 706 CAATCCATTCTGCTGGGAGGAGTATTTCAATTGCAACAGGTGCTTCGGTGTCTTCTCAAT 765  
 QY 718 GTGACTGATCCAAAGCAAGTGGCCATGGCCTTTCAGTCTCCTTTGGCTTACTCAA 777  
 Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCCTTTCAGTCTCCTTTGGCTTACTCAA 825  
 QY 778 CTCTGA 783  
 Db 826 CTCTGA 831

RESULT 7  
 US-07-805-723-10  
 ; Sequence 10, Application US/07805723  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ARMITAGE, RICHARD  
 ; APPLICANT: FANSLAW, WILLIAM  
 ; APPLICANT: SPRIGGS, MELANIE  
 ; TITLE OF INVENTION: NOVEL CYTOKINE  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: IMMUNEX CORPORATION  
 ; STREET: 51 UNIVERSITY STREET  
 ; CITY: SEATTLE  
 ; STATE: WASHINGTON  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS



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Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGCGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165
QY 121 CTTTTCGTGCTGATCTTCATAGAGATGGATAGGTGCAAGAGAGATTAACCTTCAT 180
Db 166 CTTTTCGTGCTGATCTTCATAGAGATGGATAGGTGCAAGAGATTAACCTTCAT 225
QY 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTATCC 285
QY 241 TTCTGAACTGTGAGGAGATGAGAGCAATTTGAAGACCTTTGTCAAGGATATAAGTTA 300
Db 286 TTACTGAACGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
QY 301 AACAAGAGA---GAAAGAGAAACAGCTTGAATGCAAAAGGTGATCAGATCCT 357
Db 346 AACAAGAGGAGACGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT 405
QY 358 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 525
QY 478 CTGACGGTTTAAAGAGCAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTCCAAT 537
Db 526 CTGACGGTTTAAAGAGCAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTCCAAT 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGGAGAGCTCTGCTAAAGTCCCGGTAGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGGAGAGCTCTGCTAAAGTCCCGGTAGA 645
QY 598 TTGAGAGATCTTACTAGAGTGCATATACCCAGATTCGCGCAAACTTCGCGGCAA 657
Db 646 TTGAGAGATCTTACTAGAGTGCATATACCCAGATTCGCGCAAACTTCGCGGCAA 705
QY 658 CAATCATTACCTTGGAGGAGTATTTGAATGCAACAGGCTGCTTCGCTGTGTGCAAT 717
Db 706 CAATCATTACCTTGGAGGAGTATTTGAATGCAACAGGCTGCTTCGCTGTGTGCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGGAGCCAGTGGCTTCACGTCCTTTGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGGAGCCAGTGGCTTCACGTCCTTTGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

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RESULT 9
US-07-969-703B-11
; Sequence 11, Application US/07969703B
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLON, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: NOVEL CYTOKINE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07969,703B
; FILING DATE: 19921023
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
; US-07-969-703B-11

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Query Match 92.8%; Score 726.8; DB 3; Length 840;

Best Local Similarity 96.2%; Pred. No. 1.4e-160;

Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

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QY 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCGCGCCACTGGACTGCCCATCAGC 60
Db 46 ATGATCGAAACATACAAACAACTTCTCCCGCATCGCGCCACTGGACTGCCCATCAGC 105
QY 61 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 120
Db 106 ATGAAATTTTATGATTTACTTACTTCTTCTTATCACCAGATGATGGGTGAGCA 165
QY 121 CTTTTCGTGCTGATCTTCATAGAGATGGATAGGTGCAAGAGAGATTAACCTTCAT 180
Db 166 CTTTTCGTGCTGATCTTCATAGAGATGGATAGGTGCAAGAGAGATTAACCTTCAT 225
QY 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTATCC 240
Db 226 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTATCC 285
QY 241 TTGCTGAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300
Db 286 TTACTGAACGTGAGGAGATTAAGAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345
QY 301 AACAAGAGA---GAAAGAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT 357
Db 346 AACAAGAGGAGACGAGAGAGAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT 405
QY 358 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCATAGTGGAGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465
QY 418 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGATACACCATGAGCAACACTTGGTAAACCTGGAAAAATGGAAACAG 525
QY 478 CTGACGGTTTAAAGAGCAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTCCAAT 537
Db 526 CTGACGGTTTAAAGAGCAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTCCAAT 585

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QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 597
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGCGTAGA 645
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 705
QY 658 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTTCGCGTGTGTTGTCAAT 717
Db 706 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTTCGCGTGTGTTGTCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGAAGCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGAAGCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

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RESULT 10

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US-08-009-258-7
; Sequence 7, Application US/08009258
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: WIDMER, MICHAEL
; TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,258
; FILING DATE: 19930122
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PERKINS, PATRICIA A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..831
US-08-009-258-7

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```

Query Match 92.8%; Score 726.8; DB 4; Length 840;
Best Local Similarity 96.2%; Pred. No. 1.4e-160;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;
QY 1 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCGCCATCAGC 60
Db 46 ATGATCGAAACATCAACCAAACTTCTCCCGCATCTGCGGCCACTGGAGTCCGCCATCAGC 105
QY 61 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACAGATGATGGGTGAGCA 120
Db 106 ATGAAATTTTATGTATTTACTTACTGTTTCTTATCACCACAGATGATGGGTGAGCA 165
QY 121 CTTTTTGTGTGTATCTTTCATAGAGATTTGATAAGGTGCAAGAGAGAACTTCAAT 180
Db 166 CTTTTTGTGTGTATCTTTCATAGAGATTTGATAAGGTGCAAGAGATGATAAGAGAACTTCAAT 225
QY 181 GAAGATTTTGTATTTATTAATAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATTTATTAATAAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTTATCC 285
QY 241 TTGCTGAAGTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGATATAAGTTA 300
Db 286 TTACTGAAGTGTGAGGAGATTTGAAGCCAGTTTGAAGGCTTTGTGAAGATATAAGTTA 345
QY 301 AACAAAGAGA---GAAAAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGATCTCT 357
Db 346 AACAAAGAGGACGACGAAGAAGAAAACAGCTTTTGAATGCAAAAAGGTGATCAGATCTCT 405
QY 358 CAAATTCGCGCACATGTCTAAGTGTAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 417
Db 406 CAAATTCGCGCACATGTCTAAGTGTAGGCGCAGCAGTAAACACATCTCTGTGTACAGTGG 465
QY 418 GCTGAAAAGAGTACTACACCATGAGCAACAACCTTGGTAACCTCGAAAATGGGAACAG 477
Db 466 GCTGAAAAGAGTACTACACCATGAGCAACAACCTTGGTAACCTCGAAAATGGGAACAG 525
QY 478 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCAACCTTCTGTTCCAAT 537
Db 526 CTGACCGTTTAAAGACAAGGACTCTATTATATCTATGCCCAAGTCAACCTTCTGTTCCAAT 585
QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAGTCCCGCGTAGA 597
Db 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAGTCCCGCGTAGA 645
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 657
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCCGCCAAAACCTTTGCGGGCAA 705
QY 658 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTTCGCGTGTGTTGTCAAT 717
Db 706 CAATCCATTCACCTGGGAGGAGTATTTGAATTGCAACAGAGTTCGCGTGTGTTGTCAAT 765
QY 718 GTGACTGATCCAAAGCAAGTGAAGCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 777
Db 766 GTGACTGATCCAAAGCAAGTGAAGCATGCGACTGCTTCACGTCCTTTGGCTTACTCAA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

```

RESULT 11

```

US-08-172-664-1
; Sequence 1, Application US/08172664
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANSLAW, WILLIAM
; APPLICANT: LONGO, DAN L.
; APPLICANT: MURPHY, WILLIAM
; TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
; TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
; TITLE OF INVENTION: EXPRESSING CD40

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IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-215-862-1

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1.4e-160;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAACAATCAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 60  
Db 46 ATGATCGAACAATCAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 105  
Qy 61 ATGAAATTTTATCTATTTACTTCTTCTTCTTATCACCACAGATGTTGGTTCAGCA 120  
Db 106 ATGAAATTTTATCTATTTACTTCTTCTTCTTATCACCACAGATGTTGGTTCAGCA 165  
Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGTTCGAAGAGAGATTAACCTTCAT 180  
Db 166 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGATTAACCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAGAGAGATCTTTTATCC 240  
Db 226 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAGAGATCTTTTATCC 285  
Qy 241 TTGCTGAATCTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATACGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTAAAGAGGCTTTGAAGGCTTTGTCAAGGATATACGTTA 345  
Qy 301 AACAAAGAGA--GAAAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 357  
Db 346 AACAAAGAGAGACAGAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 405  
Qy 358 CAAATTTGGGACATCTCATAGTGGCCAGCAGTAAACAACTCTGTGTACAGTGG 417  
Db 406 CAAATTTGGGACATCTCATAGTGGCCAGCAGTAAACAACTCTGTGTACAGTGG 465  
Qy 418 GCTGAAAGAGATACATACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAAACAG 477  
Db 466 GCTGAAAGAGATACATACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAAACAG 525  
Qy 478 CTGACCGTTAAAGACAGGACTCTATTATCTATGTCGCAAGTCACTCTGTTCCCAAT 537  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATCTATGTCGCAAGTCACTCTGTTCCCAAT 585  
Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 597  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGTGA 645  
Qy 598 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGCGGCA 657  
Db 646 TTCGAGAGAACTTACTCAGAGCTCAATACCCACAGTTCGCGCAACCTTGGCGGCA 705  
Qy 658 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGTCCTGCTGTTCTCAAT 717  
Db 706 CAATCCATCTACTTGGGAGGAGTATTGAAATGCAACAGGTCCTGCTGTTCTCAAT 765  
Qy 718 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAA 777  
Db 766 GTGACTGATCCAAAGCAAGTGGCCATGGCAGTGGCTTCAGTCTCTTTGGCTTACTCAA 825  
Qy 778 CTCTGA 783  
Db 826 CTCTGA 831

RESULT 13  
US-08-234-580-3  
Sequence 3, Application US/08234580  
GENERAL INFORMATION:

APPLICANT: KEHR, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/234,580  
FILING DATE: 28-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 22..807  
US-08-234-580-3

Query Match 92.8%; Score 726.8; DB 6; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1.4e-160;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAACAATCAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 60  
Db 22 ATGATCGAACAATCAACAACTTCTCCCGATCTGGCCACCTGGAGTGGCCATCAGC 81  
Qy 61 ATGAAATTTTATCTATTTACTTACTTCTTCTTATCACCACAGATGTTGGTTCAGCA 120  
Db 82 ATGAAATTTTATCTATTTACTTACTTCTTCTTATCACCACAGATGTTGGTTCAGCA 141  
Qy 121 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGTTCGAAGAGAGATTAACCTTCAT 180  
Db 142 CTTTTTGTCTGTATCTTCATAGAGATTGGATAGAGATTAACCTTCAT 201  
Qy 181 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAGAGAGATCTTTATCC 240  
Db 202 GAAGATTTTGTATTCATATAAAGCTTAAGAGATGCAACAAGAGAGATCTTTATCC 261  
Qy 241 TTGCTGAACTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGCAAGGATATACGTTA 300  
Db 262 TTACTGAACTGTGAGGAGATTAAGAGGCTTTGTAAGGCTTTGTGAAGGATATAATGTTA 321  
Qy 301 AACAAAGAGA--GAAAAAGAAACAGCTTTGAAATGCAAAAGGTCATCAGATCCT 357  
Db 322 AACAAAGAGGAGACCAAGAAACACACTTTGAAATGCAAAAGGTCATCAGATCCT 381  
Qy 358 CAAATTTGGGACATCTCATAGTGGCCAGCAGTAAACAACTCTGTGTACAGTGG 417  
Db 382 CAAATTTGGGACATCTCATAGTGGCCAGCAGTAAACAACTCTGTGTACAGTGG 441  
Qy 418 GCTGAAAGAGGATCTACACCATGAGCAACACTTTGGTAAACCTTGGAAATGGGAAACAG 477



APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,733A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-477-733A-11

Query Match 92.8%; Score 726.8; DB 8; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1.4e-160;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy 1 ATGATCGAAACATCAACAACTCTCCCGGATCTGGCGGCACTGGGACTGCCCATCAGC 60  
|||||  
Db 46 ATGATCGAAACATCAACAACTCTCCCGGATCTGGCGGCACTGGGACTGCCCATCAGC 105

Qy 61 ATGAAATTTTATGTATTTACTTACTGTTTTTCTTATCACCAGATGATTGGGTACGCA 120  
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Db 106 ATGAAATTTTATGTATTTACTTACTGTTTTTCTTATCACCAGATGATTGGGTACGCA 165  
Qy 121 CTTTTTCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAACTTCAT 180  
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Db 166 CTTTTTCTGTATCTTCATAGAGATTGGATAGGTCGAAGAGAGAACTTCAT 225  
Qy 181 GAACATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240  
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Db 226 GAACATTTTGTATTCATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 285  
Qy 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 300  
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Db 286 TTACTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTTGTCAAGGATATAACGTTA 345  
Qy 301 AACAAAGAGA---GAAAAAGAAAAAGCTTTGAAATGCAAAAAGTGATCAGAACTCT 357  
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Db 346 AACAAAGAGAGAGCAAGAAAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGAACTCT 405  
Qy 358 CAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 417  
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Db 406 CAAATTCGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 465  
Qy 418 GCTGAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTCGGAAAAATGGGAACAG 477  
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Db 466 GCTGAAAAGGATACACACCATGAGCAACAACTTGGTAAACCTCGGAAAAATGGGAACAG 525  
Qy 478 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCAAGTCACCTCTGTTCCAAT 537  
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Db 526 CTGACCGTTAAAGACAGGAGCTCTATTATATCTATGCCCAAGTCACCTCTGTTCCAAT 585  
Qy 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTTAGA 597  
|||||  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCGGTTAGA 645  
Qy 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAA 657  
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Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCACAGTTCGCGCAAAACCTTTGGGGCAA 705  
Qy 658 CAATCCATTTCACCTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTGTGTTCAT 717  
|||||  
Db 706 CAATCCATTTCACCTGGGAGGAGTATTTGAATTGCAACAGGTGCTTCGGTGTGTTCAT 765  
Qy 718 GTGACTGATCCAAAGCCAAAGTGAAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAA 777  
|||||  
Db 766 GTGACTGATCCAAAGCCAAAGTGAAGCCATGGCACTGGCTTCAGTCTCTTTGGCTTACTCAA 825  
Qy 778 CTCCTGA 783  
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Db 826 CTCCTGA 831

Search completed: May 30, 2002, 05:23:22  
Job time: 18681 sec



Db 706 CAATCCATTCACTTGGGAGGAGTATTGTAATGCAACCAAGGTGCTTCGGTGTGTCAT 765  
QY 718 GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCTTGGCTTACTCAA 777  
Db 766 GTGACTGATCCAAAGCCAAAGTGAGCCATGGCACTGGCTTCACGTCTTGGCTTACTCAA 825  
QY 778 CTCTGA 783  
Db 826 CTCTGA 831

Search completed: May 30, 2002, 02:52:00  
Job time: 11624 sec

Db 466 GCTGAAAGGATACACCATGAGCAACACTTGCTAAACCTGGAAAAATGGAAACAG 525  
Qy 478 CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCCTCAAGTCACTTCTGTCCAA 537  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCCTCAAGTCACTTCTGTCCAA 585  
Qy 538 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTCCCTTAAAGTCCCGGCTAGA 597  
Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTCCCTTAAAGTCCCGGCTAGA 645  
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 657  
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 705  
Qy 658 CAATCCATTCAGTTCGGAGGAGTATTGCAATTGCAACAGGCTGCTTCGGTCTTTGTCAAT 717  
Db 706 CAATCCATTCAGTTCGGAGGAGTATTGCAATTGCAACAGGCTGCTTCGGTCTTTGTCAAT 765  
Qy 718 GTGACTGATCCCAAGCCAAAGTGAGCCATGGCCTGCTTCAAGTTCAGTTCCTTACTCAA 777  
Db 766 GTGACTGATCCCAAGCCAAAGTGAGCCATGGCCTGCTTCAAGTTCAGTTCCTTACTCAA 825  
Qy 778 CTCCTGA 783  
Db 826 CTCCTGA 831

RESULT 15  
US-08-770-974-11  
Sequence 11, Application US/08770974  
Patent No. 6290972  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,974  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-770-974-11

Query Match 92.8%; Score 726.8; DB 4; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
Qy 1 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTGCGGCCACTGACTGCCCATCAGC 60  
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGGATCTGCGGCCACTGACTGCCCATCAGC 105  
Qy 61 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATTGGTTCAGCA 120  
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTCTTATCACCAGATGATTGGTTCAGCA 165  
Qy 121 CTTTTCGTGCTATCTTCATAGAAAGATTGGATAGGTTCGGAAGAGGAAGTAACCTTCAT 180  
Db 166 CTTTTCGTGCTATCTTCATAGAAAGATTGGATAGGTTCGGAAGAGGAAGTAACCTTCAT 225  
Qy 181 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATGCAACAGAGAGAGGATCTTTATCC 240  
Db 226 GAAGATTTTGTATTCATAAAAGCTTAAAGAGATGCAACAGAGAGAGGATCTTTATCC 285  
Qy 241 TTGCTGAACTGTGAGGAGATGAGAAAGCAATTTGAAGACCTTTGTCAAGGATATACGTTA 300  
Db 286 TTACTGAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCCAGTTTGTGAAGGATATATGTTA 345  
Qy 301 AACAAAGAGAAGAAAGCAAGCTTTGAAATGCAAAAGAGGTGATCAGATCCT 357  
Db 346 AACAAAGAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 405  
Qy 358 CAAATTCGCGCACATGTCATAAGTGAAGCCAGCAGTAAACAAACATCTGTGTTCAGTGG 417  
Db 406 CAAATTCGCGCACATGTCATAAGTGAAGCCAGTAAACAAACATCTGTGTTCAGTGG 465  
Qy 418 GCTGAAAAAGGATACCTACCATGAGCAACATCTGTTAACCTTGAAAAATGGGAACAG 477  
Db 466 GCTGAAAAAGGATACCTACCATGAGCAACATCTGTTAACCTTGAAAAATGGGAACAG 525  
Qy 478 CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCCTCAAGTCACTTCTGTTCCTCAAT 537  
Db 526 CTGACCGTTAAAGACAGGACTCTATTATATCTATGTCCTCAAGTCACTTCTGTTCCTCAAT 585  
Qy 538 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGCTAGA 597  
Db 586 CGGAGAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAAGTCCCGGCTAGA 645  
Qy 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 657  
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGCCGCAACCTTGGGGCAA 705  
Qy 658 CAATCCATTCAGTTCGGAGGAGTATTGCAATTGCAACAGGCTGCTTCGGTCTTTGTCAAT 717

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QY 181 GAAGATTTTGTATCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATCATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 285
QY 241 TTCTGCTGAACCTGTCAGGAGATGCAAGGCAATTTGAAGACCTTCTCAAGGATATAACGTTA 300
Db 286 TTACTGAACCTGTCAGGAGATTAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA 345
QY 301 AACAAAGAAGA---GAAAAAGAAAAAGAGCTTTTGAATGCAAAAAGGTGATCAGATCCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 358 CAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 406 CAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 418 GCTGAAAAAGGAGTACTACACCATGAGCAACAACTTGTGAACCTTGGAAAAATGGAAACAG 477
Db 466 GCTGAAAAAGGAGTACTACACCATGAGCAACAACTTGTGAACCTTGGAAAAATGGAAACAG 525
QY 478 CTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Db 526 CTGACCGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 597
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 645
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGAGTTCGCCCAACCTTCGCGGCAA 657
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCCAGAGTTCGCCCAACCTTCGCGGCAA 705
QY 658 CAATCCATTCACCTGGAGGAGATTTGAATTCGAACACAGGCTCTCGGTGTTGTCAAT 717
Db 706 CAATCCATTCACCTGGAGGAGATTTGAATTCGAACACAGGCTCTCGGTGTTGTCAAT 765
QY 718 GTCACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 777
Db 766 GTCACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 825
QY 778 CTCTGA 783
Db 826 CTCTGA 831

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RESULT 14
US-08-769-819-11
; Sequence 11, Application US/08769819
; Patent No. 6264951
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: FANLOW, WILLIAM
; APPLICANT: SPRIGGS, MELANIE
; APPLICANT: SRINIVASAN, SUBHASHINI
; APPLICANT: GIBSON, MARYLOU
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,819
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,624
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/249,189
; FILING DATE: May 24, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,703
; FILING DATE: October 23, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,723
; FILING DATE: December 5, 1991
; APPLICATION NUMBER: 07/783,707
; FILING DATE: October 25, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2802-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CD40-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..831
; US-08-769-819-11

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Query Match 92.8%; Score 726.8; DB 4; Length 840;
Best Local Similarity 96.2%; Pred. No. 1e-197;
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGCGGCCACTGACTGCGCCATCAGC 60
Db 46 ATGATCGAAACATACAAACCAACTTCTCCCGATCTGCGGCCACTGACTGCGCCATCAGC 105
QY 61 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATTGGTGTGAGCA 120
Db 106 ATGAAATTTTATGATTTTACTTACTTCTTTTCTTATCACCAGATGATTGGTGTGAGCA 165
QY 121 CTTTTGCTGTGTATCTTCATAGAAGATTGGATAGGTCGAAGAGGAAGTAAACCTTCAT 180
Db 166 CTTTTGCTGTGTATCTTCATAGAAGTTTGGACAAGATTGAGATGAAGATGAAGGAATCTTCAT 225
QY 181 GAAGATTTTGTATTTATATAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240
Db 226 GAAGATTTTGTATTTATGATTAAGCAAGATGATGATGATGATGATGATGATGATGATGAT 285
QY 241 TTGCTGAACCTGTCAGGAGATGCAAGCAATTTGAAGACCTTCTCAAGGATATAACGTTA 300
Db 286 TTACTGAACCTGTCAGGAGATTAAGACCTTCTCAAGGATATAACGTTA 345
QY 301 AACAAAGAAGA---GAAAAAGAAAAAGAGCTTTGAAATGCAAAAAGGTGATCAGATCCCT 357
Db 346 AACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 405
QY 358 CAAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 406 CAAATTCGCGCATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 418 GCTGAAAAAGGAGTACTACACCATGAGCAACAACTTGTGAACCTTGGAAAAATGGAAACAG 477

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Patent No. 6106832  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: DAVISON, BARRY  
APPLICANT: FANSLON, WILLIAM  
APPLICANT: RENSCH, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING  
DEFECTIVE CD40L (as amended)  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/589,771B  
FILING DATE: January 22, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HENRY, JANIS C. 34,347  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2810-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-589-771B-7

ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-982-272-20.rni

Query Match	92.8%;	Score 726.8;	DB 3;	Length 840;
Best Local Similarity	96.2%;	Pred. No. 1e-197;		
Matches	756;	Conservative	0;	Mismatches 27; Indels 3; Gaps 1;
QY	1	ATGATCGAACAATCAACCAACAACTCTCCCGCATCTCGGCGACCTGGAGTCCCATCAGC	60	
DB	46	ATGATCGAACAATCAACCAACAACTCTCCCGCATCTCGGCGACCTGGAGTCCCATCAGC	105	
QY	61	ATGAAATTTTATGTATTTACTTACTTCTTTTATCACCAGATGATGGGTACGCA	120	
DB	106	ATGAAATTTTATGTATTTACTTACTTCTTTTATCACCAGATGATGGGTACGCA	165	
QY	121	CTTTTGTGCTGTATCTCATAGAAGTTGGATAGGTGCGAAGAGTAACCTTCAT	180	
DB	166	CTTTTGTGCTGTATCTCATAGAAGTTGGAAGATAGAGATGAAAGGAATCTTCAT	225	
QY	181	GAAGATTTTGTATTCATAAAGGCTAAAGATGCAACAAAGAGAGATCTTTATCC	240	
DB	226	GAAGATTTTGTATTCATAAAGGCTAAAGATGCAACAAAGAGAGATCTTTATCC	285	
QY	241	TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGCTTTGTCAAGATATACGTTA	300	
DB	286	TTACTGAAGTGTGAGAGATGAGAGGCAATTTGAAGCTTTGTCAAGATATACGTTA	345	
QY	301	ACAAAGAGAA--GAAAGAGAAACAGCTTTGAATCAAAAGAGTGCATCAGATCT	357	
DB	346	ACAAAGAGAGAAAGAGAGAAACAGCTTTGAATCAAAAGAGTGCATCAGATCT	405	
QY	358	CAAAATTCGGGCACATCTATAAGTAGGCGCAGCAGTAAACACATCTGTGTACAGTG	417	
DB	406	CAAAATTCGGGCACATCTATAAGTAGGCGCAGCAGTAAACACATCTGTGTACAGTG	465	
QY	418	GCTGAAAGAGGATACACACATGACCACTTGTAACTTGTAACTTGTAACTTGTAACT	477	
DB	466	GCTGAAAGAGGATACACACATGACCACTTGTAACTTGTAACTTGTAACTTGTAACT	525	
QY	478	CTGACCGTTAAAAGACAGACCTTATATATCTATGCCCCAGTCACTTCTGTCCCAAT	537	
DB	526	CTGACCGTTAAAAGACAGACCTTATATATCTATGCCCCAGTCACTTCTGTCCCAAT	585	
QY	538	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA	597	
DB	586	CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTAAAGTCCCGGTAGA	645	
QY	598	TTGAGAGATCTTACTCAGCTGCAATACCCAGCTTCCGCAAACTTCCGCGGCA	657	
DB	646	TTGAGAGATCTTACTCAGCTGCAATACCCAGCTTCCGCAAACTTCCGCGGCA	705	
QY	658	CAATCCATTCACCTGGGAGGATTTGAATTCACACAGGTGCTTGGGTTTGTCAAT	717	
DB	706	CAATCCATTCACCTGGGAGGATTTGAATTCACACAGGTGCTTGGGTTTGTCAAT	765	
QY	718	GTGACTGATCCAGCCCAAGTGGAGCTGAGGCTGAGGCTTACGCTTGTGCTTACACAA	777	
DB	766	GTGACTGATCCAGCCCAAGTGGAGCTGAGGCTGAGGCTTACGCTTGTGCTTACACAA	825	
QY	778	CTCTGA 783		
DB	826	CTCTGA 831		



REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2845-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46...831  
US-08-763-995-1

Query Match 92.8%; Score 726.8; DB 3; Length 840;

Best Local Similarity 96.2%; Pred. No. 1e-197; Indels 3; Gaps 1;  
Matches 756; Conservative 0; Mismatches 27;

QY 1 ATGATCGAAACATACAAACAACTCTCCCGCATCTCGCGCCACTGCGACTGCCCATCAGC 60  
DB 46 ATGATCGAAACATACAAACAACTCTCCCGCATCTCGCGCCACTGCGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 120  
DB 106 ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTTCAGCA 165  
QY 121 CTTTTCGTGCTGATCTTCATAGAAGATTGGATAGCTCGAAGGAGGAAGTAAACCTTCAT 180  
DB 166 CTTTTCGTGCTGATCTTCATAGAAGTTGGACAGATAGAGATGAAGGATCTTCAT 225  
QY 181 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGGAGGATCTTTATCC 240  
DB 226 GAAGATTTTGTATTCATATAAAGCTAAAGAGATGCAACAAAGGAGGATCTTTATCC 285  
QY 241 TTGCTCACTGTCAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
DB 286 TTACTGAATGTCAGAGATGAGAGGCAATTTGAAGGCTTGTGAAGGATATAAGCTTA 345  
QY 301 AACAAAGAGA---GAAAAAGAAACAGCTTTGAATGCAAAAGGTGATCAGATCCT 357  
DB 346 AACAAAG 405  
QY 358 CAAATTCGCGCATGCTATAGTAGGCGCAGCAGTAAACACATCTGTGTACAGTGG 417  
DB 406 CAAATTCGCGCATGCTATAGTAGGCGCAGCAGTAAACACATCTGTGTACAGTGG 465  
QY 418 GCTGAAAGAGGATACACCATGAGCAACACTTGGTAACCTGGAATGGAACAG 477  
DB 466 GCTGAAAGAGGATACACCATGAGCAACACTTGGTAACCTGGAATGGAACAG 525  
QY 478 CTGACCGTTTAAAGACAAGGACTTATATATCTATGCCCCAAGTCACTCTGTTCCTCAAT 537  
DB 526 CTGACCGTTTAAAGACAAGGACTTATATATCTATGCCCCAAGTCACTCTGTTCCTCAAT 585  
QY 538 CGGGAAGCTTCGAGTCAAGCTCATTATAGCAGCCTTGCTGCTAAAGTCCCGGTAGA 597  
DB 586 CGGGAAGCTTCGAGTCAAGCTCATTATAGCAGCCTTGCTGCTAAAGTCCCGGTAGA 645  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCAAACCTTCGGGGAA 657  
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCAAACCTTCGGGGAA 705  
QY 658 CAATCCATTCCTTGGGAGGAGTATTGAATTGCAACACAGTCTTCGGGTGTTGTCAT 717

DB 706 CAATCCATTCCTTGGGAGGAGTATTGAATTGCAACACAGTCTTCGGGTGTTGTCAT 765  
QY 718 GTGACTGATCCCAAGCAAGTGAGCCATGCGACTGGCTTCACGCTCCTTTGGCTTACTCAA 777  
DB 766 GTGACTGATCCCAAGCAAGTGAGCCATGCGACTGGCTTCACGCTCCTTTGGCTTACTCAA 825  
QY 778 CTCTGA 783  
DB 826 CTCTGA 831  
RESULT 12  
US-09-088-913A-11  
Sequence 11, Application US/09088913A  
Patent No. 6087329  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/088,913A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,624  
FILING DATE:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

Db 226 GAAGATTTTGTATTTCATGAAACGATACAGAGATGCAACACAGGAGAGAAAGATCTTATCC 285  
QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTTGAAGACCTTTGTCAAGGATATACGTTA 300  
Db 286 TTACTCAACTGTGAGGAGATTTAAAGCCAGTTTGAAGCTTTGTGAAGATATATGTTA 345  
QY 301 AACAAAGAGA--GAAAAAGAAACAGCTTTTGAATGCAAAAAAGGTGATCAGATCCT 357  
Db 346 AACAAAGAGACAGCAAGAAAGAAACAGCTTTTGAATGCAAAAAAGGTGATCAGATCCT 405  
QY 358 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 417  
Db 406 CAAATTCGCGCACATGTCTATAAGTGAAGCCAGCAGTAAACACATCTCTGTGTACAGTGG 465  
QY 418 GCTGAAAAAGGATACACACATGAGCAACAACTTGGTAACCTGGAAAAATGGAAACAG 477  
Db 466 GCTGAAAAAGGATACACACATGAGCAACAACTTGGTAACCTGGAAAAATGGAAACAG 525  
QY 478 CTGACCGTTTAAAAAGACAAAGGACTCTATTATATCTATGCCCCAGTCCCTTCTGTCCCAAT 537  
Db 526 CTGACCGTTTAAAAAGACAAAGGACTCTATTATATCTATGCCCCAGTCCCTTCTGTCCCAAT 585  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGA 597  
Db 586 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCCTAAAGTCCCCCGGTAGA 645  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGCTTCGCCCAAACTTCGCGGCAA 657  
Db 646 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGCTTCGCCCAAACTTCGCGGCAA 705  
QY 658 CAATCCATTCAGTGGGAGGAGTATTGAAATGCAACAGTCTTCGGTGTGTGCAAT 717  
Db 706 CAATCCATTCAGTGGGAGGAGTATTGAAATGCAACAGTCTTCGGTGTGTGCAAT 765  
QY 718 GTGACTGATCCAAAGCAAGTGGCCAGTGGCAGTGGCTTACGCTCCTTGGCTTACTCAA 777  
Db 766 GTGACTGATCCAAAGCAAGTGGCCAGTGGCAGTGGCTTACGCTCCTTGGCTTACTCAA 825  
QY 778 CTCGTA 783  
Db 826 CTCGTA 831

RESULT 11  
US-08-763-995-1  
Sequence 1, Application US/08763995  
Patent No. 6017527  
GENERAL INFORMATION:  
APPLICANT: MARASKOVSKY, EUGENE  
TITLE OF INVENTION: METHOD OF ACTIVATING DENDRITIC CELLS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Power Macintosh 7200/90  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Macintosh, Version #6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763.995  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: USSN 08/677,762  
APPLICATION NUMBER: 10 JUL 1996  
FILING DATE: 10 JUL 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.

CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477.733B  
FILING DATE: June 07, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,189  
FILING DATE: May 24, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-477-733B-11

Query Match 92.88; Score 726.8; DB 2; Length 840;  
Best Local Similarity 96.23; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAATACAAACCAACTTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 60  
Db 46 ATGATCGAATACAAACCAACTTCTCCCGATCTGCGGCACTGGGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTACTTCTTTCTTATACCCAGATGTTGGTACGA 120  
Db 106 ATGAAATTTTATGATTTACTTCTTTCTTATACCCAGATGTTGGTACGA 165  
QY 121 CTTTGTGCTGATCTTCATAGAGATTTGATAGGTGGAAGAGTAAGTAACTTCAT 180  
Db 166 CTTTGTGCTGATCTTCATAGAGATTTGGAAGATAGAGATGAAAGATCTTCAT 225  
QY 181 GAAGATTTGATTTCAATAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCC 240

GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: SRINIVASAN, SUBHASHINI  
APPLICANT: GIBSON, MARYLOU  
APPLICANT: MORRIS, ARVIA E.  
APPLICANT: MCGREW, JEFFERY  
TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: MS Word for Apple Power Macintosh, version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,624A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,733  
FILING DATE: June 07, 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,703  
FILING DATE: October 23, 1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/805,723  
FILING DATE: December 5, 1991  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/783,707  
FILING DATE: October 25, 1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2802-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-484-624A-11

Query Match 92.8%; Score 726.8; DB 2; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAAACATACAAACCAAACTCTCCCGGCGCCACTGCGACTGCCCATCAGC 60

Db 46 ATGATCGAAACATACAAACCAAACTCTCCCGGCGCCACTGCGACTGCCCATCAGC 105  
QY 61 ATGAAATTTTATGTTTATTTACTGTTTCTTTATCACCAGATGATGGTGAGCA 120  
Db 106 ATGAAATTTTATGTTTATTTACTGTTTCTTTATCACCAGATGATGGTGAGCA 165  
QY 121 CTTTTCGCTGTATCTTCTAGAGATTGGATAAGTGAAGAGGAAGTAACCTTCAT 180  
Db 166 CTTTTCGCTGTATCTTCTAGAGATTGGATAAGTGAAGAGGAAGTAACCTTCAT 225  
QY 181 GAAGATTTTGTATTTATAAAGCTTAAAGAGATGCAACAAAGAGAGATCTTTATCC 240  
Db 226 GAAGATTTTGTATTTATGAAACGATACAGAGATGCAACACAGGAGAAAGATCTTATCC 285  
QY 241 TTGCTGAAGTGTGAGAGATGAGAGGCAATTTGAAGACCTTGTCAAGGATATAAGCTTA 300  
Db 286 TTACTGAAGTGTGAGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGCTTA 345  
QY 301 AACAAAGAGA---GAAAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 357  
Db 346 AACAAAGAGAGAGAGAGAAAGAAAACAGCTTTGAAATGCAAAAAGGTGATCAGATCCT 405  
QY 358 CAAATTCGCGCACATGTCATAAGTGAGGCGCAGCAGTAAACACACATCTGTGTACAGTGG 417  
Db 406 CAAATTCGCGCACATGTCATAAGTGAGGCGCAGCAGTAAACACACATCTGTGTACAGTGG 465  
QY 418 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 477  
Db 466 GCTGAAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGAAAAATGGAAACAG 525  
QY 478 CTGACCGTTAAAAGACAAGGACTCTATTATCTATGCCCCAGCTCTGTGTCCAAT 537  
Db 526 CTGACCGTTAAAAGACAAGGACTCTATTATCTATGCCCCAGCTCTGTGTCCAAT 585  
QY 538 CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAGTCCCCCGGTAGA 597  
Db 586 CGGAAAGCTTCGAGTCAAGCTCCATTTATAGCCAGGCTCTGCCTAAAGTCCCCCGGTAGA 645  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCCGCCAAACCTTCGCGGCGAA 657  
Db 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGTTCCGCCAAACCTTCGCGGCGAA 705  
QY 658 CAATCCATTACATTGGGAGGAGTATTGTAATTCGAACACAGGCTCTCGGTGTTGTCAAT 717  
Db 706 CAATCCATTACATTGGGAGGAGTATTGTAATTCGAACACAGGCTCTCGGTGTTGTCAAT 765  
QY 718 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGCGCTTACAGTCTTGGCTTACTCAA 777  
Db 766 GTGACTGATCCAAAGCAAGTGAGCCATGGCACTGCGCTTACAGTCTTGGCTTACTCAA 825  
QY 778 CTCTGA 783  
Db 826 CTCTGA 831  
RESULT 10  
US-08-477-733B-11  
; Sequence 11, Application US/08477733B  
; Patent No. 5981724  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: FANSLAW, WILLIAM  
; APPLICANT: SPRIGGS, MELANIE  
; APPLICANT: SRINIVASAN, SUBHASHINI  
; APPLICANT: GIBSON, MARYLOU  
; APPLICANT: MORRIS, ARVIA E.  
; APPLICANT: MCGREW, JEFFERY  
; TITLE OF INVENTION: NOVEL CYTOKINE THAT BINDS CD40  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNEX CORPORATION  
; STREET: 51 UNIVERSITY STREET  
; STREET: 51 UNIVERSITY STREET



QY 121 CTTTTCCTGCTGATCTTTCATAGAAGATTGGATAAGGTGCAAGAGGAAGTAACCTTCAT 180  
DB 142 CTTTTCCTGCTGATCTTTCATAGAAGGTGCAAGAGTAAGATGAAGGAATCTTCAT 201  
QY 181 GAAGATTTTGTATTCATATAAAGAGCTTAAGAGATGCAACAAAGAGGAAGATCTTTATCC 240  
DB 202 GAAGATTTTGTATTCATATAAAGAGCTTAAGAGATGCAACAAAGAGGAAGATCTTTATCC 261  
QY 241 TTGCTGAACCTGTCAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 262 TTACTGACCTGTGAGGAGATTAAGCCAGTTTGAAGCCTTTGTGAAGGATATAAGTTA 321  
QY 301 AACAAAGAAGA---GAAAAAGAAAACAGCTTTTGAATGCAAAAGAGTGATCAGAAATCC 357  
DB 322 AACAAAGAGGAGGAGCAAGAAAGAAAACAGCTTTTGAATGCAAAAGAGTGATCAGAAATCC 381  
QY 358 CAATTCGCGCACATGTCATAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417  
DB 382 CAATTCGCGCACATGTCATAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441  
QY 418 GCTGAAAAGAGTACTACACCATGAGCAACAACTTGGTAACCTGGGAAAATGGGAAACAG 477  
DB 442 GCTGAAAAGAGTACTACACCATGAGCAACAACTTGGTAACCTGGGAAAATGGGAAACAG 501  
QY 478 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCAT 537  
DB 502 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCAT 561  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 597  
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 621  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCAAACCTTGGGGCAA 657  
DB 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCAAACCTTGGGGCAA 681  
QY 658 CAATCCATTCACCTGGGAGGAGTATTGGAATGCAACCAAGGCTGCTGGGTGTTGTCAAT 717  
DB 682 CAATCCATTCACCTGGGAGGAGTATTGGAATGCAACCAAGGCTGCTGGGTGTTGTCAAT 741  
QY 718 GTCACTGATCCAAAGCAAGTGAGCCATGGCAGCTGCTTACGCTTCTGCTTACTCAA 777  
DB 742 GTCACTGATCCAAAGCAAGTGAGCCATGGCAGCTGCTTACGCTTCTGCTTACTCAA 801  
QY 778 CTCTGA 783  
DB 802 CTCTGA 807

## RESULT 7

US-08-690-096-1  
; Sequence 1, Application US/08690096  
; Patent No. 5945513  
; GENERAL INFORMATION:  
; APPLICANT: ARUFFO, ALEJANDRO  
; APPLICANT: HOLLEBAUGH, DIANE  
; APPLICANT: LEBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,096  
; FILING DATE: 31-JUL-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/940,605  
; FILING DATE: 04-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 22..807  
; US-08-690-096-1

Query Match 92.8%; Score 726.8; DB 2; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGCGCCACTGCGACTGCCCATCAGC 60  
DB 22 ATGATCGAAACATACACCAAACTTCTCCCGCATCTCGCGCCACTGCGACTGCCCATCAGC 81  
QY 61 ATGAAATTTTATGATATTACTTACTGTTTCTTATACCCAGATGATGGGTACAGCA 120  
DB 82 ATGAAATTTTATGATATTACTTACTGTTTCTTATACCCAGATGATGGGTACAGCA 141  
QY 121 CTTTTCCTGCTGATCTTTCATAGAAGATTGGATAAGGTGCAAGAGGAAGTAACCTTCAT 180  
DB 142 CTTTTCCTGCTGATCTTTCATAGAAGATTGGATAAGGTGCAAGAGGAAGTAACCTTCAT 201  
QY 181 GAAGATTTTCTATTATAAAGAGCTTAAGAGATGCAACAAAGAGGAAGATCTTTATCC 240  
DB 202 GAAGATTTTCTATTATGAAACGATACAGATGCAACACAGAGAAAGATCTTTATCC 261  
QY 241 TTGCTGAACCTGTCAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 262 TTACTGAACTGTGAGGAGATTAAGAGCCAGCTTTTGAAGGCTTTGTGAAGGATATAAGTTA 321  
QY 301 AACAAAGAAGA---GAAAAAGAAAACAGCTTTTGAATGCAAAAGAGTGATCAGAAATCC 357  
DB 322 AACAAAGAGGAGGAGCAAGAAAGAAAACAGCTTTTGAATGCAAAAGAGTGATCAGAAATCC 381  
QY 358 CAATTCGCGCACATGTCATAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417  
DB 382 CAATTCGCGCACATGTCATAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 441  
QY 418 GCTGAAAAGAGTACTACACCATGAGCAACAACTTGGTAACCTGGGAAAATGGGAAACAG 477  
DB 442 GCTGAAAAGAGTACTACACCATGAGCAACAACTTGGTAACCTGGGAAAATGGGAAACAG 501  
QY 478 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCAT 537  
DB 502 CTGACCGTTTAAAGAGACAGGACTCTATTATCTATGCCCCAAGTCACCTTCTGTTCAT 561  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 597  
DB 562 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCTCTGCTTAAGTCCCGCGGTAGA 621  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCAAACCTTGGGGCAA 657  
DB 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCAGATTCGCCAAACCTTGGGGCAA 681  
QY 658 CAATCCATTCACCTGGGAGGAGTATTGGAATGCAACCAAGGCTGCTGGGTGTTGTCAAT 717  
DB 682 CAATCCATTCACCTGGGAGGAGTATTGGAATGCAACCAAGGCTGCTGGGTGTTGTCAAT 741  
QY 718 GTCACTGATCCAAAGCAAGTGAGCCATGGCAGCTGCTTACGCTTCTGCTTACTCAA 777  
DB 742 GTCACTGATCCAAAGCAAGTGAGCCATGGCAGCTGCTTACGCTTCTGCTTACTCAA 801  
QY 778 CTCTGA 783  
DB 802 CTCTGA 807

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2818-A  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE: ORGANISM: Homo sapiens  
IMMEDIATE SOURCE: CLONE: CD40-L  
FEATURE: NAME/KEY: CDS  
LOCATION: 46..831  
US-08-360-923A-1

Query Match 92.8%; Score 726.8; DB 1; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCGGACCTGGAGTGGCCATCAGC 60  
DB 46 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCGGACCTGGAGTGGCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTATCACCAGATGATTTGGTGCAGCA 120  
DB 106 ATGAAATTTTATGATTTACTTACTTCTTATCACCAGATGATTTGGTGCAGCA 165  
QY 121 CTTTTCCTGCTGTATCTTCATAGAAGATTGGATAAGGTGCAAGAGAAATAACCTTAT 180  
DB 166 CTTTTCCTGCTGTATCTTCATAGAAGATTGGATAAGGTGCAAGAGAAATAACCTTAT 225  
QY 181 GAAGATTTGTTATTAATAAAGCTTAAGAGATGCAACAAAGGAGAAAGATCTTTATCC 240  
DB 226 GAAGATTTGTTATTAATAAAGCTTAAGAGATGCAACAAAGGAGAAAGATCTTTATCC 285  
QY 241 TTGCTGAAGTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 286 TTACTGAAGTGTGAGGAGATTAAGGCAAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 345  
QY 301 AACAAAGAAGAA--GAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 357  
DB 346 AACAAAGAGAGACGAAAGAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGATCCT 405  
QY 358 CAATTTGGGACATGTCATTAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGG 417  
DB 406 CAATTTGGGACATGTCATTAAGTGAGCCAGCAGTAAACACATCTGTGTACAGTGG 465  
QY 418 GCTGAAAGAGATTAACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAGAACAG 477  
DB 466 GCTGAAAGAGATTAACACCATGAGCAACAACTTGGTAACCTTGGAAATGGAAGAACAG 525  
QY 478 CTGACCGTTAAAGACAAAGGACTTATATATATCTATGCCCAGTCACTCTGTTCCTCAAT 537  
DB 526 CTGACCGTTAAAGACAAAGGACTTATATATATCTATGCCCAGTCACTCTGTTCCTCAAT 585  
QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTGCTAAAGTCCCGCGGTAGA 597  
DB 586 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCTGCTAAAGTCCCGCGGTAGA 645  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGGGCAACCTTGGGGCAA 657  
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCACAGTTCGGGCAACCTTGGGGCAA 705

QY 658 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCATCAAT 717  
DB 706 CAATCCATTCACTTGGGAGGAGTATTTGAATTCGAACACAGGTGCTTCGGTGTTCATCAAT 765  
QY 718 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGGCTTACACGTCCTTTGGCTTACTCAAA 777  
DB 766 GTGACTGATCCAAAGCAAGTGAAGCCATGAGCTGGCTTACACGTCCTTTGGCTTACTCAAA 825  
QY 778 CTCTGA 783  
DB 826 CTCTGA 831

RESULT 6  
US-08-431-055-3  
Sequence 3, Application US/08431055  
Patent No. 5817516  
GENERAL INFORMATION:  
APPLICANT: KEHRY, MERILYN R  
APPLICANT: CASTLE, BRIAN E  
TITLE OF INVENTION: METHODS FOR PROLIFERATING AND  
TITLE OF INVENTION: DIFFERENTIATING B CELLS, AND USES THEREOF  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 100 NEW YORK AVE. N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/431,055  
APPLICATION NUMBER: US/08/431,055  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,580  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 1011.1030000/RAM  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE: NAME/KEY: CDS  
LOCATION: 22..807  
US-08-431-055-3

Query Match 92.8%; Score 726.8; DB 1; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCGGACCTGGAGTGGCCATCAGC 60  
DB 22 ATGATCGAATACATACCAACAACTCTCCCGATCTGCGGCGGACCTGGAGTGGCCATCAGC 81  
QY 61 ATGAAATTTTATGATTTACTTACTTCTTATCACCAGATGATTTGGTGCAGCA 120  
DB 82 ATGAAATTTTATGATTTACTTACTTCTTATCACCAGATGATTTGGTGCAGCA 141

APPLICANT: FANSLAW, WILLIAM  
APPLICANT: RENSCHAW, BLAIR  
APPLICANT: SPRIGGS, MELANIE  
APPLICANT: WIDMER, MICHAEL  
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS  
TITLE OF INVENTION: IN A CD40 LIGAND GENE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: MS Word for Apple 5.1, Version a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/184,422  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/009,258  
FILING DATE: 01/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: PERKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2810-A  
TELEPHONE: 2065870430  
TELEFAX: 2065870606  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 840 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 46..831  
US-08-184-422-7

Query Match 92.8%; Score 726.8; DB 1; Length 840;  
Best Local Similarity 96.2%; Pred. No. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGCGGATGCCATCAGC 60  
DB 46 ATGATGAAACATACACCAAACTCTCCCGGATCTCGCGCCACTGCGGATGCCATCAGC 105  
QY 61 ATGAAATTTTATGATTTTACTTCTTTTCTTATACCCAGATGATGGTGCAGCA 120  
DB 106 ATGAAATTTTATGATTTTACTTCTTTTCTTATACCCAGATGATGGTGCAGCA 165  
QY 121 CTTTTCGCTGTCTCTCTATAGAAATGGATGCAAGAGGAAGTAACCTTCAT 180  
DB 166 CTTTTCGCTGTCTCTCTATAGAAATGGATGCAAGAGGAAGTAACCTTCAT 225  
QY 181 GAAGATTTTCTATTAATAAGCTTAAGAGATGCAACAAAGAGAGAGATCTTATCC 240  
DB 226 GAAGATTTTCTATGATGAAGATGATACAGAGATGCAACAAAGAGAGATCTTATCC 285  
QY 241 TTGCTGAACCTGTGAGGAGATGCAAGCAATTTGAAGACCTTGTCAAGGATATAACGTTA 300

DB 286 TTACTGAACCTGTGAGGAGATTAAGCCAGTTTGAAGGCTTTTGAAGGATATAATGTTA 345  
QY 301 AACAAAAGAGA---GAAAAAAGAAAAACAGCTTTGAAATGCAAAAAGTGATCAGAACTCT 357  
DB 346 AACAAAGAGAGAGAGAGAAAGAAACAGCTTTGAAATGCAAAAAGTGATCAGAACTCT 405  
QY 358 CAAATTCGCGCACATGTCATAGTGAGGCGCAGCAGTAACAAACATCTGTGTACAGTGG 417  
DB 406 CAAATTCGCGCACATGTCATAGTGAGGCGCAGCAGTAACAAACATCTGTGTACAGTGG 465  
QY 418 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTGGAAAATGGGAACAG 477  
DB 466 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTGGAAAATGGGAACAG 525  
QY 478 CTGACCGTTAAAAGACAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTCTCCAAT 537  
DB 526 CTGACCGTTAAAAGACAAGGACTCTATTATCTATGCCCCAAGTCACCTTCTCTCCAAT 585  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCAGAGCTCTGCCTAAAGTCCCGGCTAGA 597  
DB 586 CGGGAAGCTTCGAGTCAAGCTCCATTATAGCAGAGCTCTGCCTAAAGTCCCGGCTAGA 645  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCGCAACCTTCGCGGCAA 657  
DB 646 TTCGAGAGATCTTACTCAGAGCTGCAAAATACCAAGTTCCGCGCAACCTTCGCGGCAA 705  
QY 658 CAATCCATTACCTTGGGAGAGATTTTGAATTCGAACACAGGTCTTCGGTGTGTGCAAT 717  
DB 706 CAATCCATTACCTTGGGAGAGATTTTGAATTCGAACACAGGTCTTCGGTGTGTGCAAT 765  
QY 718 GTGACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 777  
DB 766 GTGACTGATCCAAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 825  
QY 778 CTCTGA 783  
DB 826 CTCTGA 831  
RESULT 5  
US-08-360-923A-1  
Sequence 1, Application US/08360923A  
Patent No. 5674492  
GENERAL INFORMATION:  
APPLICANT: ARMITAGE, RICHARD  
APPLICANT: FANSLAW, WILLIAM  
APPLICANT: LONGO, DAN L.  
APPLICANT: MURPHY, WILLIAM  
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING  
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS  
TITLE OF INVENTION: EXPRESSING CD40  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNEX CORPORATION  
STREET: 51 UNIVERSITY STREET  
CITY: SEATTLE  
STATE: WASHINGTON  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Apple Macintosh System 7.1  
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,923A  
FILING DATE: December 21, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/172,664  
FILING DATE: December 23, 1993  
CLASSIFICATION: 424

361 CAATTTGGGCACATGTCTAAGTGAGGCCAGCAGTAAACAAACATCTGTGTACAGTGG 420  
418 GCTGAAAAGGATACACTACACATCAGCAACAACTTGTAAACCTTGGAAAAATGGGAACAG 477  
421 GCTGAAAAGGATACACTACACATCAGCAACAACTTGTAAACCTTGGAAAAATGGGAACAG 480  
478 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 537  
481 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 540  
538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 597  
541 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 600  
598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 657  
601 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 660  
658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGCTTCGGTGTGTCTCAAT 717  
661 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGCTTCGGTGTGTCTCAAT 720  
718 GTCACTGATCCCAAGCAAGTGAGCCATGGCCTTCACTGCTTGGCTTACTCAAA 777  
721 GTCACTGATCCCAAGCAAGTGAGCCATGGCCTTCACTGCTTGGCTTACTCAAA 780  
778 CTCTGA 783  
781 CTCTGA 786

RESULT 3  
US-07-940-605A-1  
; Sequence 1, Application US/07940605A  
; Patent No. 5540926  
; GENERAL INFORMATION:  
; APPLICANT: ARUFFO, ALEJANDRO  
; APPLICANT: HOLLENBAUGH, DIANE  
; APPLICANT: LEBETTER, JEFFREY A.  
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,605A  
; FILING DATE: 04-SEP-1992  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 840 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:

NAME/KEY: CDS  
LOCATION: 22...807  
US-07-940-605A-1  
Query Match 92.8%; Score 726.8; DB 1; Length 840;  
Best Local Similarity 96.2%; Pred. NO. 1e-197;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGGCCACTGGAGCTGCCCATCAGC 60  
DB 22 ATGATCGAAACATACAAACAACTTCTCCCGCATCTGGGGCCACTGGAGCTGCCCATCAGC 81  
QY 61 ATGAAATTTTATGATGATTTTACTTACTTCTTTTCTTTATCACCAGATGATTTGGGTACGA 120  
DB 82 ATGAAATTTTATGATGATTTTACTTACTTCTTTTCTTTATCACCAGATGATTTGGGTACGA 141  
QY 121 CTTTTTCCTGCTGTATCTTCATAGAGATTTGGATTAAGTCTGGAAGAGAGTAACACCTTCAT 180  
DB 142 CTTTTCCTGCTGTATCTTCATAGAGATTTGGATTAAGTCTGGAAGAGAGTAACACCTTCAT 201  
QY 181 GAAGATTTTCTATTTCAATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 240  
DB 202 GAAGATTTTCTATTTCAATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC 261  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAAGCAATTTTGAAGACCTTGTCAAGGATATAACGTTA 300  
DB 262 TTACTGAACCTGTGAGGAGATTTAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAAGTTA 321  
QY 301 AACAAAGAAGA:--GAAAAAGAAAAAGAGGTTTGAATGCAAAAGGTGATCAGATCCT 357  
DB 322 AACAAAGATCCT 381  
QY 358 CAATTTGGGCACATGTCTAAGTGAGGCCAGCAGTAGTAAAAACACATCTGTGTACAGTGG 417  
DB 382 CAATTTGGGCACATGTCTAAGTGAGGCCAGCAGTAGTAAAAACACATCTGTGTACAGTGG 441  
QY 418 GCTGAAAAAGGATACACACCATGAGCAACAACTTGTGTAACCTTGGAAAAATGGGAACAG 477  
DB 442 GCTGAAAAAGGATACACACCATGAGCAACAACTTGTGTAACCTTGGAAAAATGGGAACAG 501  
QY 478 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 537  
DB 502 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCCCCAAGTCACCTTCTGTTCACAT 561  
QY 538 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 597  
DB 562 CGGGAAGCTTCAGTCAAGCTCCATTTATAGCCAGCTCTGCCTAAAGTCCCGCGGTAGA 621  
QY 598 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 657  
DB 622 TTCGAGAGAACTTACTCAGAGCTGCAAAATACCCACAGTTCGGCCAAACCTTGGGGCAA 681  
QY 658 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGAGTCTTCGGTGTGTCTCAAT 717  
DB 682 CAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACAGGAGTCTTCGGTGTGTCTCAAT 741  
QY 718 GTGACTGATCCCAAGCAAGTGAAGCCATGGCCTTCACTGCTTGGCTTACTCAAA 777  
DB 742 GTGACTGATCCCAAGCAAGTGAAGCCATGGCCTTCACTGCTTGGCTTACTCAAA 801  
QY 778 CTCTGA 783  
DB 802 CTCTGA 807

RESULT 4  
US-08-184-422-7  
; Sequence 7, Application US/08184422  
; Patent No. 5565321  
; GENERAL INFORMATION:  
; APPLICANT: ARMITAGE, RICHARD  
; APPLICANT: DAVISON, BARRY



NAME/KEY: CDS  
LOCATION: 1..783  
US-08-446-922-3

Query Match 92.8%; Score 726.8; DB 1; Length 786;  
Best Local Similarity 96.2%; Pred. No. 9.9e-198;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGGCCACTGGAGTGGCCCATCAGC 60  
DB 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGGCCACTGGAGTGGCCCATCAGC 60  
QY 61 ATGAAATTTTATGTTTATTTACTTCTTTCTTTATCACCAGATGATGGGTGAGCA 120  
DB 61 ATGAAATTTTATGTTTATTTACTTCTTTCTTTATCACCAGATGATGGGTGAGCA 120  
QY 121 CTTTTCCTGCTGATCTTCATAGAACTGGATAAGTTCGAAGAGCAAGTAAACCTTCAT 180  
DB 121 CTTTTCCTGCTGATCTTCATAGAACTGGATAAGTTCGAAGAGCAAGTAAACCTTCAT 180  
QY 181 GAAGATTTTGTATTTATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTGTATTTATGAAAGCATACAGAGATGCAACAGAGAGAGATCTTTATCC 240  
QY 241 TTCTGAATCTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
DB 241 TTCTGAATCTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
QY 301 AACAAAGAGA---GAAAGAAAGAAACAGCTTTGAAATGCAAAAGTGCATGAGATCCT 357  
DB 301 AACAAAG 360  
QY 358 CAAATTCGGGCACATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417  
DB 361 CAAATTCGGGCACATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
QY 418 GCTGAAAGAGGATACACCATGAGCAACACTTGTACCTTGGTAAAGTGGAAAGCAAG 477  
DB 421 GCTGAAAGAGGATACACCATGAGCAACACTTGTACCTTGGTAAAGTGGAAAGCAAG 480  
QY 478 CTGACCGTTTAAAGACAAAGGACTCTATTATATCTATGCCCCAAGTCACTTCTGTTCCAAT 537  
DB 481 CTGACCGTTTAAAGACAAAGGACTCTATTATCTATGCCCCAAGTCACTTCTGTTCCAAT 540  
QY 538 CGGAGAGCTTCGAGTCAAGCTCCATTATAGCAGAGCTTGCCTAAAGTCCCGGCTAGA 597  
DB 541 CGGAGAGCTTCGAGTCAAGCTCCATTATAGCAGAGCTTGCCTAAAGTCCCGGCTAGA 600  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGATTCGCCCAACCTTCGGGGCAA 657  
DB 601 TTCGAGAGATCTTACTCAGAGCTGCAATATACCCAGATTCGCCCAACCTTCGGGGCAA 660  
QY 658 CAATTCATTCACCTTGGGAGGATTTGAAATTCGAACAGGCTCTCGGTGTTTGTCAAT 717  
DB 661 CAATTCATTCACCTTGGGAGGATTTGAAATTCGAACAGGCTCTCGGTGTTTGTCAAT 720  
QY 718 GTGACTGATCCAAAGCCAAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777  
DB 721 GTGACTGATCCAAAGCCAAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 778 CTCTGA 783  
DB 781 CTCTGA 786

## RESULT 2

PCT-US93-10034-3

Sequence 3, Application PCT/US9310034  
GENERAL INFORMATION:  
APPLICANT: Sprigins, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric

TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10034  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..783  
PCT-US93-10034-3

Query Match 92.8%; Score 726.8; DB 5; Length 786;  
Best Local Similarity 96.2%; Pred. No. 9.9e-198;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGGCCACTGGAGTGGCCCATCAGC 60  
DB 1 ATGATCGAAACATACACCAAACTCTCCCGGATCTCGGGCCACTGGAGTGGCCCATCAGC 60  
QY 61 ATGAAATTTTATGTTTATTTACTTCTTTCTTTATCACCAGATGATGGGTGAGCA 120  
DB 61 ATGAAATTTTATGTTTATTTACTTCTTTCTTTATCACCAGATGATGGGTGAGCA 120  
QY 121 CTTTTCCTGCTGATCTTCATAGAACTGGATAAGTTCGAAGAGCAAGTAAACCTTCAT 180  
DB 121 CTTTTCCTGCTGATCTTCATAGAACTGGATAAGTTCGAAGAGCAAGTAAACCTTCAT 180  
QY 181 GAAGATTTTCTATTATATAAAAGCTTAAGAGATGCAACAAAGGAGAGATCTTTATCC 240  
DB 181 GAAGATTTTCTATTATGAAAGCATACAGAGATGCAACAGAGAGAGATCTTTATCC 240  
QY 241 TTCTGAATCTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
DB 241 TTCTGAATCTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAAGTTA 300  
QY 301 AACAAAGAGA---GAAAGAAAGAAACAGCTTTGAAATGCAAAAGTGCATGAGATCCT 357  
DB 301 AACAAAG 360  
QY 358 CAAATTCGGGCACATGTCATAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 10, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 22, Appl

28 580.6 74.2 1425 2 US-08-484-624A-15  
29 580.6 74.2 1425 2 US-08-477-733B-15  
30 580.6 74.2 1425 3 US-09-088-913A-15  
31 580.6 74.2 1425 4 US-08-769-819-15  
32 580.6 74.2 1425 4 US-08-770-974-15  
33 579.6 74.0 929 1 US-08-446-922-10  
34 579.6 74.0 929 2 US-08-249-189-20  
35 579.6 74.0 929 2 US-08-484-624A-20  
36 579.6 74.0 929 3 US-08-477-733B-20  
37 579.6 74.0 929 4 US-08-769-819-20  
38 579.6 74.0 929 4 US-08-770-974-20  
39 579.6 74.0 929 4 US-08-249-189-22  
40 500.2 63.9 878 2 US-08-484-624A-22  
41 500.2 63.9 878 2 US-08-477-733B-22  
42 500.2 63.9 878 3 US-09-088-913A-22  
43 500.2 63.9 878 4 US-08-769-819-22  
44 500.2 63.9 878 4 US-08-770-974-22  
45 500.2 63.9 878 4 US-08-770-974-22

28 580.6 74.2 1425 2 US-08-484-624A-15  
29 580.6 74.2 1425 2 US-08-477-733B-15  
30 580.6 74.2 1425 3 US-09-088-913A-15  
31 580.6 74.2 1425 4 US-08-769-819-15  
32 580.6 74.2 1425 4 US-08-770-974-15  
33 579.6 74.0 929 1 US-08-446-922-10  
34 579.6 74.0 929 2 US-08-249-189-20  
35 579.6 74.0 929 2 US-08-484-624A-20  
36 579.6 74.0 929 3 US-08-477-733B-20  
37 579.6 74.0 929 4 US-08-769-819-20  
38 579.6 74.0 929 4 US-08-770-974-20  
39 579.6 74.0 929 4 US-08-249-189-22  
40 500.2 63.9 878 2 US-08-484-624A-22  
41 500.2 63.9 878 2 US-08-477-733B-22  
42 500.2 63.9 878 3 US-09-088-913A-22  
43 500.2 63.9 878 4 US-08-769-819-22  
44 500.2 63.9 878 4 US-08-770-974-22  
45 500.2 63.9 878 4 US-08-770-974-22

ALIGNMENTS

RESULT 1  
US-08-446-922-3  
Sequence 3, Application US/08446922  
Patent No. 5716805  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
APPLICANT: Srinivasan, Subhashini  
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple Operating System 7.1  
SOFTWARE: Microsoft Word for Apple, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,922  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/107,353  
FILING DATE: 08-13-93  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 1003-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 786 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: CD40-L  
FEATURE:

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: May 30, 2002, 02:51:53 : Search time 139.75 Seconds  
(without alignments)  
1376.251 Million cell updates/sec

Title: US-08-982-272-20  
Perfect score: 783  
Sequence: 1 ATGATCGAACAATACAAACCA.....TTGGCTTACTCAAACTCTGCA 783

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 393533 seqs, 122816752 residues  
Total number of hits satisfying chosen parameters: 767066

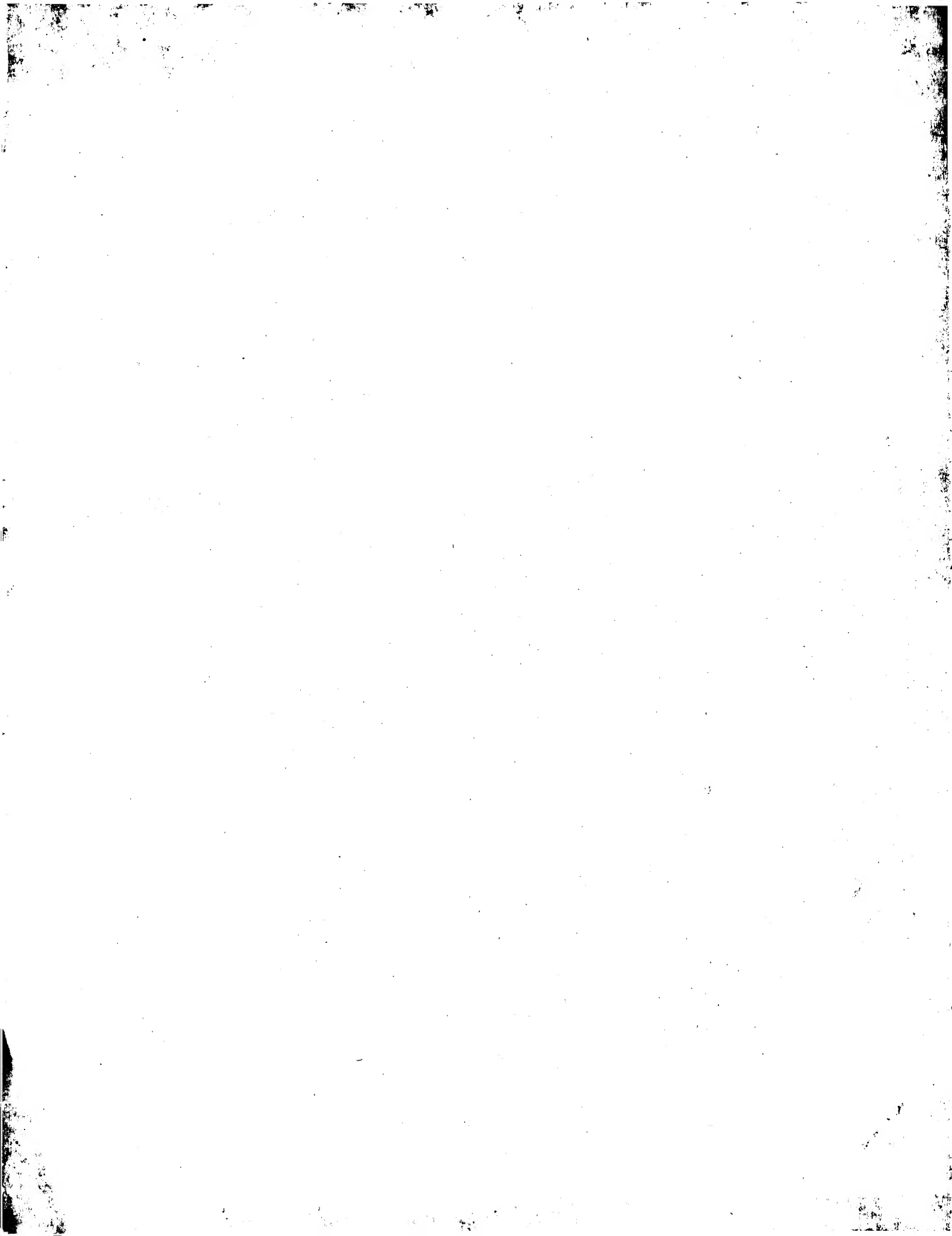
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	726.8	92.8	786	US-08-446-922-3	Sequence 3, Appl
2	726.8	92.8	786	PCT-US93-10034-3	Sequence 3, Appl
3	726.8	92.8	840	US-07-940-605A-1	Sequence 1, Appl
4	726.8	92.8	840	US-08-184-422-7	Sequence 7, Appl
5	726.8	92.8	840	US-08-360-923A-1	Sequence 1, Appl
6	726.8	92.8	840	US-08-431-055-3	Sequence 3, Appl
7	726.8	92.8	840	US-08-690-096-1	Sequence 1, Appl
8	726.8	92.8	840	US-08-249-189-11	Sequence 11, Appl
9	726.8	92.8	840	US-08-484-624A-11	Sequence 11, Appl
10	726.8	92.8	840	US-08-477-733B-11	Sequence 11, Appl
11	726.8	92.8	840	US-08-763-995-1	Sequence 11, Appl
12	726.8	92.8	840	US-09-088-913A-11	Sequence 7, Appl
13	726.8	92.8	840	US-08-589-771B-7	Sequence 11, Appl
14	726.8	92.8	840	US-08-769-819-11	Sequence 11, Appl
15	726.8	92.8	840	US-08-770-974-11	Sequence 3, Appl
16	726.8	92.8	840	US-08-858-197-3	Sequence 5, Appl
17	618.2	79.0	783	US-08-446-922-5	Sequence 1, Appl
18	618.2	79.0	783	US-08-249-189-1	Sequence 1, Appl
19	618.2	79.0	783	US-08-484-624A-1	Sequence 1, Appl
20	618.2	79.0	783	US-08-477-733B-1	Sequence 1, Appl
21	618.2	79.0	783	US-09-088-913A-1	Sequence 1, Appl
22	618.2	79.0	783	US-08-769-819-1	Sequence 1, Appl
23	618.2	79.0	783	US-08-770-974-1	Sequence 5, Appl
24	618.2	79.0	783	PCT-US93-10034-5	Sequence 1, Appl
25	616.6	78.7	818	US-08-431-055-1	Sequence 1, Appl
26	616.6	78.7	818	US-08-858-197-1	Sequence 1, Appl
27	580.6	74.2	1425	US-08-249-189-15	Sequence 15, Appl



Thu May 30 05:45:58 2002

; SEQ ID NO 10646  
; LENGTH: 57649  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-105-299-10646

Query Match 4.7%; Score 36.6; DB 6; Length 57649;  
Best Local Similarity 54.0%; Pred. No. 32;  
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 161 AAGAGGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACA 220  
Db 48584 aaggacaataaaccttttataaaattttattcttaaaaaaaatcacactgtacaa 48643  
QY 221 AAGGAGAGGATCTTTATCCCTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280  
Db 48644 attagatagaacattatcaatgcagatttataaaatgggaacagaagactaaagc 48703  
QY 281 TTGTCAAGGATATAACGTT 299  
Db 48704 tagcgaaggaacgtacatt 48722

RESULT 15  
US-10-105-299-14274  
; Sequence 14274, Application US/10105299  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, et. al  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS950  
; CURRENT APPLICATION NUMBER: US/10/105,299  
; CURRENT FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 15197  
; Prior Application removed - See File Wrapper or Palm  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14274  
; LENGTH: 57649  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-105-299-14274

Query Match 4.7%; Score 36.6; DB 6; Length 57649;  
Best Local Similarity 54.0%; Pred. No. 32;  
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 161 AAGAGGAGTAAACCTTCATGAAGATTTTGTATTCATAAAAGCTAAAGAGATGCAACA 220  
Db 48584 aaggacaataaaccttttataaaattttattcttaaaaaaaatcacactgtacaa 48643  
QY 221 AAGGAGAGGATCTTTATCCCTGCTGAACCTGTGAGGAGATGAGAAGGCAATTTGAAGACC 280  
Db 48644 attagatagaacattatcaatgcagatttataaaatgggaacagaagactaaagc 48703  
QY 281 TTGTCAAGGATATAACGTT 299  
Db 48704 tagcgaaggaacgtacatt 48722

Search completed: May 30, 2002, 05:45:48  
Job time: 17122 sec



PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 179264  
LENGTH: 1223197  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1223197)  
OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-179264

Query Match  
Best Local Similarity 5.0%; Score 39.2; DB 6; Length 1223197;  
Matches 101; Conservative 3; Mismatches 106; Indels 0; Gaps 0;

QY 92 TTCTTATACCCAGATGATTGGTCAGCAGCTTTTTCCTGCTGTATCTTCATAGAGATTGG 151  
Db 759351 TCGTGTAAGCAGATTAATGGTCTCAGTATTACTATCAAGTATCGTAGAACCTGAG 759292

QY 152 ATAAGTCGAAGGAGTAACCTTCATGAGATTTTCTATCATATAAAGCTAAAGA 211  
Db 759291 TTAGAATCTATTCTCGAAGAAGACTTTCTGAGTGATTTTGGGTATGTATTTCTGATCAC 759232

QY 212 GATGCAACAAAGGAGGAGTCTTTATCTTCTGCTGAACCTGTGAGGAGATGAGAAGGCAAT 271  
Db 759231 TCCGTTGCAATGSGAGTACGTTTATCCCTTCYTRATAGGAGGCAATATTTGGGTCA 759172

QY 272 TTGAAGACCTTGTCAAGGATATACCTTAA 301  
Db 759171 TTCAGGAATAAGTTATAGAAAAAAGCTCA 759142

RESULT 9  
US-10-027-632-45446  
; Sequence 45446, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45446  
; LENGTH: 544  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-45446

Query Match  
Best Local Similarity 4.8%; Score 37.2; DB 6; Length 544;  
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 242 TGCTGAACCTGTGAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACCTTAA 301  
Db 263 tgcttatttaacagatgaaagaaagaaatatttataatgaagaaagggattagataccaat 322

QY 302 ACAAGAAGAGAAAAAAGAACAGCTTTTCAATGCAAAAAGGTGATCATGATCTCTCAA 361  
Db 323 attaaagttacttattacattcttttatttatttaagagaaagggattagataccaat 382

QY 362 TTGCGGCACATGTCATAAGTGTAGGCCAGCAGTAA 395  
Db 383 tatggggcacaaaaataaagtttgctttcactta 416

RESULT 10  
US-10-106-698-1404  
; Sequence 1404, Application US/10106698  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 1404  
; LENGTH: 712  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (705)...(705)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-106-698-1404

Query Match  
Best Local Similarity 4.8%; Score 37.2; DB 6; Length 712;  
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 189 TGTATTCTATAAAAAAGCTAAAGAGATGCAACAAAGAGAGAGATCTTTATCTCTGCTGAA 248  
Db 470 tgctcagaataatgggaatgtgtgttaacacagcatttggctgttaggcagtgctgc 529

QY 249 CTGTCAGGAGATGAGAAGCAATTTGAAGACCTTGTCAAGGATATAACCTTAAACAAAGA 308  
Db 530 ctgtaataatagattgaaatgtattttatcagctgtatataataatttgaggaaagaaaaa 589

QY 309 AGAGAAAAAAGAACAGCTTTTGAATGCAAAAA 342  
Db 590 aaaaaaaagaaaaaagaaaaaagaaaaa 623

RESULT 11  
US-10-027-632-217675/c  
; Sequence 217675, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 179264  
LENGTH: 1223197  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1223197)  
OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-179264

Query Match  
Best Local Similarity 48.1%; Score 39.2; DB 6; Length 1223197;  
Matches 101; Conservative 3; Mismatches 106; Indels 0; Gaps 0;

QY 92 TTCTTATACCCAGATGATTGGTCAGCAGCTTTTTCCTGCTGTATCTTCATAGAGATTGG 151  
Db 759351 TCGTGTAAGCAGATTAATGGTCTCAGTATTACTATCAAGTATCGTAGAACCTGAG 759292

QY 152 ATAAGTCGAAGGAGTAACCTTCATGAGATTTTCTATCATATAAAGCTAAAGA 211  
Db 759291 TTAGAATCTATTCTCGAAGAAGACTTTCTGAGTGATTTTGGGTATGTATTTCTGATCAC 759232

QY 212 GATGCAACAAAGGAGGAGTCTTTATCTTCTGCTGAACCTGTGAGGAGATGAGAAGGCAAT 271  
Db 759231 TCCGTTGCAATGSGAGTACGTTTATCCCTTCYTRATAGGAGGCAATATTTGGGTCA 759172

QY 272 TTGAAGACCTTGTCAAGGATATACCTTAA 301  
Db 759171 TTCAGGAATAAGTTATAGAAAAAAGCTCA 759142

RESULT 9  
US-10-027-632-45446  
; Sequence 45446, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45446  
; LENGTH: 544  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-45446

Query Match  
Best Local Similarity 5.0%; Score 39.2; DB 6; Length 1223197;  
Matches 101; Conservative 3; Mismatches 106; Indels 0; Gaps 0;

QY 92 TTCTTATACCCAGATGATTGGTCAGCAGCTTTTTCCTGCTGTATCTTCATAGAGATTGG 151  
Db 759351 TCGTGTAAGCAGATTAATGGTCTCAGTATTACTATCAAGTATCGTAGAACCTGAG 759292

QY 152 ATAAGTCGAAGGAGTAACCTTCATGAGATTTTCTATCATATAAAGCTAAAGA 211  
Db 759291 TTAGAATCTATTCTCGAAGAAGACTTTCTGAGTGATTTTGGGTATGTATTTCTGATCAC 759232

QY 212 GATGCAACAAAGGAGGAGTCTTTATCTTCTGCTGAACCTGTGAGGAGATGAGAAGGCAAT 271  
Db 759231 TCCGTTGCAATGSGAGTACGTTTATCCCTTCYTRATAGGAGGCAATATTTGGGTCA 759172

QY 272 TTGAAGACCTTGTCAAGGATATACCTTAA 301  
Db 759171 TTCAGGAATAAGTTATAGAAAAAAGCTCA 759142

RESULT 9  
US-10-027-632-45446  
; Sequence 45446, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45446  
; LENGTH: 544  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-45446







Db 400 caaattgaggccatgtctataagttaggcccagcagtaaaacaacatctgtgttacagtgg 459  
QY 418 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAG 477  
Db 460 gctgaaaaggatgatacaccatgagcaacaacttggtaacccttggaatgggaacag 519  
QY 478 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCTTAAAGTCCCAAGTCCCTTCTGTTCCCAAT 537  
Db 520 ctgacgcttaaaagacaaggactcattatatactatgcccgaagtccacctctgttcccaat 579  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 597  
Db 580 cgggaagcttcgagtcagctccattatagccagcctctgcttaagtcctcccggtaga 639  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTGGCGGGCAA 657  
Db 640 ttcgagagaatctactcagagctcaaataccacagttccgcaaaccttgcgggcaa 699  
QY 658 CAATCCATTCACTTGGGAGGAGTATTGAATTGCAACCAAGGTGCTTCGGTGTTCGTCAAT 717  
Db 700 caatccattcacttgaggagtagtattgaattgcaaccaggtgcttcggtgtttgtcaat 759  
QY 718 GTGACTGATCCAAAGCAAGTGAAGCTGAGCTGGCTTACCTTGGCTTACTTCAAA 777  
Db 760 gtgactgatccaagccaagtgagcattgagcctgagctggttcacgtctcttggcttactcaaa 819  
QY 778 CTCTGA 783  
Db 820 ctctga 825

## RESULT 2

US-09-442-384B-457  
; Sequence 457, Application US/09442384B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashiev, Matvey  
; TITLE OF INVENTION: Hematology/Immunology Array  
; FILE REFERENCE: CLON-006CIP15  
; CURRENT APPLICATION NUMBER: US/09/442,384B  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 830  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-442-384B-457

Query Match 92.8%; Score 726.8; DB 5; Length 1816;  
Best Local Similarity 96.2%; Pred. No. 2.2e-169;  
Matches 756; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGATCGAAACATACAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60  
Db 40 atgataaacaatacaacaaactctcccagatctgcccagctgagctgcccacagc 99  
QY 61 ATGAAAAATTTTATCTATTACTTACTTCTTATCACCACATGATGGGTGAGCA 120  
Db 100 atgaaaaattttatgatacttacttactgttttcttataccacagatgaggttcagca 159  
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGATAAGTTCGAAGAGGAAGTAACCTTCAT 180  
Db 160 ctttttgcgtgatacttcataagaagttgacaagatagaagatgaagaatcttcat 219  
QY 181 GAAGATTTTGTATTCATAAAAAGCTAAGAGATGCACAAAGGAGAGAGATCTTTATCC 240  
Db 220 gaagattttgtattcatgaaacagatagagatgcaacagaggagaaatccattacc 279  
QY 241 TTGCTGAACCTGTGAGGAGATGAGAGGCAATTTGAAGACCTTGTCAAGATATAACGTTA 300

Db 280 ttactgaactgtgagagattataaagccagtttgaaggcttgaaggataataatgtta 339  
QY 301 AACAAGAAGA---GAAAAAGAAACAGCTTTGAAATGCAAAAGGTGATCAGAAATCCT 357  
Db 340 aacaagaaggagagcagaagaagaacagcttgaagaatgcaaaagggtgatacagaatcct 399  
QY 358 CAATTTGGGCACTGTCTATAAGTGAAGCCAGCAGTAAACAACATCTGTGTGTACAGTGG 417  
Db 400 caaattgcggcacatgtcataagttaggcagcagtaaaacaacatctgtgttacagtgg 459  
QY 418 GCTGAAAAGGATACACCATGAGCAACAACTTGGTAACCTTGGAAAATGGGAAACAG 477  
Db 460 gctgaaaaggatgatacaccatgagcaacaacttggtaacccttggaatgggaacag 519  
QY 478 CTGACCGTTAAAGCAAGGACTCTATTATATCTATGCTTAAAGTCCCAAGTCCCTTCTGTTCCCAAT 537  
Db 520 ctgacgcttaaaagacaaggactcattatatactatgcccgaagtccacctctgttcccaat 579  
QY 538 CGGGAAGCTTCGAGTCAAGCTCCATTTATAGCCAGCCTCTGCTTAAAGTCCCGGTAGA 597  
Db 580 cgggaagcttcgagtcagctccattatagccagcctctgcttaagtcctcccggtaga 639  
QY 598 TTCGAGAGATCTTACTCAGAGCTGCAATACCCAGTTCGCCCAACCTTGGCGGGCAA 657  
Db 640 ttcgagagaatctactcagagctcaaataccacagttccgcaaaccttgcgggcaa 699  
QY 658 CAATCCATTCACTTGGGAGGAGTATTGAATTGCAACCAAGGTGCTTCGGTGTTCGTCAAT 717  
Db 700 caatccattcacttgaggagtagtattgaattgcaaccaggtgcttcggtgtttgtcaat 759  
QY 718 GTGACTGATCCAAAGCAAGTGAAGCTGAGCTGGCTTACCTTGGCTTACTTCAAA 777  
Db 760 gtgactgatccaagccaagtgagcattgagcctgagctggttcacgtctcttggcttactcaaa 819  
QY 778 CTCTGA 783  
Db 820 ctctga 825

## RESULT 3

US-09-053-375B-821  
; Sequence 821, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 821  
; LENGTH: 1250  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-053-375B-821

Query Match 79.0%; Score 618.2; DB 5; Length 1250;  
Best Local Similarity 86.8%; Pred. No. 1e-142;  
Matches 680; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 1 ATGATCGAAACATACAACTTCTCCCGATCTGGCGGCACCTGGACTGCCCATCAGC 60  
Db 13 atgataaacaatacaacaaactctcccagatctgcccagctgagcttccacagcagc 72  
QY 61 ATGAAAAATTTTATCTATTACTTACTTCTTATCACCACATGATGGGTGAGCA 120  
Db 73 atgaaaattttatgatacttacttactgttttcttataccacaaatgattggtctg 132  
QY 121 CTTTGTGCTGTATCTTCATAGAAGATTGGATAAGTTCGAAGAGGAAGTAACCTTCAT 180

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2002, 05:40:08 ; Search time 627.19 Seconds  
(without alignments)  
1310.273 Million cell updates/sec

Title: US-08-982-272-20  
Perfect score: 783  
Sequence: 1 ATGATCGAATACATAACCA.....TTGCTTACTCAAACTCTGA 783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 850503 seqs, 524770293 residues

Total number of hits satisfying chosen parameters: 1701006

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	726.8	92.8	1816	5	US-09-053-375B-226
2	726.8	92.8	1816	5	US-09-442-384B-457
3	618.2	79.0	1250	5	US-09-053-375B-821
4	371	47.4	508	5	US-09-911-904-131
5	155.8	19.9	2395	5	US-09-875-453A-9
6	41.6	5.3	2865	6	US-10-027-632-111808
7	39.8	5.1	637	6	US-10-027-632-233265
8	39.2	5.0	1223197	6	US-10-027-632-179264
9	37.2	4.8	544	6	US-10-027-632-45446
10	37.2	4.8	717	6	US-10-106-698-1404
11	36.8	4.7	637	6	US-10-027-632-217675
12	36.8	4.7	637	6	US-10-027-632-217676
13	36.6	4.7	57649	6	US-10-105-299-9151
14	36.6	4.7	57649	6	US-10-105-299-10646
15	36.6	4.7	57649	6	US-10-105-299-14274
16	36.4	4.6	2580	6	US-10-027-632-258659
17	36.2	4.6	2430	6	US-10-105-694-1
18	36.2	4.6	2430	6	US-10-105-695-1
19	36.2	4.6	2430	6	US-10-106-014-1
20	36	4.6	559	6	US-10-027-632-78162
21	36	4.6	559	6	US-10-027-632-78163
22	36	4.6	573	6	US-10-027-632-263768
23	36	4.6	2217	1	PCT-US02-09944-196
24	35.6	4.5	501	6	US-10-027-632-56905
25	35.6	4.5	501	6	US-10-027-632-297776
26	35.6	4.5	626	6	US-10-027-632-239684

27	35.6	4.5	787	6	US-10-027-632-4057	Sequence 4057, Ap
28	35.6	4.5	1640	6	US-10-106-698-499	Sequence 499, App
c 29	35.6	4.5	1665	5	US-09-919-002-8655	Sequence 8655, Ap
30	35.4	4.5	780	5	US-09-540-209B-1518	Sequence 1518, Ap
31	35.4	4.5	783	5	US-09-540-209B-1516	Sequence 1516, Ap
32	35.4	4.5	837	5	US-09-540-209B-1520	Sequence 1520, Ap
c 33	35.2	4.5	66566	5	US-09-830-706B-37	Sequence 37, Appl
34	35	4.5	601	6	US-10-027-632-85186	Sequence 85186, A
35	35	4.5	601	6	US-10-027-632-85187	Sequence 85187, A
36	35	4.5	620	6	US-10-027-632-46525	Sequence 46525, A
37	35	4.5	620	6	US-10-027-632-46526	Sequence 46526, A
38	35	4.5	1216	6	US-10-027-632-210428	Sequence 210428, A
c 39	34.8	4.4	26496	6	US-10-105-299-12937	Sequence 12937, A
40	34.6	4.4	3321	5	US-09-919-002-413	Sequence 413, App
c 41	34.4	4.4	584	6	US-10-027-632-200394	Sequence 200394, A
42	34.4	4.4	608	6	US-10-027-632-233425	Sequence 233425, A
43	34.4	4.4	608	6	US-10-027-632-233426	Sequence 233426, A
c 44	34.4	4.4	919	6	US-10-137-321-444	Sequence 444, App
c 45	34.4	4.4	1169	6	US-10-027-632-200393	Sequence 200393, A

## ALIGNMENTS

RESULT 1  
US-09-053-375B-226  
; Sequence 226, Application US/09053375B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Bibilashvili, Robert  
; TITLE OF INVENTION: Nucleic Acid Arrays  
; FILE REFERENCE: CLON-006  
; CURRENT APPLICATION NUMBER: US/09/053,375B  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 1543  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226  
; LENGTH: 1816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-053-375B-226

Query Match 92.8%; Score 726.8; DB 5; Length 1816;  
Best Local Similarity 96.2%; Pred. No. 2.2e-169;  
Matches 736; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY	1	ATGATGAAATACATACACCAAACTTCTCCCGATCTGCGGCCACTGGAGTCCCATCAGC	60
DB	40	atgatgaaacatacaacaaacttctcccgatctgcgccactgagctgcccatacgc	99
QY	61	ATGAAATTTTATGATTTACTTACTGTTTCTTATCACCAGATGATGGTCAGCA	120
DB	100	atgaaattttatgtatttacttactgttttcttaccacccagatgattgggtcagca	159
QY	121	CTTTTCTGCTGATCTTCTATAGAGATTGGATAAGTTCGACGAGGAAGTAACCTTCAT	180
DB	160	cttttctgtatcttctatagaaggttgacaagatagaatgaagaatcttcat	219
QY	181	GAAGATTTCTATCATAAAAGCTAAAGAGATGCAACAAAGGAGAGATCTTTATCC	240
DB	220	gaagattttgtattcatgaacagatagacagatgcacacagagagaaatcttctatcc	279
QY	241	TTGCTGAACCTGAGGAGATGAGAAAGCAATTTTGAACACCTTGTCAAGGATATAACGTTA	300
DB	280	ttactgaactgtgagagattaaaagccagtttgaaggctttgtgaaggataataatgta	339
QY	301	AACAAAGAGA - - -GAAAAAGAAAACAGCTTTGAAATGCAAAAAGTGATCAGAACTCT	357
DB	340	aacaaaggagagacgaagaaacacagctttgaaatgcaaaaagtgatcagaaatcct	399
QY	358	CAAAATCCGCACATGTCATAAAGTGAGCGCCAGTAGTAAACCAACATCTGTGTACAGTGG	417